

CRFA

Access DB# 86298

SEARCH REQUEST FORM

Scientific and Technical Information Center

M.A. WALICKA

CRF 09/218,902
09/218702

Requester's Full Name: 09/273,957 Examiner #: 78201 Date: Feb. 6.03
Art Unit: 1652 Phone Number 305-7270 Serial Number: 09/723,957
Mail Box and Bldg/Room Location: 10 D06 Results Format Preferred (circle): PAPER DISK E-MAIL
10 D01

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Phenol oxidizing enzymes

Inventors (please provide full names): WANG et al.

Earliest Priority Filing Date: 12/22/98

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 1
: 2

Point of Contact:
Thomas G. Larson, Ph.D.
703-308-7309
CM1, Rm. 6 B 01

Thank you in advance.
Please rush.

M. Walicka

ABSSØ4
2/11
N. J. J. 2/12

1-1791(NA)
2-594(AA)
3-3677(CNA)

Point of Contact:
Thomas G. Larson, Ph.D.
703-308-7309
CM1, Rm. 6 B 01

C. Chan
Rush

STAFF USE ONLY

Searcher: Larson
Searcher Phone #: _____
Searcher Location: _____
Date Searcher Picked Up: 2/11
Date Completed: 2/13
Searcher Prep & Review Time: 15
Clerical Prep Time: _____
Online Time: 10

Type of Search

NA Sequence (#) 2
AA Sequence (#) 1
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
Dialog _____
Questel/Orbit _____
Dr. Link _____
Lexis/Nexis _____
Sequence Systems ABSSØ4
WWW/Internet _____
Other (specify) _____

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 17:10:31 ; Search time 4505.67 Seconds

(without alignments) 11568.344 Million cell updates/sec

Title: US-09-218-702-1

Perfect score: 1791
Sequence: 1 gtcataatgcgcgttcacagtc.....atcttgagatcgagagagtaa 1791

Scoring table: IDENTITY-MUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Genem1: *
1: gb_ba: *
2: gb_bt: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pal: *
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31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rpd: *
36: em_htg_mam: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1791	100.0	1791	6	AR211556	AR211556 Sequence
2	1778	99.3	7259	6	AX384798	AX384798 Sequence
3	1474	82.3	3677	6	AR211554	AR211554 Sequence
4	685.8	38.3	2126	8	AM0271104	AJ271104 Acromoniu
5	573.2	32.0	1942	8	MYRBOR	D12579 M. verrucar
6	573.2	32.0	1959	6	E05283	E05283 Biliirubin O
7	503.4	28.1	2905	6	AR211555	AR211555 Sequence
8	502.8	28.1	2063	6	AR211557	AR211557 Sequence
9	460.4	25.7	1958	6	AR122996	AR122996 Sequence
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11	460.4	25.7	1958	6	AX108672	AX108672 Sequence
12	460.4	25.7	1958	6	AX456852	AX456852 Sequence
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15	460.4	25.7	2095	6	AX108674	AX108674 Sequence
16	460.4	25.7	2095	6	AX456854	AX456854 Sequence
17	266.6	14.9	3241	8	MYRBOD	D14081 M. verrucar
18	188.6	10.5	858	6	AR211558	AR211558 Sequence
19	95.4	5.3	9531	1	AY033994	AY033994 Streptomy
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22	86.4	4.8	1422	6	AX195966	AX195966 Sequence
23	86.4	4.8	109519	6	AX195929	AX195929 Sequence
24	79.8	4.5	1533	6	AX121137	AX121137 Sequence
25	79.8	4.5	1614	6	AX063821	AX063821 Sequence
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27	79.8	4.5	349980	6	AX127146	AX127146 Sequence
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29	79.8	4.4	134673	8	AP002860	AP002860 Oryza sat
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42	54.6	3.0	125020	9	AF429315	AF429315 Homo sapi
43	53.4	3.0	12848	1	AE013953	AE013953 Yersinia
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ALIGNMENTS

RESULT 1
AR211556
LOCUS AR211556 1791 bp
DEFINITION Sequence 5 from patent US 6399329.
ACCESSION AR211556
VERSION AR211556.1 GI:21514909
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1791)
AUTHORS Wang, H. and Bodie, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 5 04-JUN-2002;
FEATURES Location/Qualifiers

source	1. 1791	/organism="unknown"
BASE COUNT	380 a 551 c 451 g	409 t
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Query Match	100.0%;	Score 1791; DB 6; Length 1791;
Best Local Similarity	100.0%;	Pred. No. 0;
Matches 1791; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	1	GTCAATATGCTTTTCAGATCATGGCAACATGGCAGCAGAGCTCCGGGCTCCTGTCTGGAGTGC 60
DB	1	GTCAATATGCTTTTCAGATCATGGCAACATGGCAGCAGAGCTCCGGGCTCCTGTCTGGAGTGC 60
OY	61	CTTGGCATCCGATGGACACCGGGCAGACCACCCATTGAGGCTGTGATCCGGAATGAAG 120
DB	61	CTTGGCATCCGATGGACACCGGGCAGACCACCCATTGAGGCTGTGATCCGGAATGAAG 120
OY	121	ACTGAGGCTTTGGCTGACACCTCCTGGCTGTGAGCAGGGGATGAGACACTGGGAGTCACT 180
DB	121	ACTGAGGCTTTGGCTGACACCTCCTGGCTGTGAGCAGGGGATGAGACACTGGGAGTCACT 180
OY	181	CCATACCACTTCTTTACAGAAATGCCCTTCCCAATTTCCACCTGTCAAGCAGCCCAAGATG 240
DB	181	CCATACCACTTCTTTACAGAAATGCCCTTCCCAATTTCCACCTGTGTCAAGCAGCCCAAGATG 240
OY	241	ATCATTTACCAACCCCTGTACCCGGCAGAGACATTTTGGTACTATGAGATCGAGATCAAGCCA 300
DB	241	ATCATTTACCAACCCCTGTACCCGGCAGAGACATTTTGGTACTATGAGATCGAGATCAAGCCA 300
OY	301	TTTTCAGCAAAAGATTATTACCCCACTTGGCCCTCGGCACACTGTGCGGCTACGATGGCATG 360
DB	301	TTTTCAGCAAAAGATTATTACCCCACTTGGCCCTCGGCACACTGTGCGGCTACGATGGCATG 360
OY	361	AGCCCTGGTCTACTTTCAATTTTCCACAGAGACAGAGACTGTAGTTAGTTTCATCAAC 420
DB	361	AGCCCTGGTCTACTTTCAATTTTCCACAGAGACAGAGACTGTAGTTAGTTTCATCAAC 420
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DB	421	AATGGCACCGTGGAGAACTGGTTCATCTGCAGGGCTCCCAATGCGTGGCCCTTTGCGAT 480
OY	481	GGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTACTTTCCCAACTAC 540
DB	481	GGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTACTTTCCCAACTAC 540
OY	541	CAATCCGCGCGCTTCTGTGGTACCATATGACACGCTTTTATAGAAGCTCTGAGAATGCC 600
DB	541	CAATCCGCGCGCTTCTGTGGTACCATATGACACGCTTTTATAGAAGCTCTGAGAATGCC 600
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DB	601	TACTTTGGCAGAGCTGGCGCCTACATTATCAACGACGAGGCTGAGAGATCTCTCGGGTCT 660
OY	661	CCTAGTGGCTATGGCGAGTTGCGATATCCCTGTGATCTTGACGCGCCAAAGTACTATAAGCC 720
DB	661	CCTAGTGGCTATGGCGAGTTGCGATATCCCTGTGATCTTGACGCGCCAAAGTACTATAAGCC 720
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DB	721	GATGTATACCCCTGCTTTCGACCGAGGGGTAGAGACACGAGACCTGTGGGAGATGTCAATCAT 780
OY	781	GTCAACGGCAGACCAATGAGCTTTCTCTTAAGTGCACAGCCCCGGAAGTACGTTCCGATTC 840
DB	781	GTCAACGGCAGCAGCAATGAGCTTTCTCTTAAGTGCACAGCCCCGGAAGTACGTTCCGATTC 840
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DB	841	CTCAACGCTGCGGTCTCTGCTTGGCTCTCTACCTCGTCAAGGACACGACTCTCCCAAC 900
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DB	901	GTCAAAATTTCTTTTCCAAATCATATGCTTGTATGCTGGTCTCTTCAAGCCCCGTTGAG 960

QY	961	ACCTCTAACCTCTACCTTGTCTTGTGCCGAGGCTTACGAGATCATTTATTGACTTACCAAC	1020
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Db	1021	TTTGTGGCGACACTTGTACCTGTGGCAACGTTGTGAGACCAACGATGTGGGCGACGAG	1080
QY	1081	GATGAGTACGCTGCGCACTCTCGAGGTGATGAGCTTGTGTCGTCAGCTGTGGCACTGTTGAG	1140
Db	1081	GATGAGTACGCTGCGCACTCTCGAGGTGATGAGCTTGTGTCGTCAGCTGTGGCACTGTTGAG	1140
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Db	1141	GACAAAGCCAGGTCCTCCCTCACTCTCGTGACGTTCTTCTTCCCTCTCACAGGAAGC	1200
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QY	1321	TGGGAGCTCGAGACTCCTCTGTGAGGCTGAGAGCCACCCGTCACATTCACCTGTTGAC	1380
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Db	1561	ATGGCTGTATTCAAGTCAACGCCCATGTGGAGAGGAAGGATATCTTCAGAGAGACTTTCGAG	1620
QY	1621	GACCCCATGAACCCCAAGTGGGCGGCCCGTCTTCAACAACCGCAAGCACTTCATGCTGGC	1680
Db	1621	GACCCCATGAACCCCAAGTGGGCGGCCCGTCTTCAACAACCGCAAGCACTTCATGCTGGC	1680
QY	1681	GCTGGAACCTTCTCGCGAGTCAATCACTGCCCCAGTGCAGAGAGCTGGCGAGCAGGAG	1740
Db	1681	GCTGGAACCTTCTCGCGAGTCAATCACTGCCCCAGTGCAGAGAGCTGGCGAGCAGGAG	1740
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LOCUS	AX384798	7559 bp	DNA
DEFINITION	Sequence 3 from Patent WO0196543.		linear
ACCESSION	AX384798		
VERSION	AX384798.1	GI:19577933	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	unclassified.		
AUTHORS	1		
TITLE	Hood, E., Howard, J.A., Bailey, M., van Gestel, F.J., Ward, M., Wang, H. and Woodard, S.		
JOURNAL	Method of increasing recovery of heterologous active enzymes produced in plants		
	Patent: WO 0196543-A 3 20-DEC-2001;		

Prodigene, Inc. (US) ; Genencor, Inc. (US)
Location/Qualifiers
1.. 7259
/organism="unidentified"
/db_xref="taxon:32644"
/note="Stachybotrys sp."
BASE COUNT 1928 a 1745 c 1583 g 1997 t 6 others
ORIGIN

Query Match 99.3%: Score 1778; DB 6; Length 7259;
Best Local Similarity 99.9%: Pred. No. 0;
Matches 1790; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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5201 GTCATATATCTGTTCAAGTCATGAGCAACTGGCAGACGCTCCGGGCTCCGTCTGGAGTC 5260
61 CTCGGCATCCGATGAGACACGGCAGCACCCCATTTAGAGCTGTGTATCCGCAAGTGAA 120
5261 CTCGGCATCCGATGAGACACGGCAGCACCCCATTTAGAGCTGTGTATCCGCAAGTGAA 5320
121 ACTGAGGTTTGGCTGACACCTCCCTTCTGTCAGCAGGCGGATACGACTGGAGTCACT 180
5321 ACTGAGGTTTGGCTGACACCTCCCTTCTGTCAGCAGGCGGATACGACTGGAGTCACT 5380
181 CCATACAACTGCTTTACAGAAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGAT 240
5381 CCATACAACTGCTTTACAGAAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGAT 5440
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5441 ATCATATTACCAACCCGTCACCGGCAAGAGCAATTTGGTACTATGATCGAGATCAAGCA 5500
301 TTTCAGCAAGAGATTTACCCCACTTGGCCCTGCCACTCTCTGGCTTACATGGCATG 360
5501 TTTCAGCAAGAGATTTACCCCACTTGGCCCTGCCACTCTCTGGCTTACATGGCATG 5560
361 ACCCCGTCCTACTTTCAATGTTCCAGAGAAAGAGACTGATTTAGGTTCAATCAAC 420
5561 ACCCCGTCCTACTTTCAATGTTCCAGAGAAAGAGACTGATTTAGGTTCAATCAAC 5620
421 AATGCCACCGTGAGAACTCGGTGTCATGCAAGGCTCCCATCGGCTGCCCTTTGCAT 480
5621 AATGCCACCGTGAGAACTCGGTGTCATGCAAGGCTCCCATCGGCTGCCCTTTGCAT 5680
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5681 GGTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAAGATTTACTACTTTCCCAACTAC 5740
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959 AGACCTTAACTCTTACCTTCTGTTGGCGAGGCTTACAGATCATTTATGACTTCACCA 1018
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6221 ACTTTCCTGGCCAGACTCTTTGACCTCGCAGACTTGTCTGAGACCAAGATGTGGGAGG 6280
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1499 AACCTGAGCTGAGGCTTACATGTGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1558
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1559 TGTATGCTGTATTCACAGCTCACCGCCCATGTGAGAGAGAGATATCTTCAAGAGACTTGG 1618
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6881 GCGCTGGAACCTTCTCGCGGAGTCCATCATCTGCGGAGTCAAGAGCTGGCCGAGCAG 6940
1739 AGCGGTACAACCGGCTTCGATGAGATCTCTGAGAGATCTTGTGAATCGAGAGTA 1790
6941 AGCGGTACAACCGGCTTCGATGAGATCTCTGAGAGATCTTGTGAATCGAGAGTA 6992

RESULT 3
AR211554
LOCUS AR211554 3677 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6399329.
ACCESSION AR211554
VERSION AR211554.1 GI:21514906
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3677)
AUTHORS Wang, H. and Bodie, E. A.

TITLE	Phenol oxidizing enzymes																												
JOURNAL	Patent: US 6393329-A 1 04 -JUN-2002;																												
FEATURES	Location/Qualifiers																												
source	1..3677																												
BASE COUNT	822 a	1057 c	849 g	948 t	1 others																								
ORIGIN																													
Query Match	82.3%; Score 1474; DB 6; Length 3677;																												
Best Local Similarity	87.0%; Pred. No.3.1e-311;																												
Matches 1791; Conservative	0;	Mismatches	0;	Indels	267;	Gaps	5;																						
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OY	61	CTG	GC	AT	CCG	CAT	CCG	AT	GGA	CA	CCG	GC	CA	CCG	CC	AT	TG	AG	CGT	GTG	AT	CCG	CA	GA	GA	G	120		
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Db	1158	ACT	GA	G	CT	CTT	CG	C	TG	AC	TCC	CTC	CTT	CG	TG	C	AG	C	AG	G	GA	G	AG	AC	TG	GA	CT	1217	
OY	181	CC	AT	C	A	CT	G	C	T	T	T	A	C	-----									198						
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OY	199	-----	A	G	A	A	T	G	C	C	C	T	G	C	A	T	T	C	A	C	C	T	G	C	A	A	G	239	
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OY	240	-----	G	A	T	C	A	T	T	A	C	C	C	-----									260						
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OY	261	C	G	G	C	A	G	A	C	A	T	T	G	T	A	C	T	A	T	A	G	A	T	C	A	T	T	C	311
Db	1398	C	G	G	C	A	G	A	C	A	T	T	G	T	A	C	T	A	T	A	G	A	T	C	A	T	T	C	1457
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OY	327	G	C	G	C	C	T	G	C	A	T	C	T	G	T	C	A	G	A	T	G	A	T	G	A	T	G	386	
Db	1518	G	C	G	C	C	T	G	C	A	T	C	T	G	T	C	A	G	A	T	G	A	T	G	A	T	G	1577	
OY	387	C	A	G	A	G	A	C	A	G	A	C	T	G	T	A	T	A	G	T	T	A	G	T	T	A	G	446	
Db	1578	C	A	G	A	G	A	C	A	G	A	C	T	G	T	A	T	A	G	T	T	A	G	T	T	A	G	1637	
OY	447	T	C	T	G	A	C	G	G	T	C	C	A	T	G	C	C	C	T	T	G	A	T	G	G	T	A	506	
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OY	567	T	G	A	C	A	G	C	T	T	A	C	A	-----									5						

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QY	748	GAGGACCAAGACCCGTGGGGGAGATGTCATCCATGTCAAGGGACAGCATGGGCTTTCGT	807
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QY	868	CTCCTCTACCTGTGACGACACGCTCTCCACGTCAGAAATTCCTTCCAACTATTTGCC	927
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QY	1054	GCTGAGACCAACGATGTCGGCGACAGAGATGATACGCTCGACCTCTGAGGTGATTTGGC	1113
Db	2358	GCTGAGACCAACGATGTCGGCGACAGAGATGATACGCTCGACCTCTGAGGTGATTTGGC	2417
QY	1114	TTTCGTCGACGCTCTGGCAGCTGTTTGAAGAACAGCCAGTCCCTCCACTTCCGTATAC	1177
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QY	1174	GTTCCCTTCCCTCTCTCAACAGGAAGGCCCGCGACAGCACTTCAAGTTTGAACGACAC	1237
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QY	1294	AAGCCCGAGCTCGGACCGTGTGAAGGTCTGGAGACTCGAAGAACCTCTGGAAGCTGAGAC	1357
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QY	1354	CACCCCGTCACATTCACCTTGTGACTTCAGATCCTCAAGCGAACTGTGGTCTGTGGC	1417
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QY	1714	CGAGTCGAGGAGCTGGCCGAGCAAGGACCGTAAACCGCTTCGATGAGATTCCTGAGAGAT	1777

Db	3018	CGAGTGCAGCAGCTGGCCGACGACGAGCCGTTACAACGCCCTCGATGAGATCCTGGAGAT	3077
Oy	1774	CTTGGATCGAGAGTAA 1791 	
Db	3078	CTTGGATCGAGAGTAA 3095	
RESULT 4			
LOCUS	AMU271104	2126 bp	linear
DEFINITION	Acromonium murorum mRNA for polyphenol oxidase (ppoa gene).		
VERSION	AJ271104		
KEYWORDS	AJ271104.1 GI:6996277		
SOURCE	oxidase; ppoa gene.		
ORGANISM	Acromonium murorum		
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Hypocreaceae; mitosporic Hypocreaceae; Acromonium.		
AUTHORS	1 (bases 1 to 2126)		
TITLE	Gouka, R.J., van der Heiden, M., Swarthoff, T. and Verrips, C.T. Cloning of a phenol oxidase gene from Acromonium murorum and its expression in Aspergillus awamori		
JOURNAL	Appl. Environ. Microbiol. 67 (6), 2610-2616 (2001)		
MEDLINE	2126885		
PUBMED	11375170		
REFERENCE	2 (bases 1 to 2126)		
AUTHORS	Gouka, R.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-JUN-2000) Gouka R.J., Biotechnology, Unilever Research Vlaardingen, Olivier van Noortlaan 120, 3133 AP Vlaardingen, NETHERLANDS		
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OY	1202	CCGCAGCAAGCACTTCAAGTTTGAACGCAGAACGGAGCACTACCTGATTCACGATGTG	1261
Db	1320	CCATGACGACACTCGTTCCGGCTTCCGCCGACCCGCGGACAGTGGAGCATCAACGGTGTCA	1379
OY	1262	GCTTTCGGATGTCANTAGGCGTGTCTCGGCCAAGCCCGAGCTCGGACCGTTGAGGCT	1321
Db	1380	CCTTCTCCGAGCTGAGAAACCGCTCGTGGCCAAAGTCGCCCTTGGACACCGTCAGCTGT	1439
OY	1322	GGGACCTGAGAACCTCTCTGGAGGCTGGAGCCACCCGCTCACATTACCTTTGTGACT	1381
Db	1440	GCCACTTAACGAAACGGCGCAGGGCGCTGGAGCATCTTATTCATTCATCTTTTGTACT	1499
OY	1382	TCAAATATCCTCAAGGAAGTGGTGGCT-----GGCCAGGTCATGCCCT	1426
Db	1500	TCAAATTCCTGTCTTCGACGGGTGCTTACGGGTGTCAACACCCGTGGTGTGAGCCGT	1559
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Db	1560	ACGAGTCTGTGCTGTGAAGGACGTGTCTACTCTGCGCAAGGAGAAAGACGGTGTGTGCG	1619
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Db	1620	AGGCTCACTACCCCTCTTGGCCCGCGTGTACATTTCTACATCCACACCAACCTCATTCACG	1679
OY	1547	AGGATPACGACATGATGGCTGTATTCAACGTACACGCCCATGGAGAGAAAGGATATTCCTC	1606
Db	1680	AGGACAAACGACATGATGGCCGCTTCAACGTACACGCTCTCCCCGACTACGGCTTCAACT	1739
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Db	1740	CGACGCGCCCTCGCTACCCCATGAGGAGCAGATTCGCGGCCAAGCCGTAACGTGAGCAACG	1799
OY	1667	ACTTCATGCTGTGGCGCTGGAANAATTCTTCGCCGAGTTCATCACTGCCCCGAGTGCAGAGC	1726
Db	1800	ACGTGAGGTGGCGCAGAACGCTTTCACACCGACGAGATCGAGCGCAGGTCCAGCTGA	1859
OY	1727	TGGCCGAGCAGGAGCGGTACAAACCCCTCGA	1757
Db	1860	TGGCCAGCTACTGCTCCCTACGACAACCCGGA	1890
RESULT 5			
LOCUS	MYROR		
DEFINITION	M. verrucaria mRNA for bilirubin oxidase, complete cds.		
ACCESSION	D12579		
VERSION	D12579.1 GI:456711		
KEYWORDS	bilirubin oxidase.		
SOURCE	Myrothecium verrucaria (strain:M-1) cDNA to mRNA.		
ORGANISM	Myrothecium verrucaria		
REFERENCE	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.		
AUTHORS	Kojikawa,S., Ando,K., Kajii,H., Inoue,T., Murao,S., Takeuchi,K. and Samejima,T.		
TITLE	Molecular cloning of the gene for bilirubin oxidase from Myrothecium verrucaria and its expression in yeast		
JOURNAL	J. Biol. Chem. 268 (25), 18809-18809 (1993)		
REFERENCE	93366794		
AUTHORS	2 (bases 1 to 1942)		
TITLE	Ando,K.		
JOURNAL	Direct Submission		
COMMENT	Submitted (07-JUL-1992) Keiichi Ando, Amano Pharmaceutical Co., Ltd., Tsukuba Research Laboratories; 22 Miyukiyaoka, Tsukuba, Ibaragi 305, Japan (Tel:0298-56-5026, Fax:0298-56-5012) On Feb 26, 1994 this sequence version replaced gi:436235. Submitted (07-JUL-1992) to DDBJ by: Keiichi Ando Tsukuba Research Laboratories Amano Pharmaceutical Co., Ltd.		

[illegible]

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Db      1777  ACAG 1781
RESULT 6
E05283
LOCUS      Biliirubin oxidase gene.      1959 bp      RNA      linear      PAT 29-SEP-1997
DEFINITION      E05283
ACCESSION      E05283.1 GI:2173473
VERSION      JP 1993199882-A/1.
KEYWORDS      Myrothecium verucaria.
SOURCE      Myrothecium verucaria.
ORGANISM      Myrothecium verucaria
REFERENCE      Ando, K., Koike, S. and Samejima, T.
AUTHORS      1 (bases 1 to 1959)
TITLE      PRODUCTION OF BILIRUBIN OXIDASE
JOURNAL      Patent: JP 1993199882-A 1 10-AUG-1993;
              AMANO PHARMACEUT CO LTD
COMMENT      OS      Myrothecium verucaria
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              PD      10-AUG-1993
              PE      24-JUN-1992, JP 1992034126
              PI      ANDO KEIICHI, KOIKEDA SATOSHI, SAMEJIMA TATSUYA PC
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              FH      key      Location/Qualifiers
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source      location/Qualifiers
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Best Local Similarity 62.1%; Pred. No. 1.2e-114;
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RESULT 7
AR211555
LOCUS AR211555
DEFINITION Sequence 3 from patent US 6399329.
ACCESSION AR211555
VERSION AR211555.1 GI:21514907
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2905)
AUTHORS Wang, H., and Bodle, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 3 04 -JUN-2002;
FEATURES
Source location/Qualifiers
1..2905
BASE COUNT 714 a 792 c 664 g 734 t 1 others
ORIGIN

Query Match 28.1%; Score 503.4; DB 6; Length 2905;
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Oy 581 -----TGAAGACTGCTGAATG 598
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Db 2040 CGCTGAGAGAGCTTACAGAGCAACTGC 2066

RESULT 8
AR211557

LOCUS AR211557 2063 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6399329.
ACCESSION AR211557
VERSION AR211557.1 GI:21514910
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2063)
AUTHORS Wang, H. and Bodle, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 6 04-JUN-2002;
FEATURES
source 1. 2063
BASE COUNT 501 a 604 c 510 g 448 t
ORIGIN
Query Match 28.1%; Score 502.8; DB 6; Length 2063;
Best Local Similarity 60.4%; Pred. No. 2.8e-99;
Matches 1000; Conservative 0; Mismatches 522; Indels 134; Gaps 5;
QY 244 ATTACCAACCCGTGACCGGCAAGGACATTTGTACTATGATGAGATCGAGTCAAGCCATT 303
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QY 484 TGGGCTGAAGATGTACCTTCCCTGGCGAGTACAA----- 518
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QY 519 -----GATTAATCTTCCCACTAC 541
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QY 542 AATCGCCCGCTTCTGTGTACATGACACGCTTC----- 579
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[illegible]

AUTHORS	Mang, H.
TITLE	Phenol oxidizing enzymes
JOURNAL	Patent: US 6168936-A 1 02-JAN-2001;
FEATURES	Location/Qualifiers
source	1..1958
BASE COUNT	/organism="unknown"
ORIGIN	394 a 593 c 490 g 481 t
Query Match	25.7%; Score 460.4; DB 6; Length 1958;
Best Local Similarity	59.3%; Pred. No. 5e-90;
Matches 996:	Conservative 0; Mismatches 521; Indels 163; Gaps
QY	241 ATCATTACCAACCCCTGTCCCGGCAAGACATTTGCTACTATGAGATGCAGATCAAGCA 300
DB	257 ACCGTCGCCCAACCCCAACACTGAGAGGCACTCTGTACTAGAGATGAGATTAGGCC 316
QY	301 TTTCAGCAAGAAGATTACCCCACTGGCCCTGGCCACTGCTGGCGGCAATGGCATG 360
DB	317 TTCTCCCAACAGATCTACCCCTGATCTGGAGCCGGCCACATGTTGATGATGATG 376
QY	361 AGCCCTGTCTACTTTCATATGTTCCCAAGAGACAGAGACTGTAGTTAGTTTCATCA 420
DB	377 TCCCAAGACCTTACCATCTGCTCTCTGGACACTGAGAGTGTGTCCGTTGCAAC 436
QY	421 A-----ATGCCACCGTGGAGAACTCGTTCATCTGCAGAGGCTCCCATCGGCTCCT 474
DB	437 ACCGAGAAACACCTCTCCCAACAGCGCTCCACTTGCACGGCTCTTCTCTGAGCTCC 496
QY	475 TTTCAGTGTGGGCTGGAAGATGTGACCTTCCCTGGGAGATACAGAGATTACTTTC 534
DB	497 TTTCAGTGTGGGCTGAGAGACACTACCCAGCGCTGGGAGTACAGAGATTACTATCCC 556
QY	535 AACTACCAATCCGCCCGCTCTGTGTGTACATGACACGACGTTTCATGAAAGCTGTG 594
DB	557 AACAGGACAGGCTGCCCGCATGCTTGTGTACCTGACATGACATGCCATGCTACATCC 616
QY	595 AATGCTACTTGTGTACAGGCTGGCCCTCATTTTCAACGAGAGAGGCTTAGATGCTTC 654
DB	617 AACGCTCAATGTGGTACGCTGTGTGTACATGATCCAGAGCCGGCTGAGATGCCCTG 676
QY	655 GGTCTTCCTAGTGGATATGAGGATGTCATATCCCTGATCCTGCAGGCCAAGTACT 714
DB	677 AACCTCCCAAGGGGCTAGCGGAGTTGATATCCCTGTGCTGACTGCCAAGCATATC 736
QY	715 AACGCCAGTGTACCTGCTGTCGACCGAGGCTGAGGACACAGACCTGTGGAGATGTC 774
DB	737 AACCGAGAGCGGACACTCTCTTCCACCAATGAGAGAGTTCCAGCTTGGGGTGACGT 796
QY	775 ATTCAGTGT----- 782
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DB	917 TCCAGCCCGGCAAGTACCCCTTTCGCTTCTCAAGCTCCGCTTCACGCTCTTTACGTC 976
QY	872 TCTACTGTGTGAGACACACTCTCCCAAGTGTGAGATTCCTTCCAAAGTCAATGGCTCG 931
DB	977 TCTATCTGTCTACCTCTGTGAGATTACAGACAGAGATCTCTTCCAGGTCATGCGCGTG 1036
QY	932 ATGCTGTCTCTTCAAGGCCGCTTTCAGACCTTCAACCTTACCTTACCTTGTGTGCGAGC 991
DB	1037 ACGGTGTGTGCTTGTAGGGCCCTGTGTGACATGACACTGTGTACATCTGTATGCGGAGC 1096
QY	992 GTTACGAGATCATTTATGACTTTCACCAACTTTCGTGGCCAGACTCTTTCAGCTGGCAACG 1051
DB	1097 GCTGGAGAGTTGTATGCACTTCTCACCTTGTGCGGCGGCAATGATATGATCCGCAAC 1156

Accession	Source	Organism	LOCUS	DEFINITION	VERSION	KEYWORDS	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
OY 1169	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1214	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1337	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1394	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1454	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1509	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1521	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1574	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1599	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1634	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1694	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1754	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1814	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1701	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers
OY 1874	GenBank	Stachybotrys chartarum	AX108672	Sequence 1 from Patent WO0121748.	AX108672.1	GI:13923900	1	de Vries, C. H. and Wang, H.	Detergent compositions comprising phenol oxidizing enzymes	WO 0121748-A 1 29-MAR-2001	location/Qualifiers

BASE COUNT	394 a	593 c	490 g	481 t
ORIGIN				

Query Match	25.7%;	Score 460.4;	DB 6;	Length 1958;
Best Local Similarity	59.3%;	Pred. No. 5e-90;		
Matches 996;	Conservative 0;	Mismatches 521;	Indels 163;	Gaps 6;

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D	1277	GAGATGTTCTCTTCCCGAGGCGCGCAACTGTGGAGACCCCGAAACCCCACTGTATGACAGGA	1336
Q	1214	ACTTCAAGTTGAACGACGACGACGACACTGATCAACAGATGTGTGGCTTTGGCCATG	1273
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Db	1457	ACAACTCCACAGCGTTGGACTACCCCTGTTCATTACCTCGTTACCTTCGAGTCCCTTT	1516		
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QY	1581	CGCCATGGAGGAGAAAGGATATCTTCAGAGAGACTTCGAGACCCCATGAAACCCCAAGTG	1640		
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QY	1641	GCGGCCGCTTCTTTCACACCGCAACGACTTCCATGCTGGCGTGGAAACTTCTCCGCCGA	1700		
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Db	1874	TGCCATCACTGACCGCATTTCAAGAAATGGCTTCAACCCCTACGCCCAAGGCTGATGA	1933		
RESULT 12	AX456852	1958 bp	DNA	Linear	PAT 06-JUL-2002
LOCUS	AX456852	1958 bp	DNA	Linear	
DEFINITION	Sequence 1 from Patent WO0220711.				
ACCESSION	AX456852				
VERSION	AX456852.1	GI:21715723			
KEYWORDS					
SOURCE	Stachybotrys chartarum.				
ORGANISM	Stachybotrys chartarum.				
REFERENCE	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.				
AUTHORS	Aehle, M., Convents, D., Doornink, M., van Gastel, F., Rodriguez, A. M.,				
TITLE	Topozada, A., de Vries, C. H., and Wang, H.				
JOURNAL	Detergent compositions comprising phenol oxidizing enzymes				
FEATURES	Patent: WO 02/02711-A 1 14-MAR-2002;				
	UNILEVER PLC (GB); LEVER HINDUSTAN LTD (IN); UNILEVER NV (NL)				
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	/db_xref="taxon:74722"				
BASE COUNT	394 a 593 c 490 g 481 t				
ORIGIN					
Query Match	25.7%; Score 460.4; DB 6; Length 1958;				
Best Local Similarity	59.3%; Pred. No. 5e-90;				
Matches	996; Conservative 0; Mismatches 521; Indels 163; Gaps 6;				
QY	241	ATCATTTACCAACCTGTGACCGGCAAGCACTTTGTACTATGAGATCGAGATCAAGCCA	300		
Db	257	ACCGTCCCAACCCCAACACTGAGAGACATCTGTACTACGAGATGAGATTAAGGCC	316		
QY	301	TTTTCAGCAAGATTTATCCCACTTGGGCCCTGGCACTCTGTCGGCTAGCATGSCATG	360		
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QY	361	AGCCTGGTCTACTTTCATATGTTCCAGAGGAACAGACTGTACTTATAGTTTCATCAAC	420
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QY	475	TTTCGATGGTTGGGCTGGAAGATGTGACCTTCCCTGGCGAGTCAAGAGTACTATTTCC	534
Db	497	TTTGTATGGTTGGGCTGAGAGACACTACCCAGCCCTGGGAGTACAAGGATTACTATCAACC	556
QY	535	AACTACCAATCCGCCCGCTTCTGTGTACCATATGACCAGGCTTTCATGAAAGCTGTGAG	594
Db	557	AACGAGGAGCGCTGCCCGATGCTTTTGGTACCATGACCATCCATGTCCATCAACCGCGAG	616
QY	595	AATGCTCATTTGGTCAAGGCTGGCGCCCTACATTATCAGAGAGCAGGCTAGAGTGTCTC	654
Db	617	AACGCTACATGGGTCAAGGCTGGGTCTACATGATTCAGAGACCCGGCTAGAGATGGCTCG	676
QY	655	GGTCTTCCTAGTGGCTATAGCGAGTTTCGATCCCTCTGATCCTCGACGGCCAAAGTACTAT	714
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QY	715	AAAGCCGATGTGATACCTCGCTTGCGACCGAGGGTGAAGACCAAGGACTGTGGGAGATGTC	774
Db	737	AACGAGAGCGGCACTCTCTTCTCCACCAATGAGAGGTTTCCAGCTTTCGGGGTGACGTT	796
QY	775	ATCCATGT-----	782
Db	797	ATTCAAGTGGTAAGTTGAGCCCATTTGAGATGCTTCAGATCTAGAAATATCATGTATGA	856
QY	783	-----CAAGGACAGCCATGGCCCTTTCCTTAAAG	811
Db	857	AATTGTGATGCTCTAAACGATGCTATCAAGAAACGATGACGCTTGCCCTATGCTCAAG	916
QY	812	TCCAGCCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCCGTGTCTGTGGTCTG	871
Db	917	TGCACCCCGCAAGTACCGGCTCCGCTCTTCAACCGTGGCGTCACTGCTTTTCGCTC	976
QY	872	TCTACTCTGTGAGGACCAAGCTCTCCCAAGCTCAAGATTCCTTCCAAAGTCAATGGCTCTG	931
Db	977	TGTATCTGTCACTCTGAGAGATTCAAGACCAAGACTTCCCTTCCAGTCAATGGCTCTG	1036
QY	932	ATGCTGTCTCTTCAAGCCCGCTTGAGACCTCTAACTCTCACTGCTGTGTTGGAGCAG	991
Db	1037	ACGGTGTCTGCTTGAGGGCCCTTTCACACTGACACTCTGTACACTCTATGCGCCAGAC	1096
QY	992	GTTACGAGATCATTTATGACTTTCACCAACTTTCTGCGCCAGACTTGTGAACGTGCCAAG	1051
Db	1097	GCTGGAGGTTGTTATCGACTTTTCCACCTTCCTGCGGACGTCATCGATATTCGGAAAC	1156
QY	1052	TTTGCTGAACCAAGATGTGGGCGAGAGATGATGACGTGCGCACTCTCGAGGTGATGTC	1111
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QY	1112	GCTTGTGCTGAGCTGTGGCACTGTTGAG---GACAAACAGCCAGTCCCTCCACACTCC	1166
Db	1217	GATTGTGTGTTGATGAAGTCTTGTAGTCGCCCACTTCTGTAGGTGCTTGCCAACTTCC	1276
QY	1169	GTAGCTCTTTCCTC-----TCTCAACAAGGAAGGCCCGCCGACAGAC	1213
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QY	1214	ACTTCAATTTGAACGCAAGCAGGACACTTACTGATCAACGATGTTGGCTTTGCCGATG	1273
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QY	1274	TCAATGACCGTGTCTGGCCAAAGCCGAGTGGGAGACCGGTGAGAGTCTGGAGGCTTCGAGA	1333
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RESULT 14

AX101098 2095 bp DNA linear PAT 10-APR-2001
LOCUS AX101098 Sequence 3 from Patent WO0121809.
DEFINITION AX101098
ACCESSION AX101098.1 GI:13619952
VERSION AX101098.1
KEYWORDS
SOURCE Stachybotrys chartarum.
ORGANISM Stachybotrys chartarum.
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.

REFERENCE 1 (bases 1 to 2095)
AUTHORS Wang, H.
TITLE Stachybotrys phenol oxidizing enzyme
JOURNAL Patent: WO 0121809-A 3 29-MAR-2001.
GENECOR INTERNATIONAL, INC. (US)
FEATURES
source location/Qualifiers
1..2095

BASE COUNT 437 a 618 c 510 g 530 t
ORIGIN
Query Match 25.7%; Score 460.4; DB 6; Length 2095;
Best Local Similarity 59.3%; Pred. No. 5e-90;
Matches 996; Conservative 0; Mismatches 521; Indels 163; Gaps 6;

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QY 535 AACTACCAATCCGCGCGCTTCTGTGTGTACATGACACCAAGCTTTTCATGAAGACTGCTGAG 594
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LOCUS	AX108674	2095 bp	DNA	linear	PAT 30-APR-2001
DEFINITION	Sequence 3 from Patent WO0121748.				
ACCESSION	AX108674				
VERSION	AX108674.1	GI:13923901			
KEYWORDS					
SOURCE	Stachybotrys chartarum.				
ORGANISM	Stachybotrys chartarum. Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.				
REFERENCE	1 (bases 1 to 2095)				
AUTHORS	Convents D.U., Doornink M.U., de Vries C.H. and Wang H.				
TITLE	Defergent compositions comprising phenol oxidizing enzymes				
JOURNAL	Patent: WO 0121748-A 3 29-MAR-2001;				
FEATURES	Location/Qualifiers				
source	1..2095				
BASE COUNT	437 a 618 c 510 g 530 t				
ORIGIN	/organism="Stachybotrys chartarum" /db_xref="taxon:74722"				
Query Match	25.7%; Score 460.4; DB 6; Length 2095;				
Best Local Similarity	59.3%; Pred. No. 5e-90;				
Matches	996; Conservative 0; Mismatches 521; Indels 163; Gaps 6;				
OY	241 ATCATTTACCAACCCCTGTACACCGGCAAGACATTTGGTACTATGAGATGAGATCAAGCCA 300				
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OY	655 GGTCTCTGATGAGTGATGGAGATGGATTCGATATCCCTGATCTCTGACGGCGCAAGACTAT 714				
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OY	715	AACCCGATGGTACCCCTGCTTGACCCAGGAGAGACAGACACTGCGGGAGATATC	774
Db	801	AAGCGAACGGCACTCTTCTCCACCAATGAGAGATTTCCAGCTTCTGGGGTACGTT	860
OY	775	ATCCATGT-----	782
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Db	1818	TGTTTCTGGGTACTATGTGCTACAACTACACCGAGTTTCATTTGACCCCATGAGACCTCTCTG	1877
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Job time : 4537.67 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 17:04:56 : Search time 351.125 Seconds
(without alignments)
11486.872 Million cell updates/sec

Title: US-09-218-702-1

Perfect score: 1791

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1791	100.0	1791	24	AA147584
5	1790	99.7	1791	20	AA225727
6	1786.2	99.7	1791	20	AA225727
7	1474	82.3	3677	20	AA225728
8	1474	82.3	3677	20	AA227602
9	1474	82.3	3677	21	AAA50018

10	1474	82.3	3677	21	AAA51313	Stachybotrys chart
11	1474	82.3	3677	24	AA147582	S chartarum phenol
12	1470	82.1	2067	20	AA225735	Stachybotrys chart
13	1470	82.1	2067	20	AA227609	Stachybotrys pheno
14	685.8	38.3	2110	21	AA261243	DNA encoding a phe
15	573.2	32.0	1959	14	AA047790	Bilirubin oxidase
16	503.4	28.1	2905	21	AAA50020	Bipolaris spicifer
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18	503.4	28.1	2905	24	AA147583	B spicifera phenol
19	502.8	28.1	2063	21	AA450021	Curvularia pallasc
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21	502.8	28.1	2063	21	AA147585	C pallascens pheno
22	460.4	25.7	1958	22	AAE30028	Stachybotrys chart
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24	460.4	25.7	1958	24	ABK53881	Stachybotrys chart
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26	460.4	25.7	2095	22	AAE30029	Stachybotrys chart
27	460.4	25.7	2095	24	ABK50919	DNA encoding pheno
28	460.4	25.7	2095	24	ABK53882	Stachybotrys chart
29	458.8	25.6	1958	22	AAE82585	Stachybotrys chart
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33	86.4	4.8	109519	22	AA080693	Micromonospora DNA
34	79.8	4.5	1533	22	AAH66018	C glutamicum codin
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37	59.4	3.3	3446	23	AB150557	Micromonospora car
38	45.8	2.6	4338	12	AAQ11826	Encodes N-terminal
39	45.8	2.6	4649	10	AAAN9059	Sequence encoding
40	45.8	2.6	5721	11	AAO06613	Adenyl cyclase gen
41	45.8	2.6	6381	10	AAAN91167	Sequence encoding
42	45.8	2.6	6442	24	ABK50870	Botryella pertus
43	44.6	2.5	1470	24	ABK74913	Bacillus lichenifo
44	43.4	2.4	32502	23	AA559542	Propionibacterium
45	43	2.4	426	20	AAV89078	EST clone CB15. H

ALIGNMENTS

RESULT 1	AA227601	standard; DNA; 1791 BP.
ID	AA227601	
AC	AA227601	
XX		
XX		
DT	16-DEC-1999	(first entry)
XX		
DE	Stachybotrys phenol oxidase coding sequence.	
XX		
KW	Phenol oxidase; enzyme; coloured compound; dye transfer prevention;	
KW	fabric washing; stain bleaching; anti-dye transfer; detergent; ss.	
XX		
OS	Stachybotrys chartarum.	
XX		
PN	WO949020-A2.	
XX		
PD	30-SEP-1999.	
XX		
PF	23-MAR-1999;	99WO-US06327.
XX		
PR	24-MAR-1998;	98US-0046969.
PR	22-DEC-1998;	98US-0218702.
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XX		
PA	(GENEV) GENENCOR INT INC.	
XX		
PI	Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;	
XX		
DR	WPI; 1999-591088/50.	
XX		
DR	P-PSDB; AA33992.	
XX		

PT Novel enzyme for modifying coloured compounds used to prevent
PT dye-transfer -

XX Claim 21; Fig 5; 64pp; English.

XX
CC This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
CC of the invention. The invention is used to modify a coloured compound and
CC prevent dye transfer during fabric washing, or for stain bleaching or
CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC and food industries.

XX
SQ Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other:

Query Match 100.0%; Score 1791; DB 20; Length 1791;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCATATGCTGTTCAAGTCATGCGACATGCGACAGCTCCGGGCTCCTGTCTGGAGTC 60
DB 1 GTCATATGCTGTTCAAGTCATGCGACATGCGACAGCTCCGGGCTCCTGTCTGGAGTC 60
QY 61 CTCGGCATCCCGATGGACACCGCGACGCCACCCATTGAGGCTGTTGATCCGCAAGTGAAG 120
DB 61 CTCGGCATCCCGATGGACACCGCGACGCCACCCATTGAGGCTGTTGATCCGCAAGTGAAG 120
QY 121 ACTGAGGCTCTGCTGACTCCCTCCTTGTCTGACAGCAGGCGGATGACGACTGGAGTCACT 180
DB 121 ACTGAGGCTCTGCTGACTCCCTCCTTGTCTGACAGCAGGCGGATGACGACTGGAGTCACT 180
QY 181 CCATACACTTGTCTTACAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATG 240
DB 181 CCATACACTTGTCTTACAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATG 240
QY 241 ATCATATACCAACCTGTGACCGGCAAGAGCATTTGGTACTATGATGATGATCAAGCA 300
DB 241 ATCATATACCAACCTGTGACCGGCAAGAGCATTTGGTACTATGATGATGATCAAGCA 300
QY 301 TTTTCAGCAAAAGATTTTACCACACCTTGGCGCCTGCGCACTCTGCTGGCTACGATGGCATG 360
DB 301 TTTTCAGCAAAAGATTTTACCACACCTTGGCGCCTGCGCACTCTGCTGGCTACGATGGCATG 360
QY 361 ACCCGTGTCTACTTTTCAATGTCCCNAGAGAACAGACACTGTAGTTAGTTCAATCAG 420
DB 361 ACCCGTGTCTACTTTTCAATGTCCCNAGAGAACAGACACTGTAGTTAGTTCAATCAG 420
QY 421 AATGCGACCGGTGAGAACTCGGTCCATCTGCAGGCGTCCCATCGGCTGCCCTTTCGAT 480
DB 421 AATGCGACCGGTGAGAACTCGGTCCATCTGCAGGCGTCCCATCGGCTGCCCTTTCGAT 480
QY 481 GGTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAGAGATTTACTTCCCAACTAC 540
DB 481 GGTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAGAGATTTACTTCCCAACTAC 540
QY 541 CAATCGGCCGCGCTCTGTGTGATGACCAAGCGCTTATGAAGCTCTGAGATGGC 600
DB 541 CAATCGGCCGCGCTCTGTGTGATGACCAAGCGCTTATGAAGCTCTGAGATGGC 600
QY 601 TACTTGTGTCAGGCTGGCGCTACATTATCAAGAGAGAGGCTGAGGATGCTCTCGGCTTT 660
DB 601 TACTTGTGTCAGGCTGGCGCTACATTATCAAGAGAGAGGCTGAGGATGCTCTCGGCTTT 660
QY 661 CCTAGTGGCTATGGCGAGTTGATATCCTGTGATCCTGAGCGCCCAAGTACTATAAGCC 720
DB 661 CCTAGTGGCTATGGCGAGTTGATATCCTGTGATCCTGAGCGCCCAAGTACTATAAGCC 720
QY 721 GATGGTACCTGCTGTGACCGAGAGGTGAGAGACAGAGACTGTGGGGAATGTCAATCAT 780
DB 721 GATGGTACCTGCTGTGACCGAGAGGTGAGAGACAGAGACTGTGGGGAATGTCAATCAT 780
QY 781 GTCAACGAGACAGCATGGCTTTCTTAAGTGTGACGCCCGGCAAGTACGTTTCGATTC 840
DB 781 GTCAACGAGACAGCATGGCTTTCTTAAGTGTGACGCCCGGCAAGTACGTTTCGATTC 840

QY 841 CTCAACGCTGCCGTGTCTGTCTGTGGCTCTCTACTCTGTCAAGACACAGCTCTCCCAAC 900
DB 841 CTCAACGCTGCCGTGTCTGTCTGTGGCTCTCTACTCTGTCAAGACACAGCTCTCCCAAC 900
QY 901 GTCAGAAATTCCTTCCAAATCAATGCTGTGATGCTGTGCTTCAAGCCCGGCTGAG 960
DB 901 GTCAGAAATTCCTTCCAAATCAATGCTGTGATGCTGTGCTTCAAGCCCGGCTGAG 960
QY 961 ACCCTTAACCTTACTCTTGTGCTGCGAGCCTTACGAGATCATTTAGCTTCAACCAAC 1020
DB 961 ACCCTTAACCTTACTCTTGTGCTGCGAGCCTTACGAGATCATTTAGCTTCAACCAAC 1020
QY 1021 TTTGTGCGCAGACTCTTGACCTGCGCAACTTGTCTGAGACCAAGAGTGGCGAGAG 1080
DB 1021 TTTGTGCGCAGACTCTTGACCTGCGCAACTTGTCTGAGACCAAGAGTGGCGAGAG 1080
QY 1081 GATGAGTACGCTGCGACCTGAGGATGGGCTTGTGCTGAGCTGTGGACTGTGAG 1140
DB 1081 GATGAGTACGCTGCGACCTGAGGATGGGCTTGTGCTGAGCTGTGGACTGTGAG 1140
QY 1141 GACAACAGCCAGGTCCCTCCACTCTCGGTGACGTTCTTTCCTTCCTCACAAGAGAGGC 1200
DB 1141 GACAACAGCCAGGTCCCTCCACTCTCGGTGACGTTCTTTCCTTCCTCACAAGAGAGGC 1200
QY 1201 CCCGCCGACACGACTTCAAGTTTGAAGCAGCAGCAACGACACTACCTGATCAACGATGTT 1260
DB 1201 CCCGCCGACACGACTTCAAGTTTGAAGCAGCAGCAACGACACTACCTGATCAACGATGTT 1260
QY 1261 GCGTTTCCGAGTGTCAATGAGGCTGCTGCGCAGCCGACCTGCGGACCGTTGAGGTC 1320
DB 1261 GCGTTTCCGAGTGTCAATGAGGCTGCTGCGCAGCCGACCTGCGGACCGTTGAGGTC 1320
QY 1321 TGGGAGCTGAGAACTCTCTGTGAGGCTGAGACCAACCCGCTCACATTACCTTTGTGAC 1380
DB 1321 TGGGAGCTGAGAACTCTCTGTGAGGCTGAGACCAACCCGCTCACATTACCTTTGTGAC 1380
QY 1381 TTCAAGATCTTCAAGCGAAGCTGGTGTGCTGCGCAGGTCATGCCCTTACGATGCTGTGT 1440
DB 1381 TTCAAGATCTTCAAGCGAAGCTGGTGTGCTGCGCAGGTCATGCCCTTACGATGCTGTGT 1440
QY 1441 CTTAAGGATGCTGTGTTGGGAGGGGTGAGACCTGACATGAGGCGCACTACCA 1500
DB 1441 CTTAAGGATGCTGTGTTGGGAGGGGTGAGACCTGACATGAGGCGCACTACCA 1500
QY 1501 CCCGTGACTGAGACTTACTGTGTGCACTGTCAACACCTTACAGAGGATTAACGACATG 1560
DB 1501 CCCGTGACTGAGACTTACTGTGTGCACTGTCAACACCTTACAGAGGATTAACGACATG 1560
QY 1561 ATGGCTGTATTCAACGTCACCGCATGAGAGAGAGGATATCTTACAGAGACTTCCGAG 1620
DB 1561 ATGGCTGTATTCAACGTCACCGCATGAGAGAGAGGATATCTTACAGAGACTTCCGAG 1620
QY 1621 GACCCCATGAACCCCAAGTGGGCGCGCTTCTTACCAACCGCAAGCACTTCCATGCTGCC 1680
DB 1621 GACCCCATGAACCCCAAGTGGGCGCGCTTCTTACCAACCGCAAGCACTTCCATGCTGCC 1680
QY 1681 GCTGGAACCTTCCGCGCAGTTCATCACTGTGCCGAGTCCAGAGAGCTGGCCGAGCAGAG 1740
DB 1681 GCTGGAACCTTCCGCGCAGTTCATCACTGTGCCGAGTCCAGAGAGCTGGCCGAGCAGAG 1740
QY 1741 CCGTACAAACCGCTGATGAGATCCTGTGAGAGATCTTGAATGAGAGATTA 1791
DB 1741 CCGTACAAACCGCTGATGAGATCCTGTGAGAGATCTTGAATGAGAGATTA 1791

RESULT 2

AAA50019 standard; DNA; 1791 BP.

AAA50019;

10-OCT-2000 (first entry)

DE Stachybotrys chartarum phenol oxidising enzyme cDNA.
XX Phenol oxidising enzyme; detergent; bleaching; ss.
XX Stachybotrys chartarum.
OS
FH Key Location/Qualifiers
FT CDS 7..1791
FT /tag=a
PN WO200039306-A2.
XX
XX 06-JUL-2000.
XX
XX 20-DEC-1999; 99WO-EPI0287.
XX
XX 23-DEC-1998; 98US-0220871.
XX 23-JUN-1999; 99US-0338723.
XX
XX (UNIT.) UNILEVER NV.
XX (UNIT.) UNILEVER PLC.
XX (HIND.) HINDUSTAN LEYER LTD.
XX
XX Bodie EA, Van Der Velden S, De Vries CH, Wang H;
XX WPI: 2000-514528/46.
XX P-PSDB: AAY95537.
XX
XX Detergent composition comprising novel phenol oxidising enzyme obtained
XX from fungus or bacteria, useful for pulp and paper bleaching, bleaching
XX color of stains on fabric and for anti-dye redeposition
XX
XX Disclosure: Fig 5A-B; 45pp; English.
XX
XX The present sequence is that of the Stachybotrys chartarum MUC1 38898
XX cDNA encoding a phenol oxidising enzyme (see AAY95537). The invention
XX relates to detergent compositions comprising novel phenol oxidising
XX enzymes that are encoded by nucleic acids capable of hybridising to
XX the S. chartarum phenol oxidising enzyme gene (see AA50018), provided
XX the enzymes are capable of modifying the colour associated with dyes
XX or coloured compounds, and are produced from a bacterium, yeast or
XX fungus (see AAY9538-40). The phenol oxidising enzymes can be used
XX for pulp and paper bleaching, for bleaching the colour of stains on
XX fabric and for anti-dye transfer in detergent and textile
XX applications. They may also be capable of modifying the colour in
XX the absence or presence of an enhancer. Expression vectors and host
XX cells comprising a nucleic acid encoding a phenol oxidising enzyme,
XX methods for producing the phenol oxidising enzyme, and methods for
XX constructing expression hosts are provided.
XX
XX Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other:
SQ
Query Match 100.0%; Score 1791; DB 21; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 ATCATTACCAACCGCTGTACCGGCAAGACGACATTGGTACTATGAGATCGAGATCAAGCCA 300
QY 301 TTTTCAGCAAGAGATTATACCCACCTTGGCCCTGCCACTCTGTGGGCTACAGATGGCATG 360
Db 301 TTTTCAGCAAGAGATTATACCCACCTTGGCCCTGCCACTCTGTGGGCTACAGATGGCATG 360
QY 361 AGCCCTGGTCTACTTCAATGTTCACAGAGACGAGACTGTAGTTGATTCAATCAAC 420
Db 361 AGCCCTGGTCTACTTCAATGTTCACAGAGACGAGACTGTAGTTGATTCAATCAAC 420
QY 421 AATGCCACCGGTGAGAACTCGGTTCATCTGCACGGCTCCCATCGGTCGCCCTTTCGAT 480
Db 421 AATGCCACCGGTGAGAACTCGGTTCATCTGCACGGCTCCCATCGGTCGCCCTTTCGAT 480
QY 481 GGTGGGCTGAAGANTGTACCTTCCCTGGCGAGTACAGAGATTACTCTTCCCAATAC 540
Db 481 GGTGGGCTGAAGANTGTACCTTCCCTGGCGAGTACAGAGATTACTCTTCCCAATAC 540
QY 541 CAATCGCGCGGCTTCTGTGTACCATGACACAGGCTTTCATGAAGCTGTGAGAAATGCC 600
Db 541 CAATCGCGCGGCTTCTGTGTACCATGACACAGGCTTTCATGAAGCTGTGAGAAATGCC 600
QY 601 TACTTTGTACAGGCTGGCCCTACATTATCAACGACGAGCTGAGGATGCTCGGCTTT 660
Db 601 TACTTTGTACAGGCTGGCCCTACATTATCAACGAGGCTGAGGATGCTCGGCTTT 660
QY 661 CCTAGTGGCTATGGGAGATTTCGATATCCTCTGATCTCGACGGCCCAATATTAAGGCC 720
Db 661 CCTAGTGGCTATGGGAGATTTCGATATCCTCTGATCTCGACGGCCCAATATTAAGGCC 720
QY 721 GATGGTACCGCTGTTCGACGAGGCTGAGACACAGGACTGTGGGAGATGTCATCCAT 780
Db 721 GATGGTACCGCTGTTCGACGAGGCTGAGACACAGGACTGTGGGAGATGTCATCCAT 780
QY 781 GTCAACGACGACGATGCGCTTTCCTTAACGTTCACGCCCGCAAGTACGTTCCGATTTC 840
Db 781 GTCAACGACGACGATGCGCTTTCCTTAACGTTCACGCCCGCAAGTACGTTCCGATTTC 840
QY 841 CTCACGCTGCGGTCTGTCTGTGGCTCTCTACCTGTGACGACGACGCTCTCCCAAC 900
Db 841 CTCACGCTGCGGTCTGTCTGTGGCTCTCTACCTGTGACGACGACGCTCTCCCAAC 900
QY 901 GTGAGATTCCTTCCAACTAATGCTGCTGATGCTGTGCTTCAACCCCGGTTGAG 960
Db 901 GTGAGATTCCTTCCAACTAATGCTGCTGATGCTGTGCTTCAACCCCGGTTGAG 960
QY 961 ACCCTTAACCTTACCTTGTCTGTGGCGAGCTTACGAGATCATTTACTTCAACCAAC 1020
Db 961 ACCCTTAACCTTACCTTGTCTGTGGCGAGCTTGTGCGGAGCTTACGAGATCATTTACTTCAACCAAC 1020
QY 1021 TTTTGTGGCCAGACTCTGTGACCTGCGCAAGCTTCTGTGACACCAAGATGCGGACGAG 1080
Db 1021 TTTTGTGGCCAGACTCTGTGACCTGCGCAAGCTTGTGACACCAAGATGCGGACGAG 1080
QY 1081 GATGAGTACGCTGCGACTGTGAGGATGAGGCTGCTGTGAGCTGTGAGCTGTGAG 1140
Db 1081 GATGAGTACGCTGCGACTGTGAGGATGAGGCTGCTGTGAGCTGTGAGCTGTGAG 1140
QY 1141 GACACAGGCGAGGTCCTCTCACTCTGCTGACGTTCTCTTCCCTCCTCAAGAGAGAGC 1200
Db 1141 GACACAGGCGAGGTCCTCTCACTCTGCTGACGTTCTCTTCCCTCCTCAAGAGAGAGC 1200
QY 1201 CCGCGCGACAGCACTTCAAGTTTGAACGACGACGACACTTACCTGTATCAACGATGTT 1260
Db 1201 CCGCGCGACAGCACTTCAAGTTTGAACGACGACGACACTTACCTGTATCAACGATGTT 1260
QY 1261 GGGTTGGCGATGTCAATGAGGCTGTGCGCAGCGGCACTGTGGGCGGCTTGAAGTTC 1320
Db 1261 GGGTTGGCGATGTCAATGAGGCTGTGCGCAGCGGCACTGTGGGCGGCTTGAAGTTC 1320
QY 1321 TGGGAGCTGGAAGACTCTCTGTGAGGCTGAGACCAACCCGCTCAATTCACCTTGTGAC 1380
Db 1321 TGGGAGCTGGAAGACTCTCTGTGAGGCTGAGACCAACCCGCTCAATTCACCTTGTGAC 1380

Db	1321	TGAGAGCTCGAGAAACTCCTCTGTGAGAGCTGGAGACCAACCCCGTCCACATTCACCTTGTTCAC	1380
Qy	1381	TTCAAGATCCTCAAGCCAACTGATGATCTGTGCGCCAGATCATGCCCTACGAGTCTGTGCT	1440
Db	1381	TTCAAGATCCTCAAGCCAACTGATGATCTGTGCGCCAGATCATGCCCTACGAGTCTGTGCT	1440
Qy	1441	CTTAAGATGTCGTCTGTGCTGTGGCCAGGGGTGAGACCCCTGACCATGAGGCCACACTACCA	1500
Db	1441	CTTAAGATGTCGTCTGTGCTGTGGCCAGGGGTGAGACCCCTGACCATGAGGCCACACTACCA	1500
Qy	1501	CCCTGAGACTGGAGCTTACATGATGTGGACCTGTCAACCTTATTCACAGAGATTAACGACATG	1560
Db	1501	CCCTGAGACTGGAGCTTACATGATGTGGACCTGTCAACCTTATTCACAGAGATTAACGACATG	1560
Qy	1561	ATGCGCTGATTTCAACGCTCACCCCATGAGAGAGAGATATCTTCAGAGGACTTGCAG	1620
Db	1561	ATGCGCTGATTTCAACGCTCACCCCATGAGAGAGAGATATCTTCAGAGGACTTGCAG	1620
Qy	1621	GACCCCAATGAACCCCAAGTGGGCGCGCGCTTCTTACAAACCGAAGACACTTCATCTGTGC	1680
Db	1621	GACCCCAATGAACCCCAAGTGGGCGCGCGCTTCTTACAAACCGAAGACACTTCATCTGTGC	1680
Qy	1681	GCTGGAAACTTCTCCGCGGAGTCCATCACTGCCGAGTCCAGAGACTGGCCGACGAGAG	1740
Db	1681	GCTGGAAACTTCTCCGCGGAGTCCATCACTGCCGAGTCCAGAGACTGGCCGACGAGAG	1740
Qy	1741	CCGTACCAACGCGCTCGATGAGATCTTGAGAGATCTTTGGAATGAGAGATGA	1791
Db	1741	CCGTACCAACGCGCTCGATGAGATCTTGAGAGATCTTTGGAATGAGAGATGA	1791

RESULT 3	
AA51314	
ID	AA51314 standard; DNA; 1791 BP.
XX	
AC	AA51314;
XX	
DT	09-OCT-2000 (first entry)
XX	
DE	Stachybotrys chartarum phenol oxidizing enzyme cDNA.
XX	
KW	Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
RW	pulp; paper bleaching; ss.
XX	
OS	Stachybotrys chartarum.
XX	
PH	Key
FT	Location/Qualifiers
FT	7..1791
FT	/*tag= a
FT	/product= Phenol_Oxidizing_Enzyme
XX	
PN	WO200037654-A2.
XX	
PD	29-JUN-2000.
XX	
PF	20-DEC-1999; 99WO-US31009.
XX	
PR	23-DEC-1998; 98US-0220871.
PR	23-JUN-1999; 99US-0338723.
XX	
PA	(GENV) GENENCOR INT INC.
XX	
PL	Wang H, Bodie EA;
XX	
DR	WPI; 2000-452191/39.
DR	P-PSDB; AAY96761.
XX	
PT	New phenol oxidizing enzyme for modifying colors associated with dyes
PT	or colored compounds, is obtained from fungus and is encoded by a
PT	nucleic acid comprising a specific nucleotide sequence
PS	Disclosure; Fig 5A-B; 45pp; English.
XX	

Query Match	100.0%	Score 1791;	DB 21;	Length 1791;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1791;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
CC	Phis cDN encodes stachybotrys chartarum phenoloxidizing enzyme.			
CC	Phenol oxidizing enzymes encoded by nucleic acid sequences which			
CC	hybridize to this DNA are claimed, as long as the enzyme is capable of			
CC	modifying the colour associated with dyes or coloured compounds. The			
CC	enzymes are useful in detergent compositions and for modifying colors			
CC	associated with dyes or colored compounds which occur in stains in a			
CC	sample. The enzymes are also useful for pulp and paper bleaching,			
CC	anti-dye transfer in detergent and other textile applications.			
XX	Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other:			
QY	1	GTCAATATGCTTTCAAGTCATGGCAACCTGCGAGCAGCCCTCCGGCTCTGTCTGGATGC	60	
DB	1	GTCAATATGCTTTCAAGTCATGGCAACCTGCGAGCAGCCCTCCGGCTCTGTCTGGATGC	60	
QY	61	CTCGGATCCCATGGACACCGGACGCCACCCATTGAGGCTGTGATCCCAATGTGAAG	120	
DB	61	CTCGGATCCCATGGACACCGGACGCCACCCATTGAGGCTGTGATCCCAATGTGAAG	120	
QY	121	ACTGAGGCTTTCGCTGACTCCCTCTTGTGAGCAGGCGATGACACTGGAGTCACT	180	
DB	121	ACTGAGGCTTTCGCTGACTCCCTCTTGTGAGCAGGCGATGACACTGGAGTCACT	180	
QY	181	GCATCAACTTCCTTACAGGAATGCCCTGGCAATTCCACTGTCGAAGAGGCCAAGATG	240	
DB	181	GCATCAACTTCCTTACAGGAATGCCCTGGCAATTCCACTGTCGAAGAGGCCAAGATG	240	
QY	241	ATCATTTACCAACCCCTGTACCGGCAAGGACATTTGGTACTATGAGATGAGATCAAGCA	300	
DB	241	ATCATTTACCAACCCCTGTACCGGCAAGGACATTTGGTACTATGAGATGAGATCAAGCA	300	
QY	301	TTTTCAGCAAGAATTTACCCCACTTGGCCCTGCCACTCTGTGGCTAGCATGCGATG	360	
DB	301	TTTTCAGCAAGAATTTACCCCACTTGGCCCTGCCACTCTGTGGCTAGCATGCGATG	360	
QY	361	AGCCCGTGCTCACTTTCATGATGCCAAGAGAACAGAGACTGTAGTTAGTTCAATCAC	420	
DB	361	AGCCCGTGCTCACTTTCATGATGCCAAGAGAACAGAGACTGTAGTTAGTTCAATCAC	420	
QY	421	AATGCCACCGTGAAGACTCGGTCCATGCAAGGCTCCCATCGCGTCCCTTTTCAT	480	
DB	421	AATGCCACCGTGAAGACTCGGTCCATGCAAGGCTCCCATCGCGTCCCTTTTCAT	480	
QY	481	GGTTGGGCTGAAGATGTGACTTCCCTGGCGAGTACAAAGATTACTACTTCCCAATAC	540	
DB	481	GGTTGGGCTGAAGATGTGACTTCCCTGGCGAGTACAAAGATTACTACTTCCCAATAC	540	
QY	541	CAATCGCGCCGCTTCTGTGTGATACATGACACGCGTTTCATGAAGACTGCTGAGATGCC	600	
DB	541	CAATCGCGCCGCTTCTGTGTGATACATGACACGCGTTTCATGAAGACTGCTGAGATGCC	600	
QY	601	TACTTTGGTCAAGCTGCGCTTACATTTAACAACGACGAGCTGAGAGATGCTCTCGGTCT	660	
DB	601	TACTTTGGTCAAGCTGCGCTTACATTTAACAACGACGAGCTGAGAGATGCTCTCGGTCT	660	
QY	661	CCTAGGAGGTATGCGAGATGTGCATATCCCTGTGATCTTACGCGCCCAAGTACTATAAGCC	720	
DB	661	CCTAGGAGGTATGCGAGATGTGCATATCCCTGTGATCTTACGCGCCCAAGTACTATAAGCC	720	
QY	721	GATGTACCTCGTTGACGCGAGGCTGAGACCAAGACCTGTGGGAGATGTACATCAT	780	
DB	721	GATGTACCTCGTTGACGCGAGGCTGAGACCAAGACCTGTGGGAGATGTACATCAT	780	
QY	781	GTCACGAGACCAATGCGCTTCTTACAGTCACAGCCCGCAAGTACGTTCCGATTCC	840	
DB	781	GTCACGAGACCAATGCGCTTCTTACAGTCACAGCCCGCAAGTACGTTCCGATTCC	840	
QY	841	CTCAACGCTGCGGTGTCTGTGCTTGGCTCTCTACTGTGAGACCAAGCTCTCCCAAC	900	

Db	841	CTAAGCGTCGGTGTCTGTGGCTCTCTCACTCACTGTCAGGACCAAGCTCTCCAAC	900
Qy	901	GTCGAATTCCTTTCCAAAGTCATTGCTCTGTATGCTGTCTCTTCAAGCCCGGTTCAG	960
Db	901	GTCGAATTCCTTTCCAAAGTCATTGCTCTGTATGCTGTCTCTTCAAGCCCGGTTCAG	960
Qy	961	ACCTCTAACTCTACCTTGTGTGTGGCGAGCGTTACGAGATATTATGTACTTACCCAAC	1020
Db	961	ACCTCTAACTCTACCTTGTGTGTGGCGAGCGTTACGAGATATTATGTACTTACCCAAC	1020
Qy	1021	TTTTCTGGCAGACTGTGACCTGGCCCAACGTTGGCTGAGAACCAAGATGTGGCGAGAG	1080
Db	1021	TTTTCTGGCAGACTGTGACCTGGCCCAACGTTGGCTGAGAACCAAGATGTGGCGAGAG	1080
Qy	1081	GATGAGTAGCGCTCGCACTCTCGAGGTGATGCGCTTCTGTCAGCTCTGGCACTGTTGAG	1140
Db	1081	GATGAGTAGCGCTCGCACTCTCGAGGTGATGCGCTTCTGTCAGCTCTGGCACTGTTGAG	1140
Qy	1141	GACAAAGCCAGGTCCTCCCTCCTCACTCTCCGTGACGTTCTTTCCCTCTCACAAGGAAGC	1200
Db	1141	GACAAAGCCAGGTCCTCCCTCCTCACTCTCCGTGACGTTCTTTCCCTCTCACAAGGAAGC	1200
Qy	1201	CCCGCCGACAGACTTCAAGTTTGAACGACAGACGAGACTACTCTATCAAGATGTT	1260
Db	1201	CCCGCCGACAGACTTCAAGTTTGAACGACAGACGAGACTACTCTATCAAGATGTT	1260
Qy	1261	GCGTTTCCGATGTCAATGAGCGTGTCTGTGGCAAGCCCGAGACTTGGCACTGTTGAGTTC	1320
Db	1261	GCGTTTCCGATGTCAATGAGCGTGTCTGTGGCAAGCCCGAGACTTGGCACTGTTGAGTTC	1320
Qy	1321	TGGGAGCTCGAAGACTCTCTGTGGAGGCTGGAGCCACCCGCTCACAATTCACCTTGTGTAC	1380
Db	1321	TGGGAGCTCGAAGACTCTCTGTGGAGGCTGGAGCCACCCGCTCACAATTCACCTTGTGTAC	1380
Qy	1381	TTTCAAGTCTCTCAAGGGAAGCTGGTGGTCTGTGGCCAGAGTCATGCCCTAGAGCTGTGCTGT	1440
Db	1381	TTTCAAGTCTCTCAAGGGAAGCTGGTGGTCTGTGGCCAGAGTCATGCCCTAGAGCTGTGCTGT	1440
Qy	1441	CTTAAAGGATCTGCTGTGTGTGGGCAAGGGGTGAGACCCCTGACCTGAGAGCCACTACCAA	1500
Db	1441	CTTAAAGGATCTGCTGTGTGTGGGCAAGGGGTGAGACCCCTGACCTGAGAGCCACTACCAA	1500
Qy	1501	CCCTGCACTGGAGCTTACATGTGGCACTGTCAACAACCTTATCAAGAGGATTAACGACATG	1560
Db	1501	CCCTGCACTGGAGCTTACATGTGGCACTGTCAACAACCTTATCAAGAGGATTAACGACATG	1560
Qy	1561	ATGGCTGTATTCAACGCTCAACCGGCAAGGAGGAGAGGATATCTTCAGAGAGACTTGCAG	1620
Db	1561	ATGGCTGTATTCAACGCTCAACCGGCAAGGAGGAGAGGATATCTTCAGAGAGACTTGCAG	1620
Qy	1621	GACCCCATGAAACCCCAAGTGTGGGCGCGCTTCTTCAACCCGCAAGAGCTTCCATGTCTCC	1680
Db	1621	GACCCCATGAAACCCCAAGTGTGGGCGCGCTTCTTCAACCCGCAAGAGCTTCCATGTCTCC	1680
Qy	1681	GCTGTGAATCTTCTCCGCCAGTTCATCACTGCCGCAAGTGCAGAGAGCTGGCCAGACAGAG	1740
Db	1681	GCTGTGAATCTTCTCCGCCAGTTCATCACTGCCGCAAGTGCAGAGAGCTGGCCAGACAGAG	1740
Qy	1741	CCGTACAAACCGCTCGATGAGATCTCTGGAGAGATCTTGGAAATCGAGAGATAA	1791
Db	1741	CCGTACAAACCGCTCGATGAGATCTCTGGAGAGATCTTGGAAATCGAGAGATAA	1791

RESULT 4	
AA147584	
ID	AA147584 standard; cDNA; 1791 BP.
XX	
AC	AA147584;
XX	
DT	13-SEP-2002 (first entry)
XX	
DE	S charactrum phenol oxidising enzyme cDNA
XX	

KM		phenol oxidizing enzyme; enzyme; fungus; redox reaction; detergent;
KW		paper industry; pulp industry; textile; food industry; gene; ss.
XX		
OS		Stachybotrys chartarum.
XX		
FH	Key	Location/Qualifiers
FT	CDS	7..1791
FT		/tag= a
FM		/product= "phenol oxidizing enzyme"
XX		
PN		US6399329-B1.
XX		
PD		04-JUN-2002.
XX		
PF		21-DEC-1999; 99US-0468578.
XX		
PR		12-DEC-1998; 98US-0220871.
PR		23-JUN-1999; 99US-0338723.
XX		
PA	(GEMV) GENENCOR INT INC.	
XX		
PI	Mang H, Bodie EA;	
DR		WI: 2002-498835/53.
PS	P-PSDB; AA018210.	
XX		
PT	New polynucleotides encoding phenol oxidizing enzymes, useful for	
PT	preventing the transfer of dyes in solution from one textile to another	
PT	during detergent washing -	
PS		
PS	Disclosure: Fig 5; 37pp: English.	
XX		
CC	The present invention provides the protein and coding sequences of phenol	
CC	oxidizing enzymes from Stachybotrys chartarum, Bipolaris spicifera and	
CC	Curvularia pallescens. These enzymes are useful in the textiles, paper,	
CC	pulp, detergent and food industries. In particular they are useful for	
CC	preventing the transfer of dyes in solution from one textile to another	
CC	during detergent washing (dye transfer inhibition). The present sequence	
CC	is the S. chartarum phenol oxidizing enzyme cDNA.	
XX		
SO	Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other:	
	Query Match	100.0%; Score 1791; DB 24; Length 1791;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 1791; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	GTCATATAGCTGTTCAAATCATGTGCACACTCGGGCTCTGTTGTGAGTIC 60
DB	1	GTCATATAGCTGTTCAAATCATGTGCACACTCGGGCTCTGTTGTGAGTIC 60
QY	61	CTCGCATCCCGATGAGACCGGCAAGCCCATTTGAAGCTTGATCCCAAGTGAAG 120
DB	61	CTCGGCATCCCGATGAGACCGGCAAGCCCATTTGAAGCTTGATCCCAAGTGAAG 120
QY	121	ACTGAGGCTTTCGCTGACTCCTCTCTGCTGACGAGGCGATGACGACTGGAGTCACT 180
DB	121	ACTGAGGCTTTCGCTGACTCCTCTCTGCTGACGAGGCGATGACGACTGGAGTCACT 180
QY	181	CCATATCAACTTGCTTTACAGCAATGTCCTGCCAATTCCACCTGTACAAGCCCCAAGATG 240
DB	181	CCATATCAACTTGCTTTACAGCAATGTCCTGCCAATTCCACCTGTACAAGCCCCAAGATG 240
QY	241	ATCATTTACCACCCCTGTACACGGGCAAGACATTTGTAATGATAGTAGAGATCAAGCCA 300
DB	241	ATCATTTACCACCCCTGTACACGGGCAAGACATTTGTAATGATAGTAGAGATCAAGCCA 300
QY	301	TTTTGCAAAAGATTTCACCCACCTTTGGCCCTGGCACTTCTGTCGGCTAGAGTGCATG 360
DB	301	TTTTGCAAAAGATTTCACCCACCTTTGGCCCTGGCACTTCTGTCGGCTAGAGTGCATG 360
QY	361	AGCCCTGTCTACTTTTAAATGTTCACAGAGAACAGAGACTGTAGTTAGTTTCATCAAC 420
DB	361	AGCCCTGTCTACTTTTAAATGTTCACAGAGAACAGAGACTGTAGTTAGTTTCATCAAC 420

OY	421	AATGCCACCTGGGAGAACTCGTGCATCTGCAAGGCTCCCAATCGCGTCCCTTTGCAT	480
Db	421	AATGCCACCTGGGAGAACTCGTGCATCTGCAAGGCTCCCAATCGCGTCCCTTTGCAT	480
OY	481	GGTTGGGCGTGAAGATGTGACCTTCCCGGGGAGATCAAGAGTTACTCTTCCCAACTAC	540
Db	481	GGTTGGGCGTGAAGATGTGACCTTCCCGGGGAGATCAAGAGTTACTCTTCCCAACTAC	540
OY	541	CAATCCGCGCCCTTCTGTGTGTACCATGACCAACGCTTTCATGAAGACTGTGAGANTGCC	600
Db	541	CAATCCGCGCCCTTCTGTGTGTACCATGACCAACGCTTTCATGAAGACTGTGAGANTGCC	600
OY	601	TACTTTGGTCAGGCGTGGCGCTACATTATCAACAGAGAGGTGAGAGTCTCTGGCTTT	660
Db	601	TACTTTGGTCAGGCGTGGCGCTACATTATCAACAGAGAGGTGAGAGTCTCTGGCTTT	660
OY	661	CCTAGTGCTATGGCGAGTTCCGATATCCCTGTGATCCTGACGGCCAAAGTACTATAAACCC	720
Db	661	CCTAGTGCTATGGCGAGTTCCGATATCCCTGTGATCCTGACGGCCAAAGTACTATAAACCC	720
OY	721	GATGGTACCTTGCGCTTGACCCGAGGGTGAGAGACCAAGACCTGTGGGAGATGTCAATCAT	780
Db	721	GATGGTACCTTGCGCTTGACCCGAGGGTGAGAGACCAAGACCTGTGGGAGATGTCAATCAT	780
OY	781	GTCACAGCAGACGATGAGCTTTCTCTTAAAGTGCACACCCCGGAAGTACCGTTTCGATTTC	840
Db	781	GTCACAGCAGACGATGAGCTTTCTCTTAAAGTGCACACCCCGGAAGTACCGTTTCGATTTC	840
OY	841	CTCAACGCTGCGGTGTCTGCTGTGGCTCTCTACTCTGTAGAGCAACAGCTCTCCCAAC	900
Db	841	CTCAACGCTGCGGTGTCTGCTGTGGCTCTCTACTCTGTAGAGCAACAGCTCTCCCAAC	900
OY	901	GTCAGAAATCCCTTCCCAAGCATTTGGCCTCGATGCTGAGTCTCTTCAAGCCCCCGTTAG	960
Db	901	GTCAGAAATCCCTTCCCAAGCATTTGGCCTCGATGCTGAGTCTCTTCAAGCCCCCGTTAG	960
OY	961	ACCTCTAACTCTTACCTTGTGCTGTGGCGAGCGTTACGAGATCATTTATGACTTCCACAC	1020
Db	961	ACCTCTAACTCTTACCTTGTGCTGTGGCGAGCGTTACGAGATCATTTATGACTTCCACAC	1020
OY	1021	TTTGTGGCCAGACTCTTGAGACTCGGCGAACGTTGGTGAAGCAACAGATGTGGCGGACAG	1080
Db	1021	TTTGTGGCCAGACTCTTGAGACTCGGCGAACGTTGGTGAAGCAACAGATGTGGCGGACAG	1080
OY	1081	GATGAGTACGCTGCGACTCTCGAGATGATCGGCTGTGTAGGCTGTGGCACTGTTGAG	1140
Db	1081	GATGAGTACGCTGCGACTCTCGAGATGATCGGCTGTGTAGGCTGTGGCACTGTTGAG	1140
OY	1141	GACAAACGCCAGGTGCCCTCCACTCTCCGAGACTTCCCTTCCCTCTCACAAGAAAGCC	1200
Db	1141	GACAAACGCCAGGTGCCCTCCACTCTCCGAGACTTCCCTTCCCTCTCACAAGAAAGCC	1200
OY	1201	CCCGCGCAGCAAGCACTTGAAGGATTTGAACGAGCAAGCACTACTCTATCAACAGATGTT	1260
Db	1201	CCCGCGCAGCAAGCACTTGAAGGATTTGAACGAGCAAGCACTACTCTATCAACAGATGTT	1260
OY	1261	GCGTTTGGCCGATGTCAATGAGCGTGTCTGCGCAAGCCCGAGCTGTGGCACCGTTGAGGTC	1320
Db	1261	GCGTTTGGCCGATGTCAATGAGCGTGTCTGCGCAAGCCCGAGCTGTGGCACCGTTGAGGTC	1320
OY	1321	TGGGAGGCTCGAAGCTCTCTGGAAGGCTGAGGCAACCCGCTCCAACTTCACTTGTGTAC	1380
Db	1321	TGGGAGGCTCGAAGCTCTCTGGAAGGCTGAGGCAACCCGCTCCAACTTCACTTGTGTAC	1380
OY	1381	TTCAAGATCTCAAGCGCAACTGTGTGCTGTGGCGACAGTCAATCCCTACGATGCTCTGGT	1440
Db	1381	TTCAAGATCTCAAGCGCAACTGTGTGCTGTGGCGACAGTCAATCCCTACGATGCTCTGGT	1440
OY	1441	CTTAAAGATGTCTGTGTGTGGCGAGGGGTGAGACCTTACATGAGGCCCACTTACCA	1500
Db	1441	CTTAAAGATGTCTGTGTGTGGCGAGGGGTGAGACCTTACATGAGGCCCACTTACCA	1500

Qy	1501	CCGGAGCTGGAGCTTACATGTGGCACTGCACAACTCATTCAGAGAGTAAGCAATG	1560
Db	1501	CCCTGGATGGAGCTTACATGTGGCACTGCACAACTCATTCAGAGAGTATGACATG	1560
Qy	1561	ATGCGCTGATTTCAACGTCACCGCCATGGAGAGAAAGGATATCTTCAGAGAGACTTTCAG	1620
Db	1561	ATGGGTGATTTCAACGTCACCGCCATGGAGAGAAAGGATATCTTCAGAGAGACTTTCAG	1620
Qy	1621	GACCCCATGAAACCCAGTGGCGCCGCCGTTCTTACAAACGGCAAGACTTTCATGCTGCG	1680
Db	1621	GACCCCATGAAACCCAGTGGCGCGCCGTTCTTACAAACGGCAAGACTTTCATGCTGCG	1680
Qy	1681	GCTGGAAACTCTTCCGCCGAGTCCATACACTGCCCGAGTCCAGAGACTGGCGAGCAGAG	1740
Db	1681	GCTGGAAACTCTTCCGCCGAGTCCATACACTGCCCGAGTCCAGAGACTGGCGAGCAGAG	1740
Qy	1741	CCGTACACACCGCTCGATGAGATCTTGGAGAGATCTTGGAAATGGAGAGTAA	1791
Db	1741	CCGTACACACCGCTCGATGAGATCTTGGAGAGATCTTGGAAATGGAGAGTAA	1791

RESULT 5
ABA92911
ID ABA92911 standard; DNA; 7248 BP.

AC ABA92911;
XX
DT 09-APR-2002 (first entry)

DE *Stachybotrys chartarum* laccase gene

KW Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;
KW copper; metal cofactor; gene; plant; ds.

05 Stachybotrys chartarum

PN W0200196543-A2.

PD 20-DEC-2001.

PF 14-JUN-2001; 2001WO-US19174.

15-JUN-2000; 2000US-211732P.

PA (PROD-) PRODIGENE INC.

XX
FH (JELV) GENENCO INC.

PI Woodard S:

XX
XX
WPB: 2003-090304/13

Two copies of
XX
DE

PT transitional metal complex

PT it to cofactor -

PS Example 5; Fig 16A-E;

CC The present invention

CC metal cofactor for act

to the metal cofactor.

preferably for improving

CC copper ion activity.

comprises adding bicar

CC fungal stacyndolys ch
CC blue conner oxidases

cc The oxidation and reduction of the

The present invention describes a method for improving the recovery of an active enzyme from a plant where the enzyme requires a transitional metal cofactor for activity. The method comprises introducing into the plant nucleotide sequences encoding the enzyme and exposing the enzyme to the metal cofactor. The method is useful for improving recovery of active enzyme which requires a transitional metal cofactor for activity, preferably for improving recovery of active laccase which requires copper for activity. The method can be used for improving recovery of active organophosphate hydrolase (OPH, E.C. 3.1.8.1) which requires zinc, nickel, cobalt or manganese for activity, where the method further comprises adding bicarbonate ion salt. The present sequence encodes the fungal *Stachyotrys chartarum* laccase enzyme. Laccases are also called blue copper oxidases and use copper to accept and donate electrons in the oxidation and reduction of substrates.

XX Sequence 7248 BP; 1928 A; 1744 C; 1579 G; 1997 T; 0 other:
SQ
Query Match 99.9%; Score 1790; DB 24; Length 7248;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1790; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAATATGCTGTTCAAGTCATGGCAACTGGCAGACGCTCCGGGCTCCTGTGTGAGTC 60
DB 5192 GTCAATATGCTGTTCAAGTCATGGCAACTGGCAGACGCTCCGGGCTCCTGTGTGAGTC 5251
QY 61 CTGCGATATCCGATGAGACACGGGACGCCACCCATTGAGGCTGTTATCCCAAGTGAAG 120
DB 5252 CTGCGATATCCGATGAGACACGGGACGCCACCCATTGAGGCTGTTATCCCAAGTGAAG 5311
QY 121 ACTGAGGCTTGGCTGACACCCCTCTTGGTGCAGCAGGCGATGACATGGGAGTACCT 180
DB 5312 ACTGAGGCTTGGCTGACACCCCTCTTGGTGCAGCAGGCGATGACATGGGAGTACCT 5371
QY 181 CCATACAACTTGTCTTACAGGAATGCCCAATTCCAACCTGTCAAGCAGCCCAAGATG 240
DB 5372 CCATACAACTTGTCTTACAGGAATGCCCAATTCCAACCTGTCAAGCAGCCCAAGATG 5431
QY 241 ATCATTTACCAACCCCTGTACCGGCAAGACATTTGCTACTATGAGATCGAGATCAAGCA 300
DB 5432 ATCATTTACCAACCCCTGTACCGGCAAGACATTTGCTACTATGAGATCGAGATCAAGCA 5491
QY 301 TTTCAGCAAAAGATTTTACCCCACTTGGCCCTGGCAGCTGTGGGTCAGATGGCATG 360
DB 5492 TTTCAGCAAAAGATTTTACCCCACTTGGCCCTGGCAGCTGTGGGTCAGATGGCATG 5551
QY 361 AGCCCTGTCTACTTTCAATGTTCCAGAGAACAGACTGATAGTTAGTTATCATCAAC 420
DB 5552 AGCCCTGTCTACTTTCAATGTTCCAGAGAACAGACTGATAGTTAGTTATCATCAAC 5611
QY 421 AATGCCACCGTGGAGAACCTGGTCCATCTGCACAGGCTCCCATCGGTCCTTTTCAT 480
DB 5612 AATGCCACCGTGGAGAACCTGGTCCATCTGCACAGGCTCCCATCGGTCCTTTTCAT 5671
QY 481 GGTGGGCTGAAGATGTGACCTTCCCTGGCGATACAAAGATTTACTTATCCCAACTAC 540
DB 5672 GGTGGGCTGAAGATGTGACCTTCCCTGGCGATACAAAGATTTACTTATCCCAACTAC 5731
QY 541 CAATCCGCGCGCTTCTGTGTGATACATGACCAAGCTTTTCATGAAGACTCTGAGATGCC 600
DB 5732 CAATCCGCGCGCTTCTGTGTGATACATGACCAAGCTTTTCATGAAGACTCTGAGATGCC 5791
QY 601 TACTTTGGTCAGGCTGGCGCTACATTTACAAGACGAGGCTGAGATCTCTCGTCTT 660
DB 5792 TACTTTGGTCAGGCTGGCGCTACATTTACAAGACGAGGCTGAGATCTCTCGTCTT 5851
QY 661 CCTAGTGGCTATGGGAGTGGATATCCCTGTATGCTGACGGCCGAAGTACTATAAGCCG 720
DB 5852 CCTAGTGGCTATGGGAGTGGATATCCCTGTATGCTGACGGCCGAAGTACTATAAGCCG 5911
QY 721 GATGTACCCCTGCTTGCAGCAGAGGTGAGACCAAGACTGTGGGAGATTCATCAT 780
DB 5912 GATGTACCCCTGCTTGCAGCAGAGGTGAGACCAAGACTGTGGGAGATTCATCAT 5971
QY 781 GTCAACGAGACCATGAGCTTTCTTAAAGTTCAGACCCCGCAAGTACCGTTTCGATTC 840
DB 5972 GTCAACGAGACCATGAGCTTTCTTAAAGTTCAGACCCCGCAAGTACCGTTTCGATTC 6031
QY 841 CTCACGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 6032 CTCACGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6091
QY 901 GTCAAGATTCCTTCCAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 6092 GTCAAGATTCCTTCCAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6151
QY 961 ACCTCTAACCTCTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 1021 ACCTCTAACCTCTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

DB 6152 ACCTCTAACCTCTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6211
QY 1021 TTTCGCTGGCCAGACCTTGTACCTGGCCAAAGCTTGTGAGACCAAGATGTGGCGACGAG 1080
DB 6212 TTTCGCTGGCCAGACCTTGTACCTGGCCAAAGCTTGTGAGACCAAGATGTGGCGACGAG 6271
QY 1081 GATGAGTACGCTGCGACCTGCGAGTGAATGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 6272 GATGAGTACGCTGCGACCTGCGAGTGAATGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 6331
QY 1141 GACACAGCCAGGTCCTCCCTCCACTCTCCGTGACGTTCTTTCCCTCTCTCAAGAGAGGC 1200
DB 6332 GACACAGCCAGGTCCTCCCTCCACTCTCCGTGACGTTCTTTCCCTCTCTCAAGAGAGGC 6391
QY 1201 CCGCGGACAAAGACACTTCAAGTTTGAACGACAGAACGACACTACCTGATCAAGATGTT 1260
DB 6392 CCGCGGACAAAGACACTTCAAGTTTGAACGACAGAACGACACTACCTGATCAAGATGTT 6451
QY 1261 GGCCTTTCGCGATGTCAATGAGCGTGTCTGGCCAAAGCCGAGCTGGCAACGCTTGAAGTC 1320
DB 6452 GGCCTTTCGCGATGTCAATGAGCGTGTCTGGCCAAAGCCGAGCTGGCAACGCTTGAAGTC 6511
QY 1321 TGGGACCTGAGAACCTCTCTGAGAGCTGAGACACCCGCTCCACATTCACCTGTTGAC 1380
DB 6512 TGGGACCTGAGAACCTCTCTGAGAGCTGAGACACCCGCTCCACATTCACCTGTTGAC 6571
QY 1381 TTCAAGATCTCAAGGAACTGGTGTGCTGGCCAGGCTATCCCTACAGAGTCTGTGCT 1440
DB 6572 TTCAAGATCTCAAGGAACTGGTGTGCTGGCCAGGCTATCCCTACAGAGTCTGTGCT 6631
QY 1441 CTTAAGATGTGCTGCTGCTGGGCAAGGCTGAGACCTGACCATGAGGCCCCACTAACCA 1500
DB 6632 CTTAAGATGTGCTGCTGCTGGGCAAGGCTGAGACCTGACCATGAGGCCCCACTAACCA 6691
QY 1501 CCTGAGCTGAGACTTACATGTGTGCACTGTGCACAACTTCATTCAGAGAGTAAAGCATG 1560
DB 6692 CCTGAGCTGAGACTTACATGTGTGCACTGTGCACAACTTCATTCAGAGAGTAAAGCATG 6751
QY 1561 ATGGCTGTATTAAGTCAAGCTCCGCAATGAGAGAGGATATCTTCAGAGAGACTTCGAG 1620
DB 6752 ATGGCTGTATTAAGTCAAGCTCCGCAATGAGAGAGGATATCTTCAGAGAGACTTCGAG 6811
QY 1621 GACCCCATGAACCCCAAGTGGCGCGCTTCTTCAACCCGCAAGACTTCCATGCTGCG 1680
DB 6812 GACCCCATGAACCCCAAGTGGCGCGCTTCTTCAACCCGCAAGACTTCCATGCTGCG 6871
QY 1681 GCTGGAACCTTCCGCGGAGTCACTGCTCCGAGTGCAGAGACTGGCGGAGAGAG 1740
DB 6872 GCTGGAACCTTCCGCGGAGTCACTGCTCCGAGTGCAGAGACTGGCGGAGAGAG 6931
QY 1741 CGGTCAACCGGCTGATGAGATCCGAGAGATCTTGGAAATGAGAGATG 1790
DB 6932 CGGTCAACCGGCTGATGAGATCCGAGAGATCTTGGAAATGAGAGATG 6981

RESULT 6
AA252727
ID AA252727 standard; cDNA; 1791 BP.
XX AA252727;
XX
XX 05-JAN-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidising enzyme encoding cDNA.
XX
XX Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
KW detergent; anti-dye transfer; stain removal; bleaching; ss.
XX
OS Stachybotrys chartarum.
XX
XX W09949010-A2.
XX
XX 30-SEP-1999.
PD

XX 23-MAR-1999; 99WO-EP02042.
PF
XX 24-MAR-1998; 98US-0046969.
PR 22-DEC-1998; 98US-0218702.
XX
PA (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
XX
PI Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A,
PI Wang C;
XX
DR WPI: 1999-601211/51.
DR P-PSDB: AAY45222.
XX
PT Detergent composition containing phenol oxidase from Stachybotrys, used
PT to bleach stains and prevent dye transfer -
XX
XX
XX Example 15; Fig 5; 56pp; English.
XX
CC The present invention describes a detergent composition containing a
CC purified phenol oxidising enzyme derived from Stachybotrys. The present
CC sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The
CC enzyme can be used to modify the colour of dyes and other coloured
CC compounds (e.g. for use in pulp and paper bleaching also for removing
CC stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
CC transfer during fabric washing.
XX
SQ Sequence 1791 BP; 380 A; 554 C; 448 G; 409 T; 0 other;

Query Match 99.7%; Score 1786.2; DB 20; Length 1791;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCATATGCTGTTGACGATGGCACTGGACAGCAGCCTCGGCGCTCTGTCGTGAGTC 60
DB 1 GTCATATGCTGTTGACGATGGCACTGGACAGCAGCCTCGGCGCTCTGTCGTGAGTC 60
QY 61 CTCGGCATCCCGATGGACACCGGACGCCACCCATTGAGGCTGTGTATCCCAAGTGAG 120
DB 61 CTCGGCATCCCGATGGACACCGGACGCCACCCATTGAGGCTGTGTATCCCAAGTGAG 120
QY 121 ACTGAGCTTTCGCTGACCTCCCTCTGCTGACAGCAGCGGATGACGATGGGAGTCAGT 180
DB 121 ACTGAGCTTTCGCTGACCTCCCTCTGCTGACAGCAGCGGATGACGATGGGAGTCAGT 180
QY 181 CCATTAACCTGTGTTACAGGATGCCCTGCCAATTCCACTGTGTCAGACGCCAAGATG 240
DB 181 CCATTAACCTGTGTTACAGGATGCCCTGCCAATTCCACTGTGTCAGACGCCAAGATG 240
QY 241 ATCATTAACCAACCTGTACACCGGACGAGCAATTTGTACTATGATGATCAAGATCAAGCA 300
DB 241 ATCATTAACCAACCTGTACACCGGACGAGCAATTTGTACTATGATGATCAAGATCAAGCA 300
QY 301 TTTACGCAAAAGATTTACCCACCTTGCGCCCTGACACTCTGCTGCTGCTGCTGCTGCTG 360
DB 301 TTTACGCAAAAGATTTACCCACCTTGCGCCCTGACACTCTGCTGCTGCTGCTGCTGCTG 360
QY 361 AGCCCTGGTCTTCACTTCAATGTTCCAGAGGAAAGAGACTGTATGAGTTGATCAATCAAC 420
DB 361 AGCCCTGGTCTTCACTTCAATGTTCCAGAGGAAAGAGACTGTATGAGTTGATCAATCAAC 420
QY 421 AATGCCACGCTGGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 AATGCCACGCTGGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 GGTGGGCTGAAGATGTGACCTTCCCTGGGAGATACAGGATTAATTAATTTCCCAACTAC 540
DB 481 GGTGGGCTGAAGATGTGACCTTCCCTGGGAGATACAGGATTAATTAATTTCCCAACTAC 540
QY 541 CAATCCGCCCGCTTCTGTGTGTAACATGACACGCTTTTATGAGAGCTGCTGAATGCC 600
DB 541 CAATCCGCCCGCTTCTGTGTGTAACATGACACGCTTTTATGAGAGCTGCTGAATGCC 600

QY 601 TACTTTGGTCAAGCTGCGGCTTACATTTATCAACGACGAGGCTGAGATGCTCTCGGTCTT 660
DB 601 TACTTTGGTCAAGCTGCGGCTTACATTTATCAACGACGAGGCTGAGATGCTCTCGGTCTT 660
QY 661 CCTAGTGGCTATGCGGAGTTGATATCCCTGTGATCTGACGCCCAAGTACTATTAAGCC 720
DB 661 CCTAGTGGCTATGCGGAGTTGATATCCCTGTGATCTGACGCCCAAGTACTATTAAGCC 720
QY 721 GATGGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 GATGGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 GTCACGAGACGACCAATGAGCTTTCTTAACTGACAGCCCGGCAAGTACCTGTTCCGATTC 840
DB 781 GTCACGAGACGACCAATGAGCTTTCTTAACTGACAGCCCGGCAAGTACCTGTTCCGATTC 840
QY 841 CTCACGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 CTCACGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 GTCAGATTCCTTTCAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 GTCAGATTCCTTTCAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 ACCCTTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 ACCCTTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 TTTGCTGGCCCAACTCTTACCTGCGCAACGTTGCTGAGACCAAGATGTCGGCCAGAG 1080
DB 1021 TTTGCTGGCCCAACTCTTACCTGCGCAACGTTGCTGAGACCAAGATGTCGGCCAGAG 1080
QY 1081 GATGAGTACGCTGCGCACTGCTGAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1081 GATGAGTACGCTGCGCACTGCTGAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1141 GACAAAGCCAGGCTCCCTCCACTCTCCGTCGAGCTTCTTCCCTCCCTCAAGAGAAAGCC 1200
DB 1141 GACAAAGCCAGGCTCCCTCCACTCTCCGTCGAGCTTCTTCCCTCCCTCAAGAGAAAGCC 1200
QY 1201 CCCGCCGACAGCACTTCAAGTTTGAACGACAGCAACGACACTTACTGTATCAACATGTT 1260
DB 1201 CCCGCCGACAGCACTTCAAGTTTGAACGACAGCAACGACACTTACTGTATCAACATGTT 1260
QY 1261 GGCTTTGCCGATGCAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 GGCTTTGCCGATGCAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 TGGAGACTGAGAACTCCTCTGAGGCTGAGACCAACCCGCTGACATTCACCTTGTGAC 1380
DB 1321 TGGAGACTGAGAACTCCTCTGAGGCTGAGACCAACCCGCTGACATTCACCTTGTGAC 1380
QY 1381 TTCAGATCTCTCAAGCGAAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 TTCAGATCTCTCAAGCGAAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 CTTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 CTTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 CCTTGAGCTGAGACTTACATGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 CCTTGAGCTGAGACTTACATGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 ATGGCTGATTTCAACGCTACCGCATGAGGAGAAAGGATATCTTCAAGAGACTTCCAG 1620
DB 1561 ATGGCTGATTTCAACGCTACCGCATGAGGAGAAAGGATATCTTCAAGAGACTTCCAG 1620
QY 1621 GACCCATTAACCCCAAGTGGGCGGCTTCTTACACCGCAAGACTTCCATGCTGCTGCT 1680
DB 1621 GACCCATTAACCCCAAGTGGGCGGCTTCTTACACCGCAAGACTTCCATGCTGCTGCTGCT 1680


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QY 1681 GCTGGAACTTCTCCGCCGAGTCCATCATCTCCCGAGTGCAGAGAGCTGCCGAGCAGAG 1740
    |||
Db 1681 GCTGGAACTTCTCCGCCGAGTCCATCATCTCCCGAGTGCAGAGAGCTGCCGAGCAGAG 1740
QY 1741 CGGTACAAACCGCTCGATCGATCGTGGAGATCTTGGATCCGAGAGTAA 1791
    |||
Db 1741 CGGTACAAACCGCTCGATCGATCGTGGAGATCTTGGATCCGAGAGTAA 1791

RESULT 7
AA25728
ID AA25728 standard; DNA; 3676 BP.
XX
AC AA25728;
XX
DT 05-JAN-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidising enzyme genomic DNA.
XX
KW Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
XX detergent; anti-dye transfer; stain removal; bleaching; ds.
XX
OS Stachybotrys chartarum.
XX
PN WO949010-A2.
XX
PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99MO-EP02042.
XX
PR 24-MAR-1998; 98US-0046969.
XX
PR 22-DEC-1998; 98US-0218702.
XX
PA (UNITL ) UNILEVER NV.
XX (UNITL ) UNILEVER PLC.
XX
PI Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;
PI Wang C;
XX
DR WPI: 1999-601211/51.
XX
DR P-PSDB: AAY45222.
XX
PT Detergent composition containing phenol oxidase from Stachybotrys, used
PT to bleach stains and prevent dye transfer
XX
PS Example 14: Fig 6: 56pp: English.
XX
CC The present invention describes a detergent composition containing a
CC purified phenol oxidising enzyme derived from Stachybotrys. The present
CC sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The
CC enzyme can be used to modify the colour of dyes and other coloured
CC compounds (e.g. for use in pulp and paper bleaching also for removing
CC stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
CC transfer during fabric washing.
XX
SQ Sequence 3676 BP; 822 A; 1056 C; 849 G; 948 T; 1 other:

Query Match 82.3%; Score 1474; DB 20; Length 3676;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

QY 1 GTCATATGCTGTTCAAGTCATGGCAACTGGACAGACCTCCGGGCTCGTGTGAGTTC 60
    |||
Db 1038 GTCATATGCTGTTCAAGTCATGGCAACTGGACAGACCTCCGGGCTCGTGTGAGTTC 1097
QY 61 CTCGGCATCCCGATGGACACCGGACCAACCCATTGAGGCTGTGATCCGAAGTGAAG 120
    |||
Db 1098 CTCGGCATCCCGATGGACACCGGACCAACCCATTGAGGCTGTGATCCGAAGTGAAG 1157
QY 121 ACTGAGGCTGTGGCTGACCTCCCTGCTGTGGAGGAGGAGTACACATCGGAGTACCT 180
    |||
Db 1158 ACTGAGGCTGTGGCTGACCTCCCTGCTGTGGAGGAGGAGTACACATCGGAGTACCT 1217
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QY 181 CCATACAACTTGGTTTAC----- 198
    |||
Db 1218 CCATACAACTTGGTTTACAGTGAAGACACCTGTCACACTGTTTCCCTGATTAACTAAC 1277
QY 199 -----AGCAATGCTGCTGCCAATTCACCTGTGACAGAGCCCAAGAT----- 239
    |||
Db 1278 TCTTATAGGAATCCCTGCGCAATTCACCTGTGACAGAGCCCAAGATGATGTTCTTGGAT 1337
QY 240 -----GATCATTAACCAACCTGTGAC----- 260
    |||
Db 1338 TTTCTACGAAGCAACTCGGCCCGGACTAATGTATTCTAGAGATCTTACCAACCTGTGAC 1397
QY 261 CGGCAAGAGATTTGGTACTATGATGAGATCGAGATCAAGCCATTTCAGCAAG----- 311
    |||
Db 1398 CGGCAAGAGATTTGGTACTATGAGATCGAGATCAAGCCATTTCAGCAAGAGGTAGTTT 1457
QY 312 -----GATTTACCCCACTT 326
    |||
Db 1458 GCTCAGAAACCTTGTGTAAATATCATTTGTTACTGACCTTTCAGATTTTACCCCACTT 1517
QY 327 GCGCCCTGCGACCTGCTGGGACATGAGATGAGACCCCTGTCCTTCAATGTTCC 386
    |||
Db 1518 GCGCCCTGCGACCTGCTGGGACATGAGATGAGACCCCTGTCCTTCAATGTTCC 1577
QY 387 CAGAGCAACAGAGACTGTAGTTAGTTCAATCAACAATGCCACGTTGAGAGAACTCGGTCCA 446
    |||
Db 1578 CAGAGCAACAGAGACTGTAGTTAGTTCAATCAACAATGCCACGTTGAGAGAACTCGGTCCA 1637
QY 447 TCTGCAAGGCTCCCATCGGCTGCCCTTTCGATGGTTGGGCTGAAGATGTGACCTTCCC 506
    |||
Db 1638 TCTGCAAGGCTCCCATCGGCTGCCCTTTCGATGGTTGGGCTGAAGATGTGACCTTCCC 1697
QY 507 TGGCGAGTACAAAGATTACTACTTTCACAACTACCAATCCGCCCTTGTGTGTGATCA 566
    |||
Db 1698 TGGCGAGTACAAAGATTACTACTTTCACAACTACCAATCCGCCCTTGTGTGATCA 1757
QY 567 TGACCAAGCTTTTCATGA----- 583
    |||
Db 1758 TGACCAAGCTTTTCATGAAGGTATGCTACGAGCTTATCTTTGCTTGGCTAACCTTTGGCTA 1817
QY 584 -----AGACTGCTGAGAAATGCCCTACTTTGGTCCAGGCTGGCGCTACATT 627
    |||
Db 1818 ACCAATTCCTTTCGTAAGACTGCTGAGAAATGCCCTACTTTGGTCCAGGCTGGCGCTACATT 1877
QY 628 ATCAAGAGAGAGGCTGAGATGCTCTCGGCTTCTCTAGTGGCTATGCGAGTTCCATATC 687
    |||
Db 1878 ATCAAGAGAGAGGCTGAGATGCTCTCGGCTTCTCTAGTGGCTATGCGAGTTCCATATC 1937
QY 688 CCTGATCTCTGACGGCCAAAGTACTATTAACGGCGATGTAACCTGCGTTTCGACCGAGGT 747
    |||
Db 1938 CCTGATCTCTGACGGCCAAAGTACTATTAACGGCGATGTAACCTGCGTTTCGACCGAGGT 1997
QY 748 GAGGACCAAGACCTGTGGGAGATGTATTCATGTCAACGGACAGCCATGGCCCTTTCCTT 807
    |||
Db 1998 GAGGACCAAGACCTGTGGGAGATGTATTCATGTCAACGGACAGCCATGGCCCTTTCCTT 2057
QY 808 AAGTCCACGCCCCGCAAGTACCGTTTCCGATTCCTTAACGCTGCGTGTCTGTGG 867
    |||
Db 2058 AAGTCCACGCCCCGCAAGTACCGTTTCCGATTCCTTAACGCTGCGTGTCTGTGG 2117
QY 868 CTCCTCTACCTGCTCGAGACACAGCTCTCCCAACGATGAGAATTCCTTCCAACTGATGGC 927
    |||
Db 2118 CTCCTCTACCTGCTCGAGACACAGCTCTCCCAACGATGAGAATTCCTTCCAACTGATGGC 2177
QY 928 TCTGATGCTGGTCTCCTTCAAGCCCCGTTTCAGACCTTACCTTACCTTCTGTTGCC 987
    |||
Db 2178 TCTGATGCTGGTCTCCTTCAAGCCCCGTTTCAGACCTTACCTTACCTTCTGTTGCC 2237
QY 988 GAGCGTTACGAGATCATTTAT----- 1008
    |||
Db 2238 GAGCGTTACGAGATCATTTATGATGATGCCCTCCCTTCACGAAATGAGTCAAGAACTTA 2297
QY 1009 -----GACTTACCAAACTTTGGTGGGCAACAGTCTTGACCTGGCGAAACGTT 1053
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Db 2298 AGACTAACACTTGTAGACTTACACCACTTGTGCGCAGACTCTTGACCTGGCCAAAGTT 2357
OY 1054 GCTGAGACCAACAGATGTCGGCGCAGAGAGATGATAGCTTCGACCTCGAGAGTATGCGC 1113
Db 2358 GCTGAGACCAACAGATGTCGGCGCAGAGAGATGATAGCTTCGACCTCGAGAGTATGCGC 2417
OY 1114 TTGTCGTACAGCTCTGTGCACTGTTGAGGACACAGCCAGAGTCCCTCCACTCTCCGTGAC 1173
Db 2418 TTGTCGTACAGCTCTGTGCACTGTTGAGGACACAGCCAGAGTCCCTCCACTCTCCGTGAC 2477
OY 1174 GTTCTTTTCCCTCTCTCAAGAGAGGCCCGCCGACACAGCATTCAAGTTTGAACGACG 1233
Db 2478 GTTCTTTTCCCTCTCTCAAGAGAGGCCCGCCGACACAGCATTCAAGTTTGAACGACG 2537
OY 1234 AAGGACACTACTGTATGATCAAGCATGTTGGCTTGGCGATGTCATAGAGCGTGCCTGGCC 1293
Db 2538 AAGGACACTACTGTATGATCAAGCATGTTGGCTTGGCGATGTCATAGAGCGTGCCTGGCC 2597
OY 1294 AAGCCGAGCTCGGACACCGCTTGAGGCTCTGGAGCTCGAGAACTCTCTGGAGGCTGGAGC 1353
Db 2598 AAGCCGAGCTCGGACACCGCTTGAGGCTCTGGAGCTCGAGAACTCTCTGGAGGCTGGAGC 2657
OY 1354 CACCCGCTCGACATTACCTTGTGACTTCAACATCTCTCAAGGAACTGGTGTCTGTGC 1413
Db 2658 CACCCGCTCGACATTACCTTGTGACTTCAACATCTCTCAAGGAACTGGTGTCTGTGC 2717
OY 1414 CAGGTATGCGCTTACAGATGTCGTCTTAAAGATGTCGTGTTGGGAGGGGAG 1473
Db 2718 CAGGTATGCGCTTACAGATGTCGTCTTAAAGATGTCGTGTTGGGAGGGGAG 2777
OY 1474 ACCCTGACATGAGGAGGAGCCACTACCAACCTGGAGCTGAGCTTACATGTGGACTGTAC 1533
Db 2778 ACCCTGACATGAGGAGGAGCCACTACCAACCTGGAGCTTACATGTGGACTGTAC 2837
OY 1534 AACCTATTTCAGAGATATACGATGATGCTGTATTCAGCTCACCGCATGGAGAG 1593
Db 2838 AACCTATTTCAGAGATATACGATGATGCTGTATTCAGCTCACCGCATGGAGAG 2897
OY 1594 AAGGATATCTTACAGAGAGACTTCGAGAGACCCATGAAACCCCAAGTGGCGCGTTCT 1653
Db 2898 AAGGATATCTTACAGAGAGACTTCGAGAGACCCATGAAACCCCAAGTGGCGCGTTCT 2957
OY 1654 TACACCGCAGAGACTTCATGCTCGCGCTGAAACTTCTCCGCGAGTCCATCACCTGCC 1713
Db 2958 TACACCGCAGAGACTTCATGCTCGCGCTGAAACTTCTCCGCGAGTCCATCACCTGCC 3017
OY 1714 CGAGTGCAGAGAGCTGGCCGAGAGAGCCGTACAACCGCTCGATGATGATCTGGAGAT 1773
Db 3018 CGAGTGCAGAGAGCTGGCCGAGAGAGCCGTACAACCGCTCGATGATGATCTGGAGAT 3077
OY 1774 CTTGAATCGAGAGATA 1791
Db 3078 CTTGAATCGAGAGATA 3095

RESULT 8
AA227602
ID AA227602 standard; DNA; 3677 BP.
XX
AC AA227602;
XX
DE 16-DEC-1999 (first entry)
XX
DE Stachybotrys phenol oxidase genomic sequence.
KW Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
KW fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
XX Stachybotrys chartarum.
OS
XX
PN MO9949020-A2.
XX
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PD 30-SEP-1999.
XX
XX 23-MAR-1999; 99WO-US06327.
XX
PR 24-MAR-1998; 98US-0046969.
PR 22-DEC-1998; 98US-0218702.
PR 22-MAR-1999; 99US-0273957.
XX
PA (GENEV) GENENCOR INT INC.
XX
PI Amory A, Wang H, Dphase P, Lambrechts-Rongvaux A, Wang C;
XX
XX WPI: 1999-591088/50.
XX
XX P-PSDB: AAY39992.
XX
PT Novel enzyme for modifying coloured compounds used to prevent
PT dye-transfer.
XX
XX Claim 21: Fig 6; 64p; English.
XX
XX This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
XX of the invention. The invention is used to modify a coloured compound and
XX prevent dye transfer during fabric washing, or for stain bleaching or
XX anti-dye transfer. It is useful in the detergent, paper and pulp, textile
XX and food industries.
XX
XX Sequence 3677 BP; 822 A; 1056 C; 849 G; 947 T; 3 other:
XX
```

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Query Match 82.3%; Score 1474; DB 20; Length 3677;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
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OY 1 GTCAATATGCTGTTCAAGTATGCAACTGACAGAGCCCTCGGCTCCTGTCGAGTC 60
Db 1038 GTCAATATGCTGTTCAAGTATGCAACTGACAGAGCCCTCGGCTCCTGTCGAGTC 1097
OY 61 CTCGGCATCCCGATGAGACACCGGACCCACCCATTGAGGCTGTGATCCGAATGAAG 120
Db 1098 CTCGGCATCCCGATGAGACACCGGACCCACCCATTGAGGCTGTGATCCGAATGAAG 1157
OY 121 ACTGAGGCTTCGCTGACATCCCTGTCGAGAGCGATGACATGAGAGTCAACCT 180
Db 1158 ACTGAGGCTTCGCTGACATCCCTGTCGAGAGCGATGACATGAGAGTCAACCT 1217
OY 181 CCATACAACTTGGCTTAC----- 198
Db 1218 CCATACAACTTGGCTTACAGATGAGACACCTGTCACCACTGTTTCCCTGATTAAC 1277
OY 199 -----AGCAATGCCCTGCCAATTTCACCTGTCAAGCAGCCCAAGAT----- 239
Db 1278 TCTTATAGCAATGCCCTGCCAATTTCACCTGTCAAGCAGCCCAAGATGTGCTTGAT 1337
OY 240 -----GATATTACCAACCCCTGTAC 260
Db 1338 TTTCTAGAAAGCACTGCGGCCCGACTAATGTATCTAGATATTATCAACCTGTAC 1397
OY 261 CGGCAAGCAATTTGGTACTATGATGATGATGATGATGATGATGATGATGATGATGAT 311
Db 1398 CGGCAAGCAATTTGGTACTATGATGATGATGATGATGATGATGATGATGATGAT 1457
OY 312 -----GATTTACCCACCTT 326
Db 1458 GCTCAGAAACCTTGTGTATTAATCATTTGTACTGACCCCTTTCAGATTATACCCACCTT 1517
OY 327 GCGCCCTGCGACATCTGCTGGCTTACGATGATGATGATGATGATGATGATGATGAT 386
Db 1518 GCGCCCTGCGACATCTGCTGGCTTACGATGATGATGATGATGATGATGATGATGAT 1577
OY 387 CAGAGGAACAGACTGTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 446
Db 1578 CAGAGGAACAGACTGTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 1637
OY 447 TCTGCAAGGCTCCCATTCGCTGCCCTTTCGATGTTGGCTGAAGATGTGACTTCCC 506
```

Db	1638	TTGTGACGAGGCTCCCAATCGCGTGGCCCTTTGATGGTTGGGCTGGAAGATGACCTTCCC	1697
Qy	507	TGGCGAGTACAAGGATTACTACTTTTCCCACTACCAATCGCCCGCGCTTCTGTGTACCA	566
Db	1698	TGGCGAGTACAAGGATTACTACTTTTCCCAACTACCAATCGCCCGCGCTTCTGTGTACCA	1757
Qy	567	TGACCAAGCTTTCATGA-----	583
Db	1758	TGACCAAGCTTTCATGAAGGATGATCAAGACGCTTATCTTCTTGGACCTTTGGCTA	1817
Qy	584	-----AGACTGGTGAAGATAGCCTACTTTGGTGCAGGCGTGGGCGCTACACT	627
Db	1818	ACCAACTTCCCTTTCGTAGACTGCTGAAATGCTCTACTTTGGTGAAGCTGGCGCTACACT	1877
Qy	628	ATCAACGACGAGGCTGAGATGCGTCTCGGCTTTCCTAGTGGGTATGAGCGAGTTGCATATC	687
Db	1878	ATCAACGACGAGGCTGAGATGCGTCTCGGCTTTCCTAGTGGGTATGAGCGAGTTGCATATC	1937
Qy	688	CCTCTGATCTGACGGCCAGTACTATACGCCGATGTAACCTTGGCTTCGACGAGGGT	747
Db	1938	CCCTGTATCTGACGGCCAGTACTATATACGCCGATGTAACCTTGGCTTCGACGAGGGT	1997
Qy	748	GAGGACGAGGACCTGTGGGAGATGTATCCATGTCAAGGACGACGATGGGCTTCTCT	807
Db	1998	GAGGACGAGGACCTGTGGGAGATGTATCCATGTCAAGGACGACGATGGGCTTCTCT	2057
Qy	808	AAGCTCCAGCCCGCCAGTACCGCTTTCCTGATTCCTCAACGCTGCGGTGTCTGTGG	867
Db	2058	AAGCTCCAGCCCGCCAGTACCGCTTTCCTGATTCCTCAACGCTGCGGTGTCTGTGG	2117
Qy	868	CTCCTTACCTGTGACGAGCACGCTCTCCCAACGTCAGAAATTCCTTCCAAAGTCAATGGC	927
Db	2118	CTCCTTACCTGTGACGAGCACGCTCTCCCAACGTCAGAAATTCCTTCCAAAGTCAATGGC	2177
Qy	928	TCTATAGTGGTCTCTTCAAGGCCCCGTTTCAAGCTGTAACTTACTCTACTTCTGTGGC	987
Db	2178	TCTATAGTGGTCTCTCTTCAAGGCCCCGTTTCAAGCTGTAACTTACTCTACTTCTGTGGC	2237
Qy	988	GAGCGTTACGAGATCAATTT-----	1008
Db	2238	GAGCGTTACGAGATCAATTTGGTATGGCTTCCCTCTCACGAATGAGTCAAGAATCTTA	2297
Qy	1009	-----GACTTCACCAACTTGTGCTGGCGAGACTCTTGCACCTGGCGAAGCTT	1053
Db	2298	AGACTTAACACTTGTAGACTTCACCAACTTGTGGCGAGACTCTTGCACCTGGCGAAGCTT	2357
Qy	1054	GCTGAGAACCAACGATGTGCGGCACAGAGATGATACGCTGCGACATCTGAGGTGATGGC	1113
Db	2358	GCTGAGAACCAACGATGTGCGGCACAGAGATGATGATGATGCTGCGACATCTGAGGTGATGGC	2417
Qy	1114	TTTCTGCTGAGCTGTGGCACTGTTTGAAGCAACAGCAGGCTGCCCTCCACATCTCCGTAC	1173
Db	2418	TTTCTGCTGAGCTGTGGCACTGTTTGAAGCAACAGCAGGCTGCCCTCCACATCTCCGTAC	2477
Qy	1174	GTTCTCTTCCCTCTCTCAAGAAGAGCCCCGCGCGAACAACACTTCAAGTTTGAAGCAGC	1233
Db	2478	GTTCTCTTCCCTCTCTCTCAAGAAGAGCCCCGCGCGAACAACACTTCAAGTTTGAAGCAGC	2537
Qy	1234	AAGGACACTTACTGATCAACGATGTTGGCTTGGCCGATGTCAATGAGCGTGTCTGGCC	1293
Db	2538	AAGGACACTTACTGATCAACGATGTTGGCTTGGCCGATGTCAATGAGCGTGTCTGGCC	2597
Qy	1294	AAGCGCGAGGCTCGGCAACCGTTGAGAGCTGAGAGAGCTGGAACATCTCTGAGAGCGTGAAGC	1353
Db	2598	AAGCGCGAGGCTCGGCAACCGTTGAGAGCTGAGAGAGCTGGAACATCTCTGAGAGCGTGAAGC	2657
Qy	1354	CACCCGCTGCACATTCACCTGTTTGAATTCAGAGTCTCAACGCAACTGTGGTGTGGC	1413
Db	2658	CACCCGCTGCACATTCACCTGTTTGAATTCAGAGTCTCAACGCAACTGTGGTGTGGC	2717
Qy	1414	CAGGTCAATGCCCTTACGAGTGTGCTGTCTTAAAGATGTGCTGTGGTTGGCAGGGGTGAC	1473

Db	2718	CAGGTCAATGCCCTACGAGTGTGCTGGTCTTAAAGATGTGCTGTGGTGGGCAAGGGGTGAG	2777
Qy	1474	ACCCGTGACCATCGAGGCCCACTACCAACCCGTGACCTGAGCTTACATGTGGCACTGTAC	1533
Db	2778	ACCCGTGACCATCGAGGCCCACTACCAACCCGTGACCTGAGCTTACATGTGGCACTGTAC	2837
Qy	1534	AACCTCATTCACGAGGATTAACGACATGATGTGCTGTATTACAAGTCAAGGCCATGGAAGAG	1593
Db	2838	AACCTCATTCACGAGGATTAACGACATGATGTGCTGTATTACAAGTCAAGGCCATGGAAGAG	2897
Qy	1594	AAGGATATCTTTCAGAGAGGACCTTCGAGAGACCCCATACACCCCAAGGGGGGACCGTTGCT	1653
Db	2898	AAGGATATCTTTCAGAGAGGACCTTCGAGAGACCCCATACACCCCAAGGGGGGACCGTTGCT	2957
Qy	1654	TACAACCGCAACGACCTTCATGCTTCGCGCTGGAACCTTCGCGAGAGTCATCACTGCC	1713
Db	2958	TACAACCGCAACGACCTTCATGCTTCGCGCTGGAACCTTCGCGAGAGTCATCACTGCC	3017
Qy	1714	CGAGTGCAGAGGCTGGCCGAGACAGAGACCGGTACACCCGCTCGATGATGATCTGAGGAT	1773
Db	3018	CGAGTGCAGAGGCTGGCCGAGACAGAGACCGGTACACCCGCTCGATGATGATCTGAGGAT	3077
Qy	1774	CTTGGATATCGAGAGTAA	1791
Db	3078	CTTGGATATCGAGAGTAA	3095
RESULT 9			
AAA50018			
ID	AAA50018 standard; DNA: 3677 BP.		
XX			
XX	AAA50018:		
XX			
DT	10-OCT-2000 (first entry)		
XX			
DE	Stachybotrys chartarum phenol oxidising enzyme gene.		
XX			
KW	Phenol oxidising enzyme; detergent; bleaching; ds.		
XX			
OS	Stachybotrys chartarum.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	1044..3095	
FT		/*lag= a	
FT	exon	1044..1237	note= "contains introns"
FT		/*tag= b	
FT	intron	1238..1285	/*number= 1
FT		/*lag= c	
FT	exon	1286..1324	/*number= 2
FT		/*tag= d	
FT	intron	1325..1376	/*number= 3
FT		/*lag= e	
FT	exon	1377..1449	/*number= 4
FT		/*tag= f	
FT	intron	1450..1503	/*number= 5
FT		/*lag= g	
FT	exon	1504..1776	/*number= 6
FT		/*tag= h	
FT	intron	1777..1835	/*number= 7
FT		/*lag= i	
FT	exon	1836..3095	/*number= 8
FT		/*tag= j	
PN	MO200039306-A2.		
XX			
PD	06-JUL-2000.		
XX			
PF	20-DEC-1999; 99NO-EP10287.		

XX 23-DEC-1998; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.
XX
XX (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
PA (HIND-) HINDUSTAN LEVER LTD.
XX
PI Bodie EA, Van Der Velden S, De Vries CH, Wang H;
XX
DR WPI: 2000-514528/46.
DR P-PSDB; AAY95537.
XX
XX Detergent composition comprising novel phenol oxidising enzyme obtained
PT from fungus or bacteria, useful for pulp and paper bleaching, bleaching
PT color of stains on fabric and for anti-dye redeposition -
XX
XX Claim 1; Fig 1A-B; 45pp: English.
XX
XX The present sequence is that of the Stachybotrys chartarum MUC1 38898
CC phenol oxidising enzyme gene, including promoter and terminator
CC sequences. The gene was isolated from genomic DNA using primers
CC (see AAY50023-24) based on isolated peptides of the enzyme. The
CC gene codes for a 594 amino acid protein (see AAY95537). The invention
CC relates to detergent compositions comprising novel phenol oxidising
CC enzymes that are encoded by nucleic acids capable of hybridising to
CC the present DNA sequence, provided the enzymes are capable of
CC modifying the colour associated with dyes or coloured compounds, and
CC are produced from a bacterium, yeast or fungus (see AAY95538-40). The
CC phenol oxidising enzymes can be used for pulp and paper bleaching,
CC for bleaching the colour of stains on fabric and for anti-dye
CC transfer in detergent and textile applications. They may also be
CC capable of modifying the colour in the absence or presence of an
CC enhancer. Expression vectors and host cells comprising a nucleic
CC acid encoding a phenol oxidising enzyme, methods for producing the
CC phenol oxidising enzyme, and methods for constructing expression
CC hosts are provided.
XX
XX Sequence 3677 BP; 822 A; 1057 C; 849 G; 948 T; 1 other;
SQ
Query Match 82.3%; Score 1474; DB 21; Length 3677;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
OY 1 GCATATATGCTTTCAGATGATGACATGGCAGCAGCCTCGGGCTCCTGCTGAGTC 60
DB 1038 GTCATATATGCTTTCAGATGATGACATGGCAGCAGCCTCGGGCTCCTGCTGAGTC 1097
OY 61 CTGGGATCCCGATGAGACACCGGACGCCACCCATTGAGGCTGTGATCCCGAAGTGAG 120
DB 1098 CTGGGATCCCGATGAGACACCGGACGCCACCCATTGAGGCTGTGATCCCGAAGTGAG 1157
OY 121 ACTGAGGCTTGGTGACTCCCTCTTGTGTCAGACGAGGATGACGATGGAGTACCT 180
DB 1158 ACTGAGGCTTGGTGACTCCCTCTTGTGTCAGACGAGGATGACGATGGAGTACCT 1217
OY 181 CCATACACTTCTTAC----- 198
DB 1218 CCATACACTTCTTACAGGTGAGACACCTTCCACCTGTTTTCTCCGATTAAC 1277
OY 199 -----AGGAATGCCCTGGCAATTCACCTGTCAAGCAGCCCAAGT----- 239
DB 1278 TCTTATAGGAATGCCCTGGCAATTCACCTGTCAAGCAGCCCAAGTATGTTGAT 1337
OY 240 -----GATCATTTACCAACCTGTGAC 260
DB 1338 TTTTACGAGCACTCGGCCCGCACTAATGATTTCTAGATCATTAACCAACCTGTGAC 1397
OY 261 CGGCAAGGACATTTGGTACTATAGATGAGATCAAGCATTTTCAGCAAG----- 311
DB 1398 CGGCAAGGACATTTGGTACTATAGATGAGATCAAGCATTTTCAGCAAGGATGATT 1457
OY 312 -----GATTTACCCACCTT 326

DB 1458 GCTCAGAAACCTTGTGTAATTAATCATTTGTTACTGACCCCTTCAGATTAACCCACCTT 1517
OY 327 GGGCCCTGCACACTCTGTCGGCTACGATGGCATGAGCCCTGGCTCTACTTCAATGTTCC 386
DB 1518 GGGCCCTGCACACTCTGTCGGCTACGATGGCATGAGCCCTGGCTCTACTTCAATGTTCC 1577
OY 387 CAGAGACAGAGACTGTAGTTAGTTTCATCAACAAATGCAACCGTGAGAACTCGGTCCA 446
DB 1578 CAGAGAACAGAGACTGTAGTTAGTTTCATCAACAAATGCAACCGTGAGAACTCGGTCCA 1637
OY 447 TCTGCAGGCTCCCATGCGCGTCCCTTTGATGATGTTGGCTGAAGATGACCTTCC 506
DB 1638 TCTGCAGGCTCCCATGCGCGTCCCTTTGATGATGTTGGCTGAAGATGACCTTCC 1697
OY 507 TGGGAGTACAGGATTTACTTCCCACTACCAATCCCGGCGCTTGTGTGTACA 566
DB 1698 TGGGAGTACAGGATTTACTTCCCACTACCAATCCCGGCGCTTGTGTGTACA 1757
OY 567 TGACCAGCTTTCANGA----- 583
DB 1758 TGACCAGCTTTCANGAGATGCTACGAGCCTTATCTTCTTGCTACCTTTGGCTA 1817
OY 584 -----AGACTCTGAGAAATGCTACTTGTGTCAGCGCTGCGCTTACAT 627
DB 1818 ACCAACTTCCTTTCGTAGACTGCTGAGAAATGCTACTTGTGTCAGCGCTTACAT 1877
OY 628 ATCAAGCAGGAGGATGATGCTCGGCTCTCTAGGGCTATGGGAGGATGCAATTC 687
DB 1878 ATCAAGCAGGAGGATGATGCTCGGCTCTCTAGGGCTATGGGAGGATGCAATTC 1937
OY 688 CCTGTGATCTTGCAGGCAAGTACTATAAGCGGATGTTGATCCTGCTTCGACAGAGGT 747
DB 1938 CCTGTGATCTTGCAGGCAAGTACTATAAGCGGATGTTGATCCTGCTTCGACAGAGGT 1997
OY 748 GAGGACAGGACCTTGGGGAGATGTCATCATGTCAACGAGACCATGECCTTTCCT 807
DB 1998 GAGGACAGGACCTTGGGGAGATGTCATCATGTCAACGAGACCATGECCTTTCCT 2057
OY 808 AACGTCCAGCCCCGCAAGTACGTTCCGATTCCTCAACGCTGCCGTGTCTGCTTGG 867
DB 2058 AACGTCCAGCCCCGCAAGTACGTTCCGATTCCTCAACGCTGCCGTGTCTGCTTGG 2117
OY 868 CTCCTCTACCTGTGAGGACACAGCTCTCTCCAACTGACAAATTCCTTCCAAATTCG 927
DB 2118 CTCCTCTACCTGTGAGGACACAGCTCTCTCCAACTGACAAATTCCTTCCAAATTCG 2177
OY 928 TCTGATGCTGTCTCTTCAAGCCCCCGTTGAGACCTTACCTTACCTTGCCTGTG 987
DB 2178 TCTGATGCTGTCTCTTCAAGCCCCCGTTGAGACCTTACCTTACCTTGCCTGTG 2237
OY 988 GAGCGTTACGAGATCATTT----- 1008
DB 2238 GAGCGTTACGAGATCATTTATTTGATGCCCTCCCTCTCAGCAATGAGTCAAGAACTTA 2297
OY 1009 -----GACTTCAACAATTTGCTGGCCAGACTCTTGACCTGGCAACGTT 1053
DB 2298 AGACTTAACACTTGTAGACTTTCACCAACTTGTGCTGGCCAGACTCTTGACCTGGCAACGTT 2357
OY 1054 GCTGAGACCAACGATGTGGCGCAGCAGAGATGATGAGTACGCTCTGAGAGTGTATGGC 1113
DB 2358 GCTGAGACCAACGATGTGGCGCAGCAGAGATGATGAGTACGCTCTGAGAGTGTATGGC 2417
OY 1114 TTGCTGTCAGCTGTGGCACTGTTGAGGACAAACAGCAGGTCCCTCACTCTCGGTGAC 1173
DB 2418 TTGCTGTCAGCTGTGGCACTGTTGAGGACAAACAGCAGGTCCCTCACTCTCGGTGAC 2477
OY 1174 GTTCCCTTCCCTCTCACAAGGAGGCCCCGCGCAAGCAATTCAGTTTGAAGCGAGC 1233
DB 2478 GTTCCCTTCCCTCTCACAAGGAGGCCCCGCGCAAGCAATTCAGTTTGAAGCGAGC 2537
OY 1234 AACGACACTTACCTGATCAACGATGTTGGCTTGGCGAATGTCATGACGTTGCTGACC 1293

```
.
Db 2538 AACGGACACTACCTGATCAAGCATGTGGCTTTGCCGATGTCATGAGCGGTCTCGGCC 2597
Oy 1294 AAGCCCGAGCTCGGACCGCTTGAGCTTGCGAGCTCGAGAACTCTCTTGAGAGCTGGAGC 1353
Db 2598 AAGCCCGAGCTCGGACCGCTTGAGCTTGCGAGCTCGAGAACTCTCTTGAGAGCTGGAGC 2657
Oy 1354 CACCCCGTCAACATTCACCTTGTTGACTTCAAGATCCCTCAACGCAAACTGGTGGTGGC 1413
Db 2658 CACCCCGTCAACATTCACCTTGTTGACTTCAAGATCCCTCAACGCAAACTGGTGGTGGC 2717
Oy 1414 CAGTCAATGCCCTACGAGTCTGCTGCTGTTAAGATGTCGTTGTTGGGAGGGGTGAG 1473
Db 2718 CAGTCAATGCCCTACGAGTCTGCTGCTGTTAAGATGTCGTTGTTGGGAGGGGTGAG 2777
Oy 1474 ACCCTGACCATTCGAGGCCCACTACCAACCCTTGAGCTTGAGCTTACATGTGGACATGTAC 1533
Db 2778 ACCCTGACCATTCGAGGCCCACTACCAACCCTTGAGCTTGAGCTTACATGTGGACATGTAC 2837
Oy 1534 AACCTCATTCACGAGGATTAACGACATGATGGCTGATTCAAGCTCACCGCCATGGAGAG 1593
Db 2838 AACCTCATTCACGAGGATTAACGACATGATGGCTGATTCAAGCTCACCGCCATGGAGAG 2897
Oy 1594 AAGGATATCTTCAGAGAGACTTCGAGAGACCCCATGAACCCCAAGTGGCGCCGTTCTCT 1653
Db 2898 AAGGATATCTTCAGAGAGACTTCGAGAGACCCCATGAACCCCAAGTGGCGCCGTTCTCT 2957
Oy 1654 TACAAACCCGCAACGACTTCCTGCTGCTGGAACCTTCCGCGAGTCCATCTACTGACC 1713
Db 2958 TACAAACCCGCAACGACTTCCTGCTGCTGGAACCTTCCGCGAGTCCATCTACTGACC 3017
Oy 1714 CGAGTCAGAGAGCTGGCGGAGAGAGCGGTCAACCGCCTCGATGATGATCTCGAGGAT 1773
Db 3018 CGAGTCAGAGAGCTGGCGGAGAGAGCGGTCAACCGCCTCGATGATGATCTCGAGGAT 3077
Oy 1774 CTTGGAATCGAGAGTAA 1791
Db 3078 CTTGGAATCGAGAGTAA 3095

RESULT 10
AAAS1313
ID AAAS1313 standard: DNA: 3677 BP.
AC AAAS1313:
XX
XX 09-OCT-2000 (first entry)
XX
XX Stachybotrys chartarum phenol oxidizing enzyme genomic DNA.
KW Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
KW pulp; paper bleaching; ds.
XX
XX Stachybotrys chartarum.
OS
XX
XX Key Location/Qualifiers
FH CDS 1044..3095
FT 1044..3095
FT 1044..1237
FT exon /product= Phenol_Oxidizing_Enzyme
FT /tag= a
FT /partial
FT 1238..1285
FT intron /tag= b
FT 1286..1324
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XX WO200037654-A2.
XX
XX 29-JUN-2000.
XX
XX 20-DEC-1999; 99MO-US31009.
XX
XX 23-DEC-1998; 98US-0220871.
XX
XX 23-JUN-1999; 99US-0338723.
XX
XX (GENV ) GENENCOR INT INC.
XX
XX Wang H, Bodie EA:
XX
XX WPI: 2000-452191/39.
XX
XX P-PSDB: AAY96761.
XX
XX New phenol oxidizing enzyme for modifying colors associated with dyes
XX or colored compounds, is obtained from fungus and is encoded by a
XX nucleic acid comprising a specific nucleotide sequence
XX
XX Claim 10; Fig 1A-B; 45pp; English.
XX
XX This genomic DNA encodes Stachybotrys chartarum phenol oxidizing enzyme.
XX Phenol oxidizing enzymes encoded by nucleic acid sequences which
XX hybridize to this DNA are claimed, as long as the enzyme is capable of
XX modifying the colour associated with dyes or coloured compounds. The
XX enzymes are useful in detergent compositions and for modifying colors
XX associated with dyes or colored compounds which occur in stains in a
XX sample. The enzymes are also useful for pulp and paper bleaching,
XX anti-dye transfer in detergent and other textile applications.
XX
XX Sequence 3677 BP; 822 A; 1057 C; 849 G; 948 T; 1 other;
XX
XX
XX Query Match 82.3%; Score 1474; DB 21; Length 3677;
XX Best Local Similarity 87.0%; Pred. No. 0;
XX Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

Oy 1 GTCAATATCTGTTCAAGTCATGACGCACTGCGAGCAGCCTCGGGCTCCTGTCGAGTC 60
Db 1038 GTCAATATCTGTTCAAGTCATGACGCACTGCGAGCAGCCTCGGGCTCCTGTCGAGTC 1097
Oy 61 CTCGGCATCCCGATGAGACACCGGACGCCAACCATTGAGCGCTGTTGATCCCGAAGTGAG 120
Db 1098 CTCGGCATCCCGATGAGACACCGGACGCCAACCATTGAGCGCTGTTGATCCCGAAGTGAG 1157
Oy 121 ACTGAGCTCTGCGTACATCCCTCTTGCTGACAGGAGGATGACATGCGGAGTACCT 180
Db 1158 ACTGAGCTCTGCGTACATCCCTCTTGCTGACAGGAGGATGACATGCGGAGTACCT 1217
Oy 181 CCATACAACTTGCTTAC-----
Db 1218 CCATACAACTTGCTTACAGGTGAGACACCTGTCACCTGTTTCCCGATTAAC 1277
Oy 199 -----AGGAATGCCCTGCAATTCACCTGTCACGACGCCCAAGT----- 239
Db 1278 TCTTATAGGAATGCCCTGCAATTCACCTGTCACGACGCCCAAGTGTATGCTTTGAT 1337
Oy 240 -----GATCATTAACAACCCGTGAC 260
Db 1338 TTTCTAGGAACAATCGGCCCGGACTAATGTAATCTAGAGATCAAGCCATTTCACAG 1397
Oy 261 CGCAGAGCAATTTGTTAGTATGAGATGAGATCAAGCCATTTCACAG----- 311
```


Db 2898 AAGGATATCTTCAGAGAGACTTCAGAGACCCATGAAACCCAGTGGCGCCCTTCT 2957
Qy 1654 TACAACCGCAAGACTTCCTCATGCTGCGGTGAAAATTCTCGCGAGATCATCACTGCC 1713
Db 2958 TACAACCGCAAGACTTCCTCATGCTGCGGTGAAAATTCTCGCGAGATCATCACTGCC 3017
Qy 1714 CGAGTGCAGAGACTGGCCGAGCAGAGACCGGTACAAACCGCTTGATGAGATCCTTGAGAGAT 1773
Db 3018 CGAGTGCAGAGACTGGCCGAGCAGAGACCGGTACAAACCGCTTGATGAGATCCTTGAGAGAT 3077
Qy 1774 CTGGAAATGAGAGATAA 1791
Db 3078 CTGGAAATGAGAGATAA 3095
RESULT 12
AA225735
ID AA225735 standard; DNA; 2067 BP.
XX
AC AA225735;
XX
DT 05-JAN-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidising enzyme PCR fragment.
XX
KW Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
KM detergent; anti-dye transfer; stain removal; bleaching; PCR primer; ss.
XX
OS Synthetic.
XX Stachybotrys chartarum.
PN WO9949010-A2.
PD 30-SEP-1999.
PE 23-MAR-1999; 99WO-EP02042.
PR 24-MAR-1998; 98US-0046969.
PR 22-DEC-1998; 98US-0218702.
XX
XX
PA (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
XX
PI Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;
PI Wang C;
XX
DR WPI: 1999-601211/51.
XX
PT Detergent composition containing phenol oxidase from Stachybotrys, used
PT to bleach stains and prevent dye transfer -
XX
PS Example 17; Fig 9; 56pp; English.
XX
CC The present invention describes a detergent composition containing a
CC purified phenol oxidising enzyme derived from Stachybotrys. The present
CC sequence represents a PCR fragment of Stachybotrys chartarum phenol
CC oxidising enzyme. The enzyme can be used to modify the colour of dyes
CC and other coloured compounds (e.g. for use in pulp and paper bleaching
CC also for removing stains, e.g. food, tea, blood etc., from fabrics) and
CC for preventing dye transfer during fabric washing.
XX
S0 Sequence 2067 BP; 445 A; 621 C; 500 G; 501 T; 0 other;
Query Match 82.1%; Score 1470; DB 20; Length 2067;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1787; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

Db 67 GGCATCCCGATGAGACCGGCGACACCCCATTTGAGGCTGTTGATCCCGAAGTGAAGACT 126
Qy 124 GAGGCTTCCTGCTGACTCCCTCTTGCTGAGCAGGAGGATGAGACTGGAGTCCACTCCA 183
Db 127 GAGGCTTCCTGCTGACTCCCTCTTGCTGAGCAGGAGGATGAGACTGGAGTCCACTCCA 186
Qy 184 TGCACCTTGCTTAC----- 198
Db 187 TCAACTGCTTTAGAGGTGAGACACCTGTCACCTGTTTTCCCTGATTAACCTACTCT 246
Qy 199 -----AGGAATGCCCTGCAATTCACCTGTCAGACAGCCCAAGT----- 239
Db 247 TATAGGAATGCCCTGCAATTCACCTGTCAGACAGCCCAAGTATGATGCTTTGATTTT 306
Qy 240 -----GATCATTAACCAACCTGTCACCG 263
Db 307 CTACGAGCACTGGGCCCCGACATAATGATTTCTAGGATCATTAACACCGTGCACGG 366
Qy 264 CAAGGACATTTGTTACTATGAGATGAGATCAAGCCATTTCAAGCAAG----- 311
Db 367 CAAGGACATTTGTTACTATGAGATGAGATCAAGCCATTTCAAGCAAGGAGTGTGCT 426
Qy 312 -----GATTTACCCACCTGCG 329
Db 427 CAGAAACCTTGTTGATTAATTAATCAATGTTACTGACCTTTCAAGATTTACCCACCTGCG 486
Qy 330 CCTGCACTCTGCTGCTGCTAGATGAGATGAGCCCTGCTACTTTCAATGTTCCAG 389
Db 487 CCTGCACTCTGCTGCTGCTAGATGAGATGAGCCCTGCTACTTTCAATGTTCCAG 546
Qy 390 AGGAACAGAGACTGTAGTTAGTTAGTTCAATCAATGCGACCGTGGAGAACTCGGTCCATCT 449
Db 547 AGGAACAGAGACTGTAGTTAGTTAGTTCAATCAATGCGACCGTGGAGAACTCGGTCCATCT 606
Qy 450 GCAGGCTCCCGATCGCGCGCCCTTTGATGTTGGGTGGAAGATGATGATCCCTCCG 509
Db 607 GCAGGCTCCCGATCGCGCGCCCTTTGATGTTGGGTGGAAGATGATGATCCCTCCG 666
Qy 510 CGAGTACAGGATTTACTACTTTCCCACTACCAATCCGCGCTTCTGTTGATACATGA 569
Db 667 CGAGTACAGGATTTACTACTTTCCCACTACCAATCCGCGCTTCTGTTGATACATGA 726
Qy 570 CCACGCTTCAATGA----- 583
Db 727 CCACGCTTCAATGAAGGTATGCTAGAGCCCTTATCTTTCTTGACTTTGGCTTAAC 786
Qy 584 -----AGACTGCTGAGAAATGCTACTTTGGTCAAGGCTGGCGCCCTACATTAAC 630
Db 787 AACTTCCTTTGCTAGACTGCTGAGAAATGCTACTTTGGTCAAGGCTGGCGCCCTACATTAAC 846
Qy 631 AACGACAGGCTGAGGATGCTCGGTCTCTAGTGTAGTGGAGATGCGATATCCCT 690
Db 847 AACGACAGGCTGAGGATGCTCGGTCTCTAGTGTAGTGGAGATGCGATATCCCT 906
Qy 691 CTGATCTGAGCGCCCAAGTACTATAACGCCGATGTAGTACCTGCTGCAAGGAGTGAG 750
Db 907 CTGATCTGAGCGCCCAAGTACTATAACGCCGATGTAGTACCTGCTGCAAGGAGTGAG 966
Qy 751 GACGAGGACTGTGGGGAATGATCCATGTCACGAGCAGACCATGAGCTTCTCTTAAC 810
Db 967 GACGAGGACTGTGGGGAATGATCCATGTCACGAGCAGACCATGAGCTTCTCTTAAC 1026
Qy 811 GTCCAGGCGCGCAAGTATGATGATTCCTCAAGGCTGGCGCTGCTGAGCTC 870
Db 1027 GTCCAGGCGCGCAAGTATGATGATTCCTCAAGGCTGGCGCTGCTGAGCTC 1086
Qy 871 GTCTACCTGCTGAGGACGCTCCCAAGTCAAGATTTCTTTCAAGTCAATGCTCT 930
Db 1087 CTCTACCTGCTGAGGACGCTCCCAAGTCAAGATTTCTTTCAAGTCAATGCTCT 1146
Qy 931 GATGCTGCTCTCTTCAAGGCGCGCTTCAAGCTCTAATCTTACTTGTCTTGGCAG 990
Db 1147 GATGCTGCTCTCTTCAAGGCGCGCTTCAAGCTCTAATCTTACTTGTCTTGGCAG 1206

Oy	991	CGTTACGAGATCAATTTAT	-----	1008
Db	1207	CGTTAAGAGATCATTTATTTGGTATAGCCCTCCCTCTCAGCAATGAGTCAAGAATCTTAAGA		1266
Oy	1009	-----GACCTTCACCAACTTTTGGCTGGCCAGACACTCTTGACCTGGCCAAAGCTTGCT		1056
Db	1267	CTAACACTTGTGAGACCTTCACCAACTTTTGGCTGGCCAGACACTTGACCTGGCCAAAGCTTGCT		1326
Oy	1057	GAGACCAACGATGTGCGCCGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATGCGCTTC		1116
Db	1327	GAGACCAACGATGTGCGCCGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATGCGCTTC		1386
Oy	1117	GTCGTCAGCTCTGGCACTGTGTAAGGAAACAGCCAGATGCCCTCCACACTCTCCGTAGAGTT		1176
Db	1387	GTCGTCAGCTCTGGCACTGTGTAAGGAAACAGCCAGATGCCCTCCACACTCTCCGTAGAGTT		1446
Oy	1177	CGTTTCCTCCTCTCAAGAGGAGCCCGCCGACAAACACTTCAAGTTTGAACGACGACAAAC		1236
Db	1447	CGTTTCCTCCTCCTCAAGAGGAGCCCGCCGACAAACACTTCAAGTTTGAACGACGACAAAC		1506
Oy	1237	GGAACACTACTGATCAACGATGTTGGCTTTGCCGATGTCAATGAGCGTGTCTTGCCCAAG		1286
Db	1507	GGAACACTACTGATCAACGATGTTGGCTTTGCCGATGTCAATGAGCGTGTCTTGCCCAAG		1566
Oy	1297	CCCGAGCTCGGACACCGTTGAGGTCTGGAGAGCTCGAATCTCTCGAGAGGCTGGAGCCAC		1356
Db	1567	CCCGAGCTCGGACACCGTTGAGGTCTGGAGAGCTCGAATCTCTCGAGAGGCTGGAGCCAC		1626
Oy	1357	CCCGCTCAGACTTCAACCTTGTGTGACTTCAAGATCTCTCAAGCAACTGAGTGTGTTGGCCAG		1416
Db	1627	CCCGCTCAGACTTCAACCTTGTGTGACTTCAAGATCTCTCAAGCAACTGAGTGTGTTGGCCAG		1686
Oy	1417	GTCATGCCCTACAGATGTGCTGGTCTTAAAGATGTCTGTGTTGGCAAGGGGTGAGACC		1476
Db	1687	GTCATGCCCTACAGATGTGCTGGTCTTAAAGATGTCTGTGTTGGCAAGGGGTGAGACC		1746
Oy	1477	CTGACACTCGAGAGGCCACTCTCAAAACCCTGAGACTGGAGCTTACATGAGCACTGTCACAAAC		1536
Db	1747	CTGACACTCGAGAGGCCACTCTCAAAACCCTGAGACTGGAGCTTACATGAGCACTGTCACAAAC		1806
Oy	1537	CTCATTCACGAGATTAACGACATGATGGCTGTATTCAACGTCACCGCCATGGAGAGAG		1596
Db	1807	CTCATTCACGAGATTAACGACATGATGGCTGTATTCAACGTCACCGCCATGGAGAGAG		1866
Oy	1597	GGAATCTTACGAGAGGACTCTCGAGAGCCCATGAGAACCCCAATGGCGCGCTTCTTAC		1636
Db	1687	GGAATCTTACGAGAGGACTCTCGAGAGCCCATGAGAACCCCAATGGCGCGCTTCTTAC		1926
Oy	1657	AACCGCAACGACTTTCATGCTCGCTGGGAAACTTCTCCGCGAATCCATCACTGACCCGA		1716
Db	1927	AACCGCAACGACTTTCATGCTCGCTGGGAAACTTCTCCGCGAATCCATCACTGACCCGA		1986
Oy	1717	GTCGAGAGAGCTGGCCGACGAGAGCCGTCACAAACCGCTCGATGAGATCCTGGAGATCTT		1776
Db	1987	GTCGAGAGAGCTGGCCGACGAGAGCCGTCACAAACCGCTCGATGAGATCCTGGAGATCTT		2046
Oy	1777	GGAATCGAGAGATTA 1790		
Db	2047	GGAATCGAGAGATTA 2060		
RESULT 13				
AA227609				
ID	AA227609 standard; DNA; 2067 BP.			
XX				
AC	AA227609:			
XX				
DT	16-DEC-1999 (first entry)			
XX				
DE	Stachybotrys phenol oxidase coding sequence.			
XX				
WM	Phenol oxidase; enzyme; coloured compound; dye transfer prevention;			

xx	fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
xx	
OS	<i>Stachybotrys chartarum</i> .
xx	
PN	WO9949020-A2.
xx	
PD	30-SEP-1999.
xx	
PF	23-MAR-1999; 99MO-US06327.
xx	
PR	24-MAR-1998; 98US-0046969.
PR	22-DEC-1998; 98US-0218702.
PR	22-MAR-1999; 99US-0273957.
xx	
PA	(GEMV) GENENCOR INT INC.
xx	
PI	Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;
xx	
DR	WPI; 1999-591088/50.
xx	
PT	Novel enzyme for modifying coloured compounds used to prevent
xx	dye-transfer -
xx	
PS	Example 17; Fig 9; 64pp; English.

CC This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
CC of the invention. The invention is used to modify a coloured compound and
CC prevent dye transfer during fabric washing, or for stain bleaching or
CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC and food industries.
XX
XQ Sequence 2057 BP; 445 A; 621 C; 500 G; 501 T; 0 other;

Query Match	82.18;	Score 1470;	DB 20;	Length 2067;
Best Local Similarity	87.08;	Pred. No. 0;		
Matches 1787; Conservative	0;	Mismatches 0;	Indels 267;	Gaps 5

QY	4	AATATGCTGTTCAAAGTCATGCAAACTGAGGACAGCCTCGGGCTCCTGTGAGAGTCTC	63
Db	7	AATATGCTGTTCAAAGTCATGCAAACTGAGGACAGCCTCGGGCTCCTGTGAGAGTCTC	66
QY	64	GGCATCCCGATGGACACCGGACGACCCCATTTGAGGCTGTTGATCCGAAGTAAGACT	123
Db	67	GGCATCCCGATGGACACCGGACGACCCCATTTGAGGCTGTTGATCCGAAGTAAGACT	126
QY	124	GAGATCTTCCCTGACACCCCTCCCTTGGTGGAGAGGAGATGAGATCTGGGAGTCAACCTCA	183
Db	127	GAGATCTTCCCTGACACCCCTCCCTTGGTGGAGAGGAGATGAGATCTGGGAGTCAACCTCA	186
QY	184	TACAACTTGGCTTAC-----	198
Db	187	TACAACTTGGCTTACAGGTGAGACACCTGCCACCTGTTTCCCTGATTAACATACCT	246
QY	199	---AGGAATGCCCGGCATCTCCACTCCCTGTCAGAGGCCAAGAT-----	239
Db	247	TATAGGATGCCCGGCATCTCCACTCCCTGTCAGAGGCCAAGATGATGCTTTGATTTT	306
QY	240	-----GATCATTTACCAACCTCTGACCGG	263
Db	307	CTACGAAGCAACTCGGCCGACATAATGATTCTAGATCATTTACCAACCTCTGACCGG	366
QY	264	CAAGGACATTTGGTACTATGAGATGCAAGTCAAGCCATTTTACGCAAG-----	311
Db	367	CAAGGACATTTGGTACTATGAGATGCAAGTCAAGCCATTTTACGCAAGGTTGCT	426
QY	312	-----GATTTACCCACCTTTGCG	329
Db	427	CAGAAACCTTGTTGTAATTAATCATTTGTAAGACCCCTTTGAGATTTACCCACCTTTGCG	486
QY	330	CCCTGCCACTCTGTCGGCTAGAGATGGCATGAGCCCTGGCTCTACTTTCAATGTTCCAG	389
Db	487	CCCTGCCACTCTGTCGGCTAGAGATGGCATGAGCCCTGGCTCTACTTTCAATGTTCCAG	546

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QY 390 AGAAGACAGACTAGTATAGTTAGTTCATCAACAATGCCACCGTGGAGACTCGGTCCATCT 449
    |||
Db 547 AGCAAGAGAGACTGTATAGTTCATCAACAATGCCACCGTGGAGAACTCCGTCCATCT 606
    |||
QY 450 GACAGGCTCCCATGCGGCCCTTTGATGGTTGGGTGGTGAAGATGATACCTTCCCTGG 509
    |||
Db 607 GACAGGCTCCCATGCGGCCCTTTGATGGTTGGGTGGTGAAGATGATACCTTCCCTGG 666
    |||
QY 510 CGAGTACAAGATTAATTAATTTCCCAACTACCAATCCGCCCTTTCTGTGTACCATGA 569
    |||
Db 667 CGAGTACAAGATTAATTAATTTCCCAACTACCAATCCGCCCTTTCTGTGTACCATGA 726
    |||
QY 570 CCACGCTTTCANGA----- 583
    |||
Db 727 CCACGCTTTCANGAAGTATGCTACGAGCCCTTATCTTTCTTGGCTACCTTTGGCTAAC 786
    |||
QY 584 -----AGACTACTGAAATGCTACTTTGGTCAGGCTGGCGCTACATTAATC 630
    |||
Db 787 AACTTCCTTTCGTAGACTGTGAGATGCTACTTTGGTCAGGCTGGCGCTACATTAATC 846
    |||
QY 631 AACGACGAGCTGAGAGATGCTCGGCTTCTAGTGGCTATGCGAGTTGCATATCCCT 690
    |||
Db 847 AACGACGAGCTGAGAGATGCTCGGCTTCTAGTGGCTATGCGAGTTGCATATCCCT 906
    |||
QY 691 CTGATCTGACGGCCCAAGTACTATAACGCCGATGGTACCCTGGCTTGCACCGAGGGTAG 750
    |||
Db 907 CTGATCTGACGGCCCAAGTACTATAACGCCGATGGTACCCTGGCTTGCACCGAGGGTAG 966
    |||
QY 751 GACCAAGGACTGTGGGGGATGTCATCATGTCACAGGACGACATGGCTTTCCTTAAC 810
    |||
Db 967 GACCAAGGACTGTGGGGGATGTCATCATGTCACAGGACGACATGGCTTTCCTTAAC 1026
    |||
QY 811 GTCCAGCCCCGCAAGTACCGTTTCGATTCCTCAACGCTGCCGTGTCTGTGCTTGGCTC 870
    |||
Db 1027 GTCCAGCCCCGCAAGTACCGTTTCGATTCCTCAACGCTGCCGTGTCTGTGCTTGGCTC 1086
    |||
QY 871 CTCTACCTGTGACGACACGCTCTCCCAACGTCAGATTCCTTTCAGTCAATGGCTCT 930
    |||
Db 1087 CTCTACCTGTGACGACACGCTCTCTCCCAACGTCAGATTCCTTTCAGTCAATGGCTCT 1146
    |||
QY 931 GATGCTGGTCTGCTTCAACCCCGCTTGACGCTCTAACCTCTACCTTGTGCGGAG 990
    |||
Db 1147 GATGCTGGTCTGCTTCAACCCCGCTTGACGCTCTAACCTCTACCTTGTGCGGAG 1206
    |||
QY 991 CGTTACGAGATCAATTAAT----- 1008
    |||
Db 1207 CGTTACGAGATCAATTAATGATCCCTCCCTCTCAGCAATGATCAAGAACTTAAGA 1266
    |||
QY 1009 -----GACTTCACCAACTTGTGCTGGCGAGCTCTTGACCTGGCAACGTTGCT 1056
    |||
Db 1267 CTAAACACTTGTAGACTTTCACCAACTTGTGCTGGCGAGACTCTTGACCTGGCAACGTTGCT 1326
    |||
QY 1057 GAGACCAACGATGCGGCGAGCGAGATGATGCTGCGAGCTCTGAGGTGATGCCCTTC 1116
    |||
Db 1327 GAGACCAACGATGCGGCGAGCGAGATGATGCTGCGAGCTCTGAGGTGATGCCCTTC 1386
    |||
QY 1117 GTGCTACGCTTGGCACTGTTAGGACAACAGCAGAGTCCCTCCACTCTCCGTGACGTT 1176
    |||
Db 1387 GTGCTACGCTTGGCACTGTTAGGACAACAGCAGAGTCCCTCCACTCTCCGTGACGTT 1446
    |||
QY 1177 CCTTTCCTCTCTACAGGAGGCCCGCGCAACAGCAGCTTCAAGTTTGAAGCAGCAAC 1236
    |||
Db 1447 CCTTTCCTCTCTACAGGAGGCCCGCGCAACAGCAGCTTCAAGTTTGAAGCAGCAAC 1506
    |||
QY 1237 GGACACTACTGATCAAGATGTTGGCTTGGCGATGTAATGAGGGTCTCTGGGCAAG 1296
    |||
Db 1507 GGACACTACTGATCAAGATGTTGGCTTGGCGATGTAATGAGGGTCTCTGGGCAAG 1566
    |||
QY 1297 CCGGAGCTGGGACCGGTTAGGCTGGAGACTGAGAACTCCTCTGGAGGCTGGAGCCAC 1356
    |||
Db 1567 CCGGAGCTGGGACCGGTTAGGCTGGAGACTGAGAACTCCTCTGGAGGCTGGAGCCAC 1626
    |||
QY 1357 CCGGTCACATTCACCTTGTGACTTCAAGATTCCTCAAGCAGAACTGTGTGCTGGCCAG 1416
    |||

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Db 1627 CCGGTCACATTCACCTTGTGACTTCAAGATCTCAACGCAACTGTGTGTGGCCAG 1686
    |||
QY 1417 GTGATGCCCTTACGAGCTCTGTGCTTAAGATGTCGTGTGGTGGGAGGGGTGAGACC 1476
    |||
Db 1687 GTGATGCCCTTACGAGCTCTGTGCTTAAGATGTCGTGTGGTGGGAGGGGTGAGACC 1746
    |||
QY 1477 CTGACCATGAGGCCCATACCAACCCCTGAGCTGAGCTTACATGTGGCATGTGCACAC 1536
    |||
Db 1747 CTGACCATGAGGCCCATACCAACCCCTGAGCTGAGCTTACATGTGGCATGTGCACAC 1806
    |||
QY 1537 CTGATTCACGAGATTAACATGATGGCTGTATTCAACGTACCGCCATGAGAGGAAG 1596
    |||
Db 1807 CTGATTCACGAGATTAACATGATGGCTGTATTCAACGTACCGCCATGAGAGGAAG 1866
    |||
QY 1597 GGATATCTTCAGAGAGACTCTCGAGGACCCCATGAACCCCAAGTGGGCGCGCTTCCATAC 1656
    |||
Db 1867 GGATATCTTCAGAGAGACTCTCGAGGACCCCATGAACCCCAAGTGGGCGCGCTTCCATAC 1926
    |||
QY 1657 AACCGCAACGACTTCCATGCTCGCGCTGGAACCTTCTCCCGAGTCCATCACTGCCCA 1716
    |||
Db 1927 AACCGCAACGACTTCCATGCTCGCGCTGGAACCTTCTCCCGAGTCCATCACTGCCCA 1986
    |||
QY 1717 GTGCAAGACTGGCGGAGCAGAGACCGCTCAACCGCTTGATGATGATCTGTGAGGATCTT 1776
    |||
Db 1987 GTGCAAGACTGGCGGAGCAGAGACCGCTCAACCGCTTGATGATGATCTGTGAGGATCTT 2046
    |||
QY 1777 GGATGAGAGAGTA 1790
    |||
Db 2047 GGATGAGAGAGTA 2060
    |||

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RESULT 14
AA261243
ID AA261243 standard; DNA; 2110 BP.
XX
AC AA261243:
XX
DT 30-MAY-2000 (first entry)
XX
DE DNA encoding a phenol oxidizing enzyme.
XX
KW Phenol oxidizing enzyme; fungus; redox reaction; detergent; bleaching;
KW fabric; pulp; paper; decolourisation; plant-derived food product;
KW coloured compound; porphyrin; tannin; polyphenol; carotenoid;
KW anthocyanin; Maillard reaction product; ss.
XX
OS Acremonium murorum.
XX
FH Key
FH CDS Location/Qualifiers
FT /tag= a
FT /product= "phenol oxidizing enzyme"
XX
PN WO200005349-A1.
XX
PD 03-FEB-2000.
XX
PF 13-JUL-1999; 99WO-EP04922.
XX
PR 21-JUL-1998; 98EP-0202454.
XX
PA (UNILE ) UNILEVER NV.
PA (UNILE ) UNILEVER PLC.
PA (HIND-) HINDUSTAN LEYER LTD.
XX
PI Convents D, Gouka RJ, Van Der Heiden M, Swarthoff T, Verrips CT;
XX
DR WPI: 2000-195101/17.
XX
P-PsDB: AAY69204.
XX
PT Phenol-oxidizing enzyme from Acremonium, used in detergent compositions
PT for bleaching stains on fabrics -

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```
PT      /*tag= a
FT      /product= BO
FT      slg_peptide
FT      66..179
FT      /*tag= b
FT      mat_peptide
FT      180..1781
FT      /*tag= c
PN      JP05199882-A.
XX      10-AUG-1993.
PD      24-JAN-1992; 92JP-0034126.
XX      24-JAN-1992; 92JP-0034126.
PR      24-JAN-1992; 92JP-0034126.
XX      (AMANO ) AMANO PHARM KK.
PA      WPI: 1993-284681/36.
DR      P-PSDB; AAR40843.
XX      Biliirubin oxidase prepn. useful as an analytical enzyme - by
PT      culturing biliirubin oxidase in transformant culture
XX      Claim 1; Page 29-32; 32pp; Japanese.
XX      The sequence encodes biliirubin oxidase. The protein produced has a
CC      38 amino acid signal peptide which is removed to give the mature
CC      protein (AAR40843).
XX      Sequence 1959 BP; 457 A; 549 C; 436 G; 517 T; 0 other:
SQ
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Query Match          32.0%; Score 573.2; DB 14; Length 1959;
Best Local Similarity 62.1%; Pred. No. 1e-143;
Matches 972; Conservative 0; Mismatches 581; Indels 12; Gaps 4;
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```
OY      206 CCCTGCCATTCACCTGCAAGCAGCCAGATGATCTTTACCAACCTGTACCCGGA 265
DB      220 CACTCCCAATTCCTCTTAAGCAGCCCGCTTGACTGTACCAATCTGTGAATGGAC 279
OY      266 AGCAATTTGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 325
DB      280 AAGAGATCTGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 339
OY      326 TGCAGCCCTGCCATCTCTGCGGCTACGATGCGATGAGCCCTGCTCTTCAATGTTTC 385
DB      340 TTGATTCGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 399
OY      386 CCAGAGGAAACAGAGCTGTAGTTAGTTATCAACATGCCACCGTGGAGAACTGGTTC 445
DB      400 CTCGTGAGGATTTGAACACAGTTGTCGCGCTTCAATTAACATGCTGAGGCTCCTTACTCCGTTTC 459
OY      446 ATCTGACGAGCTCCCATGCGGCTGCGCCCTTTGATGGTTGGGCTGAAGATGACCTTCC 505
DB      460 ACCTGACGAGATCTTCTCTGTCGCGCTTTGACGGATGGGCAAGGCAATCACCGAGC 519
OY      506 CTGGGAGTACAGAGTAACTACTTTCACCACTACCAATCCGCCGCTTCTGTGGTAC 565
DB      520 CTGGGAGCTTCAAAAGCTATTAACCAATTAAGCAAGCTGCTGTACCAATGCTGATAC 579
OY      566 ATGACCAAGCTTTTCAATGAAGCTGCTGAGATGCTTCTTGTGGTGGGCTGAGCCTTACA 625
DB      580 ACGATGATGCTATGATATCACTGCTGAGAAAGCTTACCGTGGGCTGGTGGTCTTACA 639
OY      626 TTATCAAGACGAGGCTGAGATGCTCTGCTGCTCTGATGGCTTGGCGAGTTGATGATA 685
DB      640 TCTCTCACTACCCAGCGAAGAGCTCTCACTTGGCAAGTGAATGAGCGAGTTGATA 699
OY      686 TTCCTCTGATCTGAGCGGCAAGTACTATACGCCGATGTAACCTGCTTGCAGCGAG 745
DB      700 TTCGATGATCTCTCAAGCTGCAAGCAATATACCGCAAGCGCAACTTGGTACCACTAATG 759
OY      746 GTGAGGACCAAGACCTGTGGGAGATGTATCATCGATGTCACGACGACGCAATGGCCTTTCC 805
DB      760 GAGAGCTCACTCATTTCTGGGGTGTATGTAATTCAGGTGACGCGTCAACCCGTGGCCTTTCA 819
OY      806 TTAACGTCCAGCCCGCAAGTACCGCTTTCGATTCCTCAAGCGTCCGTGTCTGCTT 865
DB      820 AAGAGCTTGAGCCTCGCAAAATATCGATTCCGCTTCTCGATGCGCGACATTCCTGCTCTT 879
OY      866 GGCTCTTACCTGCTGACGAGACAGCTCTCCCAACGTGAATTCCTTTCCAACTCATTTG 925
DB      880 TCGGCTTTACTTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 939
OY      926 CTTGTGATGCTGCTCTCTTCAAGCCCGCTTCAGACCTCTCAACCTTACCTTGTGTTG 985
DB      940 CTTCCGATTTCTGCTTCTTCAAGACCTCTCCGATACCAAGCTGCTGTATCTTCAATGG 999
OY      986 CCGAGCGTTACAGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1045
DB      1000 CCGAGCGTTACAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1059
OY      1046 GCACGTTGCTGAGACCAACGATG---TGGGAGAGAGATGATGATGATGATGATGATGATG 1102
DB      1060 GCACCTGGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1119
OY      1103 AGGTATGGGCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1159
DB      1120 AGGTATGGGCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1179
OY      1160 CCATCTCTGCTGAGACCTCTCTTCCCTCTCAACAGAGAGGCGCGCAACAGCACTTCA 1219
DB      1180 CTAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1236
OY      1220 AGTTGAACGACGACCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1279
DB      1237 GCTTTGGTGCACCCGCTCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATG 1296
OY      1280 ACCGTGCTGGCGCAAGCCGAGCGGACGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1339
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OY      1340 CTGAGGCTGAGGACCAACCCGCTCAACATTCACCTGTTGACTTCAAGATCTCAAGCGAA 1399
DB      1357 GTAAAGCTTGGAGGACCAACCCGCTCAACATTCACCTGTTGACTTCAAGATCTCAAGCGAA 1416
OY      1400 CTGTGTGCTGAGGACCAACCCGCTCAACATTCACCTGTTGACTTCAAGATCTCAAGCGAA 1456
DB      1417 CTTCGCGGCAACCAACCCGCTCAACATTCACCTGTTGACTTCAAGATCTCAAGCGAA 1476
OY      1457 GGTGGGCAAGGCTGAGGACCAACCCGCTCAACATTCACCTGTTGACTTCAAGATCTCAAGCGAA 1516
DB      1477 GGTGGGCAAGGCTGAGGACCAACCCGCTCAACATTCACCTGTTGACTTCAAGATCTCAAGCGAA 1536
OY      1517 ACATGTGACCTGTCAACATTCACGAGATTAACGATTAACGATTAACGATTAACGATTAACG 1576
DB      1537 ACATGTGACCTGTCAACATTCACGAGATTAACGATTAACGATTAACGATTAACGATTAACG 1596
OY      1577 TCACGCCATGAGGAGAGAGATTCCTCAGAGAGCTTGGAGAGCCATGAAACCCCA 1636
DB      1597 CCACGCTCTGCGAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 1656
OY      1637 AGTGGCGGCGCTTCTTCAACCCGATTAACGATTAACGATTAACGATTAACGATTAACG 1696
DB      1657 TTTGGAGGCTGCTCTTCAACCCGATTAACGATTAACGATTAACGATTAACGATTAACG 1716
OY      1697 CCGAGTTCATCACTGCGCGAGTGAAGAGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1756
DB      1717 TTTAGAGCTTACTAGAGCTTATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAG 1776
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	503.4	28.1	2905	4	US-09-468-578-3
7	502.8	28.1	2063	4	US-09-468-578-6
8	460.4	25.7	1958	4	US-09-401-476-1
9	460.4	25.7	2095	4	US-09-401-476-3
10	188.6	10.5	858	4	US-09-468-578-8
11	54.6	3.0	7218	1	US-08-232-463-14
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13	45.8	2.6	6441	4	US-08-669-785-1
14	45.8	2.6	6443	6	5183745-5
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23	42.6	2.4	5567	4	US-09-535-008-64
24	42.6	2.4	5576	4	US-09-535-008-72
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	29	38.8	2.2	4108	4	US-08-981-729-8	Sequence 8, Appl
	30	38.8	2.2	4108	4	US-08-981-729-8	Sequence 1, Appl
	31	38.6	2.2	686	4	US-08-998-416-715	Sequence 715, App
C	32	38.2	2.1	4403765	4	US-09-103-840A-2	Sequence 2, Appl
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	37	36.4	2.0	2923	1	US-08-243-542-6	Sequence 6, Appl
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C	39	36.4	2.0	2923	1	US-08-484-355-6	Sequence 6, Appl
C	40	36.4	2.0	44377	2	US-08-804-227C-7	Sequence 7, Appl
C	41	36.4	2.0	44377	2	US-08-804-198-1	Sequence 1, Appl
C	42	35.6	2.0	49372	1	US-08-614-770A-1	Sequence 1, Appl
	43	35.4	2.0	3468	1	US-07-951-715A-2	Sequence 2, Appl
	44	35.4	2.0	3468	1	US-07-951-715A-4	Sequence 4, Appl
	45	35.4	2.0	3468	2	US-08-459-448A-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-468-578-5
: Sequence 5, Application US/09468578
: Patent No. 6399329
: GENERAL INFORMATION:
: APPLICANT: Wang, Huaming
: APPLICANT: Bodie, Elizabeth A.
: TITLE OF INVENTION: Phenol Oxidizing Enzymes
: FILE REFERENCE: GC561-3
: CURRENT APPLICATION NUMBER: US/09/468,578
: CURRENT FILING DATE: 1999-12-21
: PRIOR APPLICATION NUMBER: US 09/220,871
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: US 09/338,723
: PRIOR FILING DATE: 1999-06-23
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 1791
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: cDNA
US-09-468-578-5

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Best Local Similarity 100.0%: Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTCAATATGCTGTTCAAGTATGACAACTGGCAGCAGCCCTCCGGCTCTGTCGAGTC 60
    |||||||

QY 61 CTCGGCATCCCGATGACACCGGACCGACCCATTGAGAGCTGTATCCCAAGTGAAG 120
    |||||||
DB 61 CTCGGCATCCCGATGACACCGGACCGACCCATTGAGAGCTGTATCCCAAGTGAAG 120
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QY 121 ACTGAGAGTCTGCTGACACCTCCCTTGGCTGACAGCGAGGATGACAGTGGAGTACCT 180
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DB 121 ACTGAGAGTCTGCTGACACCTCCCTTGGCTGACAGCGAGGATGACAGTGGAGTACCT 180
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QY 181 CCATTAACCTTGGCTTACAGGAATGCCCTGCCAATTCCACCTGTCAAGCAGCCCAAGATG 240
    |||||||
DB 181 CCATTAACCTTGGCTTACAGGAATGCCCTGCCAATTCCACCTGTCAAGCAGCCCAAGATG 240
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QY 241 ATCATTAACCAACCTGTACACCGGACGAGCATTTGGTACTATGAGATGATCAAGATCAAGCA 300
    |||||||
DB 241 ATCATTAACCAACCTGTACACCGGACGAGCATTTGGTACTATGAGATGATCAAGATCAAGCA 300
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QY 301 TTTCAGCAAGATTTACCCACCTTGGCCCTGACACTCTGCTGCTGAGTACATGATGATG 360
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Db	361	AGCCCTGGTCTACTTTTCAATGTTCCAGAGAACGAGACTGTAGTTAGTTCAATCAAC	420
Qy	421	AATGCAACCGGGAGACTGGGTCGACATCTGCACAGGGTCCCATCGCGCCCTTTCGAT	480
Db	421	AATGCAACCGGGAGAACTGGTCGACATCTGCACAGGGTCCCATCGCGCCCTTTCGAT	480
Qy	481	GGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTACTTTCCAACTAC	540
Db	481	GGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTACTTTCCAACTAC	540
Qy	541	CAATCCGCGCCCTTCTGTGGTACCATGACACGCTTTATGAAGCTGTGAGATGCC	600
Db	541	CAATCCGCGCCCTTCTGTGGTACCATGACACGCTTTATGAAGCTGTGAGATGCC	600
Qy	601	TACTTTGGTCAGGCTGGCCGCTCAATTATCAAGAGAGGCTGAGATGCTCGACTTT	660
Db	601	TACTTTGGTCAGGCTGGCCGCTCAATTATCAAGAGAGGCTGAGATGCTCGACTTT	660
Qy	661	CCTAGTGACTATGGCGAGTTTCGATATTCCTCTGATCTGAGSGCCAACTATATAAGCC	720
Db	661	CCTAGTGACTATGGCGAGTTTCGATATTCCTCTGATCTGAGSGCCAACTATATAAGCC	720
Qy	721	GATGGTACCCTGGCTTGCAGCGAGGGGAGAGACAGACCTGGGGGAGATGTCATCAT	780
Db	721	GATGGTACCCTGGCTTGCAGCGAGGGGAGAGACAGACCTGGGGGAGATGTCATCAT	780
Qy	781	GTCAAAGCAGACCATAGCCCTTTCCTTAACTGTCACACCCCGCAAGTACCCTTCCGATT	840
Db	781	GTCAAAGCAGACCATAGCCCTTTCCTTAACTGTCACACCCCGCAAGTACCCTTCCGATT	840
Qy	841	CTCAACGCTGCCGCTGTCTGCTGGCTCTTACCTGTGAGACACAGCTCTCCCAAC	900
Db	841	CTCAACGCTGCCGCTGTCTGCTGGCTCTTACCTGTGAGACACAGCTCTCCCAAC	900
Qy	901	GTCAGAAATCCCTTTCCAAGCATTTGGCCTCGATGCTGCTCCCTTCAAGCCCCGCTTAG	960
Db	901	GTCAGAAATCCCTTTCCAAGCATTTGGCCTCGATGCTGCTCCCTTCAAGCCCCGCTTAG	960
Qy	961	ACCTCTAACCCTCTACTTTCCTGCTGGTGGCGAGCCTTACGAAATATTATTGACTTCAACAC	1020
Db	961	ACCTCTAACCCTCTACTTTCCTGCTGGTGGCGAGCCTTACGAAATATTATTGACTTCAACAC	1020
Qy	1021	TTTTGTGGCCAGACTTCTTGACTGCTGGCAACGTTGGTGAGACCAAGATGTGGCGCAGAG	1080
Db	1021	TTTTGTGGCCAGACTTCTTGACTGCTGGCAACGTTGGTGAGACCAAGATGTGGCGCAGAG	1080
Qy	1081	GATGAGTACGCTCGACTCTGAGAGTGATGCCGTTGCTGTCAGCTTGGCACTGTTGAG	1140
Db	1081	GATGAGTACGCTCGACTCTGAGAGTGATGCCGTTGCTGTCAGCTTGGCACTGTTGAG	1140
Qy	1141	GACAACAGCCAGGTCCTCCACTCTCCGAGAGTTCTTTCCTCTCACAAGAAAGGC	1200
Db	1141	GACAACAGCCAGGTCCTCCACTCTCCGAGAGTTCTTTCCTCTCACAAGAAAGGC	1200
Qy	1201	CCCGCCGACAGACTTTCAGTTTGAACGAGCAAGGACACTTACTGTATCAACATGTT	1260
Db	1201	CCCGCCGACAGACTTTCAGTTTGAACGAGCAAGGACACTTACTGTATCAACATGTT	1260
Qy	1261	GGCTTTGGCCGATGTCAATGAGCGTGTCTGGCCAAACCCGAGACTCGGCGACCTTGAGGTTC	1320
Db	1261	GGCTTTGGCCGATGTCAATGAGCGTGTCTGGCCAAACCCGAGACTCGGCGACCTTGAGGTTC	1320
Qy	1321	TGGGAGCTCGAAGCTCCTCGGAGGGCTGGAGCACCCGCTACAAATTCACCTTGTAGAC	1380
Db	1321	TGGGAGCTCGAAGCTCCTCGGAGGGCTGGAGCACCCGCTACAAATTCACCTTGTAGAC	1380
Qy	1381	TTCAAGATCCCAAGCAGACTGTGTGTCTGTGGCGAGGTATGACCTTACGAGTCTCTGCT	1440

DB	1381	TTCAAGATCCTTCAACGAACTGGTGGTGGCCAGGTATCCCTACGAGTCTCTGGT	1440
QY	1441	CTTAAAGATGTCGTCTGTTGGGCAAGGGGTGAGACCCCTGACATGAGGCCACTACCAA	1500
DB	1441	CTTAAAGATGTCGTCTGTTGGGCAAGGGGTGAGACCCCTGACATGAGGCCACTACCAA	1500
QY	1501	CCCTGAGCTGGAGCTTACCTGTGGCACTGTCAACCTCATTCACAGAGATTAACGACATG	1560
DB	1501	CCCTGAGCTGGAGCTTACCTGTGGCACTGTCAACCTCATTCACAGAGATTAACGACATG	1560
QY	1561	ATGGCTGTAATTCACGTCACCGCATGAGAGAAAGGATATCTTCAGAGAGACTTTCGAG	1620
DB	1561	ATGGCTGTAATTCACGTCACCGCATGAGAGAAAGGATATCTTCAGAGAGACTTTCGAG	1620
QY	1621	GACCCCATTAACCCCAAGTGGGGCCGCTCTTCTTACAAACCGCAAGCACTTCCATCTGCC	1680
DB	1621	GACCCCATTAACCCCAAGTGGGGCCGCTCTTCTTACAAACCGCAAGCACTTCCATCTGCC	1680
QY	1681	GCTGGAACCTTCTCGGCGCAGTCCATCATGTGCCCGAGTGCAGAGCTGGCCGACAGAG	1740
DB	1681	GCTGGAACCTTCTCGGCGCAGTCCATCATGTGCCCGAGTGCAGAGCTGGCCGACAGAG	1740
QY	1741	CCGTACACCGCCTCGATGAGATCCTGGAGAGATCTTGGATATGAGAGACTAA	1791
DB	1741	CCGTACACCGCCTCGATGAGATCCTGGAGAGATCTTGGATATGAGAGACTAA	1791
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; Patent No. 6426410			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Huang			
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes			
; FILE REFERENCE: GC567			
; CURRENT APPLICATION NUMBER: US/09/218,702			
; CURRENT FILING DATE: 1998-12-22			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO: 1			
; LENGTH: 1791			
; TYPE: DNA			
; ORGANISM: Stachybotrys sp.			
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DB	61	CTCGGATCCGATGGACACGCGGACGCCACCCCATTTGAGGCTGTTGATCCGAAGTGAAG	120
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DB	121	ACTGAGGTCCTGCTGACTCCTCTCTGCTGGAGCAGGGGATGAGACTGGAGTACCT	180
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DB	181	GCATCAACTGCTTTACAGGAATGCCCTGCCAATTCACACCTGTCAAGAGCCCAAGAG	240
QY	241	ATCATATACCAACCTGTCTACCGGCAAGACATTTGGTATATGAGTCAAGTCAAGCA	300
DB	241	ATCATATACCAACCTGTCTACCGGCAAGACATTTGGTATATGAGTCAAGTCAAGCA	300
QY	301	TTTTCAGCAAGATTTTACCCCACTTGGCCCTGCCACTCTCTGTCGGCTAGCATGGCATG	360
DB	301	TTTTCAGCAAGATTTTACCCCACTTGGCCCTGCCACTCTCTGTCGGCTAGCATGGCATG	360

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Db	421	AATGCACACGGGGAGAACCTGGTGCATGTCGACAGGGCTGCCATGCGGGCCCCCTTGAT	480
OY	481	GGTTGGGCTGAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTACTTTCACATAC	540
Db	481	GGTTGGGCTGAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTACTTTCACATAC	540
OY	541	CAATCCGCGCGCTTCTGTGTGATGACATGACACGCTTCTATGAGACTGTGAGATGCC	600
Db	541	CAATCCGCGCGCTTCTGTGTGATGACATGACACGCTTCTATGAGACTGTGAGATGCC	600
OY	601	TACTTTGGTCAGGCTGGCGCTACATTATCAAGACGAGGCTGAGGATGCTCGCTT	660
Db	601	TACTTTGGTCAGGCTGGCGCTACATTATCAAGACGAGGCTGAGGATGCTCGCTT	660
OY	661	CCCTGAGGCTATGGCGAGTTCGATATCCCTGTGATCCTGACGGCCAAAGTATTAAGCC	720
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OY	721	GATGGTACCCCTGGCTTGACCGAGGGTGAGAGACAGACTGTGGGGAGATGTATCCAT	780
Db	721	GATGGTACCCCTGGCTTGACCGAGGGTGAGAGACAGACTGTGGGGAGATGTATCCAT	780
OY	781	GTCACAGGACAGACGCACTGCGCTTTCCTTAACGTGCACGCCCGCAATACCGTTCCGATTC	840
Db	781	GTCACAGGACAGACGCACTGCGCTTTCCTTAACGTGCACGCCCGCAATACCGTTCCGATTC	840
OY	841	CTCAACGCTGCGGTGTCTCGTCTGGGCTGCTCTACTGTGAGAGACAGCTCTCCAC	900
Db	841	CTCAACGCTGCGGTGTCTCGTCTGGGCTGCTCTACTGTGAGAGACAGCTCTCCAC	900
OY	901	GTCGAATTCCTTTCGAATGATTCGCTGTGATGCTGTCTCTCAAGCCCCCGTTCAG	960
Db	901	GTCGAATTCCTTTCGAATGATTCGCTGTGATGCTGTCTCTCAAGCCCCCGTTCAG	960
OY	961	ACCTCTAACCTTACCTTGTGCTGTGGCGAGCGTTACGAGATATTATGACTTCAACAC	1020
Db	961	ACCTCTAACCTTACCTTGTGCTGTGGCGAGCGTTACGAGATATTATGACTTCAACAC	1020
OY	1021	TTTCTGTGGCAGACTCTTGACCTGCGCACAAGTGTGAGAACCAAGATGTGGCGACAG	1080
Db	1021	TTTCTGTGGCAGACTCTTGACCTGCGCACAAGTGTGAGAACCAAGATGTGGCGACAG	1080
OY	1081	GATGAGTAGCTGTGCACTCTGAGAGTGATGCGCTTGTGTCAGCTGTGGCACTGTGGAG	1140
Db	1081	GATGAGTAGCTGTGCACTCTGAGAGTGATGCGCTTGTGTCAGCTGTGGCACTGTGGAG	1140
OY	1141	GACAAACGCCAGGTCCCTTCACATCTCCGTGACGTTCTTCCCTCTCACAGAGAGGC	1200
Db	1141	GACAAACGCCAGGTCCCTTCACATCTCCGTGACGTTCTTCCCTCTCACAGAGAGGC	1200
OY	1201	CCCGCCACAAGCACTTCAAGTTTGAACGACAGAACGAGACTACTCTGATCAAGATTT	1260
Db	1201	CCCGCCACAAGCACTTCAAGTTTGAACGAGCAGCAGCACTACTCTGATCAAGATTT	1260
OY	1261	GGCTTTGCCATGTCAATGAGCGGTGTCGAGCCAGACCCCGTCAACATTCACCTGTGTCAC	1320
Db	1261	GGCTTTGCCATGTCAATGAGCGGTGTCGAGCCAGACCCCGTCAACATTCACCTGTGTCAC	1320
OY	1321	TGGGAGCTCGAGAACTCTCTGTGAGGCTGAGAGCAACCCCGTCAACATTCACCTGTGTCAC	1380
Db	1321	TGGGAGCTCGAGAACTCTCTGTGAGGCTGAGAGCAACCCCGTCAACATTCACCTGTGTCAC	1380
OY	1381	TTTCAAGATTCCTCAAGCGCAACTGTGGTTCGAGGCGAGGCTCATGCCCTACGAGATCTGCTGCT	1440
Db	1381	TTTCAAGATTCCTCAAGCGCAACTGTGGTTCGAGGCGAGGCTCATGCCCTACGAGATCTGCTGCT	1440
OY	1441	CTTAAAGATGTCTGTGGTTGGGACAGGGGTGAGACCTGAGACCATGAGAGCCCATCTACCA	1500

Accession	Sequence	Length
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Dp 1501	CCCTGGAAGTGGAGTTCATGATGTGGCACTGTGCACAACTTATTCACGAGGATTAACGACATG	1560
Qy 1561	ATGCGCTGATTCAACGTCACCCGCCATGGAGAGAGAGATATCTTCAGAGAGACTTCCAG	1620
Dp 1561	ATGCGCTGATTCAACGTCACCCGCCATGGAGAGAGAGATATCTTCAGAGAGACTTCCAG	1620
Qy 1621	GACCCCATGAACCCCAAGTGGCGCGCGCTTCCTTACAAACGGACAGCTTCATCTCTGC	1680
Dp 1621	GACCCCATGAACCCCAAGTGGCGCGCGCTTCCTTACAAACGGACAGCTTCATCTCTGC	1680
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Dp 1741	CCGTACAAACCCCTTCATGAGATCTCTGGAGAGATCTTGGGAATCGAGAGATAA	1791

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1 RESULT 3
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3 ; Sequence 1, Application US/09468578
4 ; Patent No. 6399329
5 ; GENERAL INFORMATION:
6 ;
7 ; APPLICANT: Wang, Huming
8 ;
9 ; APPLICANT: Bodie, Elizabeth A.
10 ;
11 ; TITLE OF INVENTION: Phenol Oxidizing Enzy
12 ;
13 ; FILE REFERENCE: GC561-3
14 ;
15 ; CURRENT APPLICATION NUMBER: US/09/468, 578
16 ;
17 ; CURRENT FILING DATE: 1999-12-21
18 ;
19 ; PRIOR APPLICATION NUMBER: US 09/220, 871
20 ;
21 ; PRIOR FILING DATE: 1998-12-23
22 ;
23 ; PRIOR APPLICATION NUMBER: US 09/338, 723
24 ;
25 ; PRIOR FILING DATE: 1999-06-23
26 ;
27 ; SOFTWARE: FastSeq for Windows Version 4.0.
28 ;
29 ; SEQ ID NO 1
30 ;
31 ; LENGTH: 3677
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33 ; TYPE: DNA
34 ;
35 ; ORGANISM: Stachybotrys chartarum
36 ;
37 ; US-09-468-578-1

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Query Match	82.3%	Score 1474;	DB 4;	Length 3677;
Best Local Similarity	87.08;	Pred. No. 0;		
Matches 1791; Conservative	0;	Mismatches	0;	Indels 267; Gaps 5;

Qy	1	GTCAATATGCTGTTCAAGTACTATGGCAACTGGCACACCTCCGGGCTCTGTCTGAGTGC	60
Db	1038	GTCAATATGCTGTTCAAGTACTATGGCAACTGGCACACCTCCGGGCTCTGTCTGAGTGC	1099
Qy	61	CTCGCATCCCGATGGAGACACGGCAGCCACCCATTAGAGCTGTGTATCCCGAAGTGAAG	120
Db	1098	CTCGCATCCCGATGGAGACACGGCAGCCACCCATTAGAGCTGTGTATCCCGAAGTGAAG	1155
Qy	121	ACTGAGCTCTTCGCTGACCTCCCTCTTCGTCAGACAGGCGATGACGACTGGAGTCACT	180
Db	1158	ACTGAGCTCTTCGCTGACCTCCCTCTTCGTCAGACAGGCGATGACGACTGGAGTCACT	121
Qy	181	CCATACCACTTCGCTTAC-----	198
Db	1218	CCATACCACTTCGCTTACAGGTGAGACACCTGTCCTCCACTGTTTTCCCTCGATAACTAAC	127
Qy	199	-----AGCAATGCCCTGCGCAATATCCACCTGTGCAAGGACGCCAAGAT-----	239
Db	1278	TCTTATAGGAATGCCCTGCGCAATATCCACCTGTGCAAGGACGCCAAGATGTATGCTTTGAT	133
Qy	240	-----GATCATTTACCAACCTGTGCAC-----	260

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Db 1338 TTTTACGAGCAACTCGGCCCCGAGCTAATGTATCTAGAGATCATACCAACCTGTCAC 1397
Oy 261 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTCAGCAAG----- 311
Db 1398 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTCAGCAAGAGGTGAGTTT 1457
Oy 312 -----GATTTACCCACCTT 326
Db 1458 GCTCAGAAACCTTGTGTATTAATCATTTGTTACTGACCCCTTTCAGATTTTACCCACCTT 1517
Oy 327 GGGCCCTGGCAGCTCTGCTGGGCTAGCATGAGCATAGCCCTGGCTTCTTCAATTTTCC 386
Db 1518 GGGCCCTGGCAGCTCTGCTGGCTAGCATGAGCATAGCCCTGGCTTCTTCAATTTTCC 1577
Oy 387 CAGAGGAAAGAGACTGTAGTTAGTTCAACAATGCGCCGCTGAGAGAACCTGCTCA 446
Db 1578 CAGAGGAAAGAGACTGTAGTTAGTTCAACAATGCGCCGCTGAGAGAACCTGCTCA 1637
Oy 447 TCTGCAGGCTCCCATCGCGTGCCTCTTTCGATGTTGGGCTGAAGATGTGACCTTCCC 506
Db 1638 TCTGCAGGCTCCCATCGCGTGCCTCTTTCGATGTTGGGCTGAAGATGTGACCTTCCC 1697
Oy 507 TGGCGGATCAAGGATTAATCTTCCCAACTACCAATCGCCGCTTCTGTGATGACA 566
Db 1698 TGGCGGATCAAGGATTAATCTTCCCAACTACCAATCGCCGCTTCTGTGATGACA 1757
Oy 567 TGACCAAGCTTTCATGA----- 583
Db 1758 TGACCAAGCTTTCATGAATGATGCTACGAGCCTTATCTTTCTTGGCTACCTTTGGCTA 1817
Oy 584 -----AGACTGCTGAGAAATGCCCTACTTTGGTCAAGCTTGGCCCTTACATTT 627
Db 1818 ACCAACTTCTTTCGATGACTGCTGAGAAATGCCCTACTTTGGTCAAGCTTGGCCCTTACATTT 1877
Oy 628 ATCAACGAGAGAGCTGAGATGCTCGGCTCTCTAGTGGCTATGGCGAGTTGATTC 687
Db 1878 ATCAACGAGAGAGCTGAGATGCTCGGCTCTCTAGTGGCTATGGCGAGTTGATTC 1937
Oy 688 CCTGTGATCTTGAAGGCAAGTACTATAACGCCGATGATACCTTGGCTTGCAGCGAGGT 747
Db 1938 CCTGTGATCTTGAAGGCAAGTACTATAACGCCGATGATACCTTGGCTTGCAGCGAGGT 1997
Oy 748 GAGAGACGAGACTGTGGGAGATGTATCATCATGTCAACGGAGACCATGGCTTTCTT 807
Db 1998 GAGAGACGAGACTGTGGGAGATGTATCATCATGTCAACGGAGACCATGGCTTTCTT 2057
Oy 808 AAGCTCAGCCCCGCAAGTACGTTCCGATTCCTCAACGGCTGCGTGTGCTGG 867
Db 2058 AAGCTCAGCCCCGCAAGTACGTTCCGATTCCTCAACGGCTGCGTGTGCTGG 2117
Oy 868 CTCCTCTACCTGCTCAGACCAAGCTCTCCCAACGTCAGAAATTCCTTCCAAAGTCATTTGCC 927
Db 2118 CTCCTCTACCTGCTCAGACCAAGCTCTCCCAACGTCAGAAATTCCTTCCAAAGTCATTTGCC 2177
Oy 928 TCTGATGCTGTCTCTTCAAGCCCCGTTTCAAGCTCTTAACCTTAACCTTGTGTGCC 987
Db 2178 TCTGATGCTGTCTCTTCAAGCCCCGTTTCAAGCTCTTAACCTTAACCTTGTGTGCC 2237
Oy 988 GAGCGTTAGAGATCATTAAT----- 1008
Db 2238 GAGCGTTAGAGATCATTAATGTTATGCTTATGCCCTCCCTCTCAGCAAGATGTCAGAACTCTA 2297
Oy 1009 -----GACTTCACCACTTTGCTGGCCAGACTTTGACCTGCGCAACGTT 1053
Db 2298 AGACTAACACTTGTATACCTTTCACCACTTTGCTGGCCAGACTTTTACCTGCGCAACGTT 2357
Oy 1054 GCTGAGACCAAGATGTGCGCGACGAGATGATGATGCTGCGACTCTCGAGGTGATGCGC 1113
Db 2358 GCTGAGACCAAGATGTGCGCGACGAGATGATGATGCTGCGACTCTCGAGGTGATGCGC 2417
Oy 1114 TTGCTGTGAGCTGTGGCACTGTTGAGGACAAACAGCAGAGTCCCTCCACTCCCTGAGC 1173
Db 2418 TTGCTGTGAGCTGTGGCACTGTTGAGGACAAACAGCAGAGTCCCTCCACTCCCTGAGC 2477
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Oy 1174 GTTCTTTTCCCTCTTCCACAAAGGAGGCCGCCGACAAACACTTCAAGTTTGAAGCCAGC 1233
Db 2478 GTTCTTTTCCCTCTTCCACAAAGGAGGCCGCCGACAAACACTTCAAGTTTGAAGCCAGC 2537
Oy 1234 AACGACACTTACCTGATFCAACGATGTTGGCTTTGCCGATGTCAATAGAGTGTCCTGCC 1293
Db 2538 AACGACACTTACCTGATFCAACGATGTTGGCTTTGCCGATGTCAATAGAGTGTCCTGCC 2597
Oy 1294 AAGCCCGAGCTGGCGCCGCTTGAAGTCTGAGAGCTCGAAGACTCCTCTGAGGCTGGAGC 1353
Db 2598 AAGCCCGAGCTGGCGCCGCTTGAAGTCTGAGAGCTCGAAGACTCCTCTGAGGCTGGAGC 2657
Oy 1354 CACCCCGTCACATTCACCTTGTGACTTTCAGATCCTCAAGGAACTGTGTGCTGGCC 1413
Db 2658 CACCCCGTCACATTCACCTTGTGACTTTCAGATCCTCAAGGAACTGTGTGCTGGCC 2717
Oy 1414 CAGGTATGCCCTACGAGTCTGTGTTAAGATGTGTCTGTGTTGGGAGAGGCTGAG 1473
Db 2718 CAGGTATGCCCTACGAGTCTGTGTTAAGATGTGTCTGTGTTGGGAGAGGCTGAG 2777
Oy 1474 ACCCTGACCATGAGGCCCACTACCAACCTGGACTGAGACTTACATGTGGCACTGTAC 1533
Db 2778 ACCCTGACCATGAGGCCCACTACCAACCTGGACTGAGACTTACATGTGGCACTGTAC 2837
Oy 1534 AACCTTATTCAGAGGATTAACGACATGATGCTGTATTCACGTACCGCCATGAGAGAG 1593
Db 2838 AACCTTATTCAGAGGATTAACGACATGATGCTGTATTCACGTACCGCCATGAGAGAG 2897
Oy 1594 AAGGATATCTTCAGAGAGACTTCGAGAGACCCCATATAACCCCAAGTGGGCGCCCTTCT 1653
Db 2898 AAGGATATCTTCAGAGAGACTTCGAGAGACCCCATATAACCCCAAGTGGGCGCCCTTCT 2957
Oy 1654 TACAACCGCAAGACTTTCATGCTCGCGTGAACCTTCTCGCGAGTCCATCACTGCGC 1713
Db 2958 TACAACCGCAAGACTTTCATGCTCGCGTGAACCTTCTCGCGAGTCCATCACTGCGC 3017
Oy 1714 CGAGTCCAGAGCTGGCCGAGAGAGCCGTACAAACCGCTCGATGATGATCTGAGAGAT 1773
Db 3018 CGAGTCCAGAGCTGGCCGAGAGAGCCGTACAAACCGCTCGATGATGATCTGAGAGAT 3077
Oy 1774 CTTGGAATGAGAGATTA 1791
Db 3078 CTTGGAATGAGAGATTA 3095

RESULT 4
US-09-218-702-3
; Sequence 3, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el phenol oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-218-702-3

Query Match 82.3%: Score 1474; DB 4; Length 3677;
Best Local Similarity 87.0%: Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

Oy 1 GTCATATATGCTGTTCAAGTCATGGAAGTGGCAGAGCTCCGGGCTCCTGTCTGAGATC 60
Db 1038 GTCATATATGCTGTTCAAGTCATGGAAGTGGCAGAGCTCCGGGCTCCTGTCTGAGATC 1097
Oy 61 CTCGGCATCCCGATGAGAACCGGCGACCAACCCCATTTGAGGCTGTGTGATCCCGAAGTGAAG 120
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Db	1098	CTCGGCAATCCGGATGGACACCGGACGCCACCCATTGAGCGTGTGATCCGAACTGAAG	1157
Qy	121	ACTGAGGTCTTCGCTGACCTCCCTCTTGGCTGCAGCAGGGGATAGACACTGGGAGTACCT	180
Db	1158	ACTGAGGCTCTTCGGTGACTCCCTCCCTTGGCTGCAGCAGGGGATAGACACTGGGAGTACCT	1217
Qy	181	CCATACCACTTGCTTAC-----	198
Db	1218	CCATACCACTTGCTTACAGGTGAGACACTGTGCCACCTGTTCCTCCGTAACTAAC	1277
Qy	139	-----AGGAATGCCCGGCAATTCACCGTCCCAACGACCCCAAGT-----	239
Db	1278	TCCTTATGGAATGCCCTGCCAATTCACCGTCCCAACGACCCCAAGTGTATGTCTTGTAT	1337
Qy	240	-----GATCATTCACCAACCTGTGAC	260
Db	1338	TTTTCAGGAAGCAACTGCGGCCCGGACATAATGTATTTCTAGATCATATTACCAACCTGTGAC	1397
Qy	261	CGGCAAGACATTTTGGTACTATGATGAGATCGAGATCAAGCAATTCACGCAAA-----	311
Db	1398	CGGCAAGACATTTTGGTACTATGATGAGATCGAGATCAAGCAATTCACGCAAAAGGTTGAT	1457
Qy	312	-----GATTACCCCACTT	326
Db	1458	GCTCAGAAACCTTGTTGATTAATCATGTTACTGACCTTTCAGATTAATTCACCCACCTT	1517
Qy	337	GGCGCCCTGCGCACTTCGTCGGCTACAGTGGCATGAGCCCGGCGCTACTTTCATTAATTTCC	386
Db	1518	GGCGCCCTGCGCACTTCGTCGGCTACAGTGGCATGAGCCCGTGTCTACTTTCATTAATTTCC	1577
Qy	387	CAGAGGAACAGAGACTGTAGTTAGTTTCATCAACAATGCGACCGGTGAGAACTCGTCA	446
Db	1578	CAGAGGAACAGAGACTGTAGTTAGTTTCATCAACAATGCGACCGGTGAGAACTCGTCA	1637
Qy	447	TCTGCAAGGCTCCCATTCGCGTGCCCTTTGCATGCTTGGGCTGAAGATGTACCTTCCC	506
Db	1638	TCTGCAAGGCTCCCATTCGCGTGCCCTTTGCATGCTTGGGCTGAAGATGTACCTTCCC	1697
Qy	507	TGGGAGTACAAAGATTAATCACTTTCGCAACTGCAGATCGCGCGGCTTCGTGTGTACCA	566
Db	1698	TGGGAGTACAAAGATTAATCACTTTCGCAACTGCAGATCGCGCGGCTTCGTGTGTACCA	1757
Qy	567	TGACCACGCTTTCATGA-----	583
Db	1758	TGACCACGCTTTCATGAAGGTATGCTACGAGCCTTATCTTCTTGGGCTACCTTTGGCTA	1817
Qy	584	-----AGACTGCTGAGAAATGCCACTTTGGTCAAGCTGGCGCTTACATT	627
Db	1818	ACCAACTTCTTTCGTGTGACTGCTGGAATGCTCACTTGTGTGACAGGCTGGCGCTTACATT	1877
Qy	628	ATCAACGACGAGGCTGAGATGCTGTCGCGCTTCCAGTGGGCTATGGCGAGTTCGATATC	687
Db	1878	ATCAACGACGAGGCTGAGATGCTGTCGCGCTTCCAGTGGGCTATGGCGAGTTCGATATC	1937
Qy	688	CCTCTGATCTGAGCGGCAAGTACTATTAACGCGGATGATACCTCGTTTCGACGAGAGT	747
Db	1938	CCTCTGATCTGAGCGGCAAGTACTATTAACGCGGATGATACCTCGTTTCGACGAGAGT	1997
Qy	748	GAGACAGAGAACTGTGGGAGATGTTCATCATGTTCACGACGACGACATGGCCTTTCCTT	807
Db	1998	GAGACAGAGAACTGTGGGAGATGTTCATCATGTTCACGACGACGACATGGCCTTTCCTT	2057
Qy	808	AAGTCACAGCCCGCAAGTACCGCTTTCGATTCCTCAACGCTGGCGGTGTCTGCTGTGG	867
Db	2058	AAGTCACAGCCCGCAAGTACCGCTTTCGATTCCTCAACGCTGGCGGTGTCTGCTGTGG	2117
Qy	868	CTCCTTACCTGTGCAGAGACACTCTCCCAACGTCAGAAATTCTTTCCAAAGTCAATGGC	927
Db	2118	CTCCTTACCTGTGCAGAGACACTCTCCCAACGTCAGAAATTCTTTCCAAAGTCAATGGC	2177
Qy	928	TCGTATGCTGGTCTCTTCAAGGCCCGCTTCAAGACTTCAACCTCTACCTTCGTTGGC	987

Db	2178	TCTGATGCTGGTCTCTTCAAGCCGCCCGTTGAGACTTAACCTCTACCTTGTCTGTGCC	2233
Qy	988	GAGCGTTACGAGATCATTTATTT-----	1008
Db	2238	GAGCGTTACGAGATCATTTATTTGGATATGGCCCTGCCCTCTCAGCAATGAGTCAAGAACTCTA	2297
Qy	1009	-----GACTTTCACCAATTTTGGTGGCCAGACTCTTGAACCTGGCCAAAGCTT	1053
Db	2298	AGACTAACACTTGTAGACTTTCACCAACTTTGTGGCCAGACTCTTGAACCTGGCCAAAGCTT	2357
Qy	1054	GCTGAGAACCAAGATGTGCGCGAGAGAGATAGATACGCTGGCACTCTGAGGTGATGTGGC	1113
Db	2358	GCTGAGAACCAAGATGTGCGCGAGAGAGATAGATACGCTGGCACTCTGAGGTGATGTGGC	2417
Qy	1114	TTTCGTCGACACTTGTGGCACTGTTTGAAGCAACAGCAGAGTCCCTCCACTCTCCGTGAC	1173
Db	2418	TTTCGTCGACACTTGTGGCACTGTTTGAAGCAACAGCAGAGTCCCTCCACTCTCCGTGAC	2477
Qy	1174	GTTCCTTTCCCTCCTCAAGGAAGGCCCGCCGACAGACACTTCAAGTTTGAACGCAAGC	1233
Db	2478	GTTCCTTTCCCTCCTCCTCAAGGAAGGCCCGCCGACAGACACTTCAAGTTTGAACGCAAGC	2537
Qy	1234	AACGGAACACTACCTGATCAACAGATGTTGGTGTGGCGATGTCAATGAGCGTGTCTGGCC	1293
Db	2538	AACGGAACACTACCTGATCAACAGATGTTGGTGTGGCGATGTCAATGAGCGTGTCTGGCC	2597
Qy	1294	AAGCCCGAGCTCGGCGACCGTTTGAAGGTCTGGGACCTCGAGAACCTCCCTCGAAGCGTCGAGC	1353
Db	2598	AAGCCCGAGCTCGGCGACCGTTTGAAGGTCTGGGACCTCGAGAACCTCCCTCGAAGCGTCGAGC	2657
Qy	1354	CACCCCGTCCACTTTCACCTTGTGTGAATTCAGATCCTCAAGCAGAACTGTTGGTGTGGC	1413
Db	2658	CACCCCGTCCACTTTCACCTTGTGTGAATTCAGATCCTCAAGCAGAACTGTTGGTGTGGC	2717
Qy	1414	CAGGTCAATGCCATACGAGTCTGCTGGTCTTAAGGATGTCTGTGTTGGGCAAGGGGTGAG	1473
Db	2718	CAGGTCAATGCCATACGAGTCTGCTGGTCTTAAGGATGTCTGTGTTGGGCAAGGGGTGAG	2777
Qy	1474	ACCCTGACATCGAGGGCCACTCAACACCTGGACGTGAGACTTCAATGTTGGGCACTGTAC	1533
Db	2778	ACCCTGACATCGAGGGCCACTCAACACCTGGACGTGAGACTTCAATGTTGGGCACTGTAC	2837
Qy	1534	AACCTCAATTCAGAGATTAACGAGATGATGGCTGTATTAACAGTCAACGCCATGAGGAG	1593
Db	2838	AACCTCAATTCAGAGATTAACGAGATGATGGCTGTATTAACAGTCAACGCCATGAGGAG	2897
Qy	1594	AAGGATATCTTTCAGAGAGACTTCGAGAGACCCCATGAAACCCCAAGTGGCGGCGTCTCT	1653
Db	2898	AAGGATATCTTTCAGAGAGACTTCGAGAGACCCCATGAAACCCCAAGTGGCGGCGTCTCT	2957
Qy	1654	TACAAACGCAACGACTTCGATGCTGCGCGGTGGAAATTTCTCGGCGAGATCCATCACTGCC	1713
Db	2958	TACAAACGCAACGACTTCGATGCTGCGCGGTGGAAATTTCTCGGCGAGATCCATCACTGCC	3017
Qy	1714	CGAGTCGAGAGAGCTGGCGCGAGAGAGCCGTACAACCCGCTCGATGAGATCCTGGAGAT	1773
Db	3018	CGAGTCGAGAGAGCTGGCGCGAGAGAGCCGTACAACCCGCTCGATGAGATCCTGGAGAT	3077
Qy	1774	CTTGGAAATCGAGAGTAA 1791	
Db	3078	CTTGGAAATCGAGAGTAA 3095	
RESULT 5 :			
US-09-218-702-5			
: Sequence 5, Application US/09218702			
: Patent No. 6426410			
: GENERAL INFORMATION:			
: APPLICANT: Mang, Huaming			
: TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes			
: FILE REFERENCE: GC567			
: CURRENT APPLICATION NUMBER: US/09/218,702			
: CURRENT FILING DATE: 1998-12-22			

RESULT 5.
US-09-218-702-5
Sequence 5, Application US/09218702
Patent No. 6426410
GENERAL INFORMATION:
APPLICANT: Wang, Huang
TITLE OF INVENTION: NO. 6426410el Phenol Oxidizing Enzymes
FILE REFERENCE: GC567
CURRENT APPLICATION NUMBER: US/09/218.702
CURRENT FILING DATE: 1998-12-22

NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid
us-09-218-702-5

Query Match 82.1%; Score 1470; DB 4; Length 2067;
Best Local Similarity 87.0%; Pred No. 0;
Matches 1787; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

QY 4 AATATGCTTTCAGTCAATGAGCACTGGCAGCAGCCTCCGGCTCCTGTCGTGAGTCTC 63
DB 7 AATATGCTTTCAGTCAATGAGCACTGGCAGCAGCCTCCGGCTCCTGTCGTGAGTCTC 66
QY 64 GGCATCCCGATGGACACCGGACCCACCCATTGAGGCTGTGATCCGAACTGGAAGACT 123
DB 67 GGCATCCCGATGGACACCGGACCCACCCATTGAGGCTGTGATCCGAACTGGAAGACT 126
QY 124 GAGGCTTCGCTGACTCCCTCCCTGCTGACGAGGCGGATGAGCAGTGGAGTCACTTCA 183
DB 127 GAGGCTTCGCTGACTCCCTCCCTGCTGACGAGGCGGATGAGCAGTGGAGTCACTTCA 186
QY 184 TCAACTTCCTTTAC-----GATCATTTACCAACCCCTGTACCCG 198
DB 187 TCAACTTCCTTTACGATGAGACACCTGTCCACCTGTTTTCCCTGCAATCACTCTC 246
QY 199 ---AGGAATGCCCTGGCAATTCACCTGTCAAGCAGCCCAAGAT----- 239
DB 247 TATAGGAATGCCCTGGCAATTCACCTGTCAAGCAGCCCAAGATGATGTCCTTGAATTT 306
QY 240 -----GATCATTTACCAACCCCTGTACCCG 263
DB 307 CTACGAAGCACTCGCCCGGACTAATGTAATTCAGGATCATTTACCAACCCCTGTACCCG 366
QY 264 CAAGGACATTTGGTACTATGAGATGAGATCAAGCCATTTACAGCAAG----- 311
DB 367 CAAGGACATTTGGTACTATGAGATGAGATCAAGCCATTTACAGCAAGGATGATTTGCT 426
QY 312 -----GATTACCCCACTTTGG 329
DB 427 CAGAAACCTTGGTAAATTAATCATTTGTAATGACCCTTTCAGATTTTACCCCACTTTGG 486
QY 330 CCTGTCATCTGCTGGGCTAGAGATGAGCATGAGCCCTGGCTGACTTTCATTAATTTCCCA 389
DB 487 CCTGTCATCTGCTGGGCTAGAGATGAGCATGAGCCCTGGCTGACTTTCATTAATTTCCCA 546
QY 390 AGGAACAGAGACTGTAGTGAAGTTTCATCAACAATGCCACCGTGGAGAACTGGTGCATCT 449
DB 547 AGGAACAGAGACTGTAGTGAAGTTTCATCAACAATGCCACCGTGGAGAACTGGTGCATCT 606
QY 450 GCACGCTCCCTGCGGCTGCGGCTTTCATGAGTGGGCTGAAAGATGACCTTCCCTGG 509
DB 607 GCACGCTCCCTGCGGCTGCGGCTTTCATGAGTGGGCTGAAAGATGACCTTCCCTGG 666
QY 510 CGAGTCAAGAGTACTACTCTTCCCAACTACCAATCGCCCGCTCTGTGGTACCATGA 569
DB 667 CGAGTCAAGAGTACTACTCTTCCCAACTACCAATCGCCCGCTCTGTGGTACCATGA 726
QY 570 CCACGCTTTCATGA----- 583
DB 727 CCACGCTTTCATGAAGGTATGCTACGAGCCTTATCTTTCTTGGTACCTTTGGCTAAC 786
QY 584 -----AGACTGCTGAATGCTTACTTTGGTCAAGCTGCGCTTACATTAATC 630
DB 787 AACTTCCTTTCATGAAGTCTGAGAAATGCTTACTTTGGTCAAGCTGCGCTTACATTAATC 846
QY 631 AAGGAGAGGCTGAGATGCTCGGTCCTGAGTGGCTAGTGGCAGTTCGATATCCCT 690
DB 847 AAGGAGAGGCTGAGATGCTCGGTCCTGAGTGGCTAGTGGCAGTTCGATATCCCT 906

QY 691 CTGATCTCTGAGGCGCAAGTACTATAACGCCGATGGTACCTTGCTTCCAGCCAGGGTGA 750
DB 907 CTGATCTCTGAGGCGCAAGTACTATAACGCCGATGGTACCTTGCTTCCAGCCAGGGTGA 966
QY 751 GACGAGGACCTGGGGGAGATGCAATCCATGTCACAGGACGCAATGGCTTTCCTTAC 810
DB 967 GACGAGGACCTGGGGGAGATGCAATCCATGTCACAGGACGCAATGGCTTTCCTTAC 1026
QY 811 GTCCAGCCCCGCAAGTACGTTTCGATTCCTCAACGCTGCGGTGTCTGCTTGGCTC 870
DB 1027 GTCCAGCCCCGCAAGTACGTTTCGATTCCTCAACGCTGCGGTGTCTGCTTGGCTC 1086
QY 871 CTCATCTCTGTCAGACCACTCTCCCAACGTCAGAAATTCCTTCCAAATGCTTCT 930
DB 1087 CTCATCTCTGTCAGACCACTCTCCCAACGTCAGAAATTCCTTCCAAATGCTTCTCT 1146
QY 931 GATGCTGCTCCTTCAACGCCCGTTCAGACCTCAACCTGACTGCTGTTGGCGAG 990
DB 1147 GATGCTGCTCCTTCAACGCCCGTTCAGACCTCAACCTGACTGCTGTTGGCGAG 1206
QY 991 CGTTACGATCATTTAT----- 1008
DB 1207 CGTTACGATCATTTATGCTATGCCCTCCCTCCCTCAGCAATGAGTCAAGAACTTA 1266
QY 1009 -----GACTTACCAACTTTGCTGGCCAGACTCTTGACCTGGCAACTTGC 1056
DB 1267 CTACACTTGTGACTTCAACAACTTGTGCGGCAACACTCTTGACCTGGCAACTTGC 1326
QY 1057 GAGACCAAGATGTGGGCGCAGGAGTGAATGCTGCGACCTGAGGTGATGGCTTC 1116
DB 1327 GAGACCAAGATGTGGGCGCAGGAGTGAATGCTGCGACCTGAGGTGATGGCTTC 1386
QY 1117 GTCGTGAGCTGTGGGCACTGTTGAGGACAACAGCAGAGTCCCTCACTGCTGAGCTT 1176
DB 1387 GTCGTGAGCTGTGGGCACTGTTGAGGACAACAGCAGAGTCCCTCACTGCTGAGCTT 1446
QY 1177 CTTTCCCTCTCACAAGGAAGGCCCGCGACAGCACTTCAAGTTTGAAGCAGCAAC 1236
DB 1447 CTTTCCCTCTCACAAGGAAGGCCCGCGACAGCACTTCAAGTTTGAAGCAGCAAC 1506
QY 1237 GGAACATCTGATCAACGATGTGGCTTGGCGATGTCAAATGAGGTGCTGGCGCA 1296
DB 1507 GGAACATCTGATCAACGATGTGGCTTGGCGATGTCAAATGAGGTGCTGGCGCA 1566
QY 1297 CCGAGCTCGGCGACCTGTGAGGTGTGGAGCTGGAAGCTCTCTGGAGCTTGGAGCCAC 1356
DB 1567 CCGAGCTCGGCGACCTGTGAGGTGTGGAGCTGGAAGCTCTCTGGAGCTTGGAGCCAC 1626
QY 1357 CCGGTCCACATTCACCTTGTGACTTCAAGATCTCAAGCGAAGCTGGTGGCTGCGCAG 1416
DB 1627 CCGGTCCACATTCACCTTGTGACTTCAAGATCTCAAGCGAAGCTGGTGGCTGCGCAG 1686
QY 1417 GTGATCCCTCAGAGTGTGTGCTTAAAGATGTGCTGCTTGGGAGGGGTGAGAC 1476
DB 1687 GTGATCCCTCAGAGTGTGTGCTTAAAGATGTGCTGCTTGGGAGGGGTGAGAC 1746
QY 1477 CTGACCATGAGGCGCCACTTACCAACCTGTGAGCTTACATGTGGCACTGTCAAC 1536
DB 1747 CTGACCATGAGGCGCCACTTACCAACCTGTGAGCTTACATGTGGCACTGTCAAC 1806
QY 1537 CTCATTCACGAGATTAACGACATGATGCTGTATTCACGTCACGCCCATGAGGAGAAG 1596
DB 1807 CTCATTCACGAGATTAACGACATGATGCTGTATTCACGTCACGCCCATGAGGAGAAG 1866
QY 1597 GATATCTTCAGAGAGACTTCGAGGAGCCCATTAACCCCAAGTGGGCGGCTTCTTAC 1656
DB 1867 GATATCTTCAGAGAGACTTCGAGGAGCCCATTAACCCCAAGTGGGCGGCTTCTTAC 1926
QY 1657 AACCGAAGACATTCATGCTGCGCTGGAACCTTCTCCGCGAGTCCATCATGCGCGA 1716
DB 1927 AACCGAAGACATTCATGCTGCGCTGGAACCTTCTCCGCGAGTCCATCATGCGCGA 1986

Db 2040 CGCTGAGCAGCCTTACAGCGACTCG 2066

RESULT 7

US-09-468-578-6

; Sequence 6, Application US/09468578

; Patent No. 639329

; GENERAL INFORMATION:

; APPLICANT: Wang, Huaming

; APPLICANT: Bodie, Elizabeth A.

; TITLE OF INVENTION: Phenol Oxidizing Enzymes

; FILE REFERENCE: GC561-3

; CURRENT APPLICATION NUMBER: US/09/468,578

; CURRENT FILING DATE: 1999-12-21

; PRIOR APPLICATION NUMBER: US 09/220,871

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: US 09/338,723

; PRIOR FILING DATE: 1999-06-23

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 2063

; TYPE: DNA

; ORGANISM: Curvularia pallescens

US-09-468-578-6

Query Match 28.1%; Score 502.8; DB 4; Length 2063;

Best Local Similarity 60.4%; Pred. No. 1.2e-128;

Matches 1000; Conservative 0; Mismatches 522; Indels 134; Gaps 5;

QY 244 ATTACCAACCTGTCCACCGCAAGACATTGGTACTAGATGATCAACCATTT 303

Db 310 ATGACCAATCTCTGCAACAAGAGATGTGTACTAGAGATGTCAAAACCTTT 369

QY 304 CAGCAAGATTTTACCCCACTTGGCCCTGCACTCTGCGGTACATGAGATGAGC 363

Db 370 AACCAAGCTTATCTCAAGTCTAGCTCTGCTGCTGCTGATGATGATGATTTA 429

QY 364 CCTGTCTACTTCAATGTCCACAGAGACAGATGATGATGATGATGATGATGAT 423

Db 430 CCAGGCCCTACAGATCTGCGGAGAGACAGAGAGCGGTTGTAGATTCGTAACCA 489

QY 424 GCCACGCTGAGACATCGGTCTGACGCGCTCCCAATCGCGTCCCTTTGATGAT 483

Db 490 GGTGATCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549

QY 484 TGGGCTGAAGATGTGACCTTCCCTGCGGAGTACAA----- 518

Db 550 TGGGCTGAAGATTTGATTTATGAAGGCCAATTCAAAGGTACACAGACAATCTTATGCA 609

QY 519 -----GATTACTACTTTCCCACTACC 541

Db 610 TCAGGGTGCCTCTTTTATACATAACAGACTCGTTCTTACACTACTACTACCGAACAAC 669

QY 542 AATCGCCCGCTCTGTGTGATACATGACACGCTTT----- 579

Db 670 AGGCTGCGAATTTCTGTGTGATACAGATCATGTATGATGATGATGATGATGAT 729

QY 580 -----ATGAAGTCTGTGATGATGCT 601

Db 730 AATCATGGAGCGAAACGAAAGATGGGCTGACACTTATGACAGACTGTGGAATAATGCTT 789

QY 602 ACTTGTGTCAGGCTGAGCTACATATATACAGACAGAGGCTGAGATGCTGCTGCTTC 661

Db 790 ATTGTGACAGGCTGCGGCTACCTGATCAAGACCCAGCTGAGGAGCGGCTGCGCTTC 849

QY 662 CTATGTCGATGCGAGTTCGATATCCCTGTGATCTGATGCTGATGCTGATGCTGAT 721

Db 850 CTTGCGGTTACGAAATACAGATCCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 909

QY 722 ATGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781

Db 910 ATGGAATCTTCCAGACAGCTGTGGAGAGACAAAGCTCTGTGGGCGGACGTCATCCATG 969

QY 782 TCAAGGAGCCATGCGCTTTCCCTTAACGTCCAGCCCGCAAGTACCGTTCGATTC 841

Db 970 TCAAGGTCAGCCCTGCGCATTTCAACGTGAGCTCGAAGATGCGCTTCATTC 1029

QY 842 TCAAGGTCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 901

Db 1030 TCAAGGTCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1089

QY 902 TCAAGTCTCTTCCAAAGCATTTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961

Db 1090 CTAGACTCTTCTTCCAAAGCATTTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1149

QY 962 CCTTAACTCTTCCAAAGCATTTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1021

Db 1150 CCTCAAGATTTTACGTCGAG 1209

QY 1022 TTGCTGCGCAGACTCTTCAACCTGCGCAGAGCTGCTGAGACCAAGATGCTGCGCAGAG 1081

Db 1210 ATGCAAGGCGCAGAGATGATTTGCTGATGCTGCAAAAGGCCAATGGGCTGCGCAGAG 1269

QY 1082 ATGAGTACGCTGCACTCTGAGGTGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1141

Db 1270 ACATTTATCAAAACACTGACCAAGGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1329

QY 1142 ACAACAGCCAGGTCCTTCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1201

Db 1330 ATAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386

QY 1202 CCGCGCAGACACTTCAAGTTTGAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1261

Db 1387 GCATGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1446

QY 1262 GCTTTCCTGATGATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321

Db 1447 GGTTCGACAGCTCCAGAACGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1506

QY 1322 GGGAGCTGAGAACTCTCTGAGAGCTGAGAGCCACCCCTGCAATTCACCTTTGACT 1381

Db 1507 GGGAACTCGAAGAAAGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1566

QY 1382 TCAAGATCTTCAAGGAGACTGCTG-----GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1435

Db 1567 TCCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1626

QY 1436 CTGTCTTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1495

Db 1627 CCGGTCTCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686

QY 1496 ACCAACCTGAGCTGAGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1555

Db 1687 ACGCCCTGCGGAGAGAGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1746

QY 1556 ACATGATGCTGATTTCAACAGCTGACCGCATGAGAGAGAGAGATATCTTCA-----GGAGG 1612

Db 1747 ACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1806

QY 1613 ACTTGAAGAGCCCAATGAAGCCCAAGTGGCGGCTTCTTCAACCAAGCAGCACTTCC 1672

Db 1807 ATTTCACAGACCCGGAAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1866

QY 1673 ATGCTGCGCTGAGAACTTCTGCGCGAGTTCATCACTGCTGCGAGTGCAGAGCTGCGCG 1732

Db 1867 CCGCGGATCGGGATATCTTCTCAGAAAGCATTCATGAGGCTGAGAGTGAAGAGTGGCGC 1926

QY 1733 ACAGAGAGCTGTAACACCCCTGCTGATGATCTGCG 1768

Db 1927 TGAACAGCGTAAACAGCAAGTGGCACAGTCAAG 1962

RESULT 8

US-09-401-476-1

; Sequence 1, Application US/09401476


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? Patent NO. 6168936
?
? GENERAL INFORMATION:
?
? APPLICANT: Wang, Huaming
? TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
? FILE REFERENCE: GC584
? CURRENT APPLICATION NUMBER: US/09/401,476
? CURRENT FILING DATE: 1999-09-22
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 1
?
? LENGTH: 1958
?
? TYPE: DNA
?
? ORGANISM: Stachybotrys chararum
? US-09-401-476-1

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Query Match	25.7%	Score 460.4	DB 4	Length 1958
Best Local Similarity	59.3%	Pred. No. 5.3e-117		
Matches 996: Conservative	0	Mismatches 521	Indels 163	Gaps 6

Dd	1037	ACGGGTGCTGCTGTTGAGGGCCCTGTTGACATGACATCTGTACATCTCTCATATGCGCCAGC	1096
Oy	992	GTTACGAGATCATATTATTTAGACTTCCACCACACTTGGTCTGGCCAGACTCTTGGACCTGGCCACG	1051
Dd	1097	GCTGGGAGGTTGTTATGATCTTCTCCACCCTTGGCTGGCCAGTTCATGATATCCGCACAC	1156
Oy	1052	TTGCTGAGACCAACGATGTGGCGACGAGATGAGTACGCTTGGCACTCTCGAGTGTATGC	1111
Dd	1157	TTTCTGGGTGAGCGGCTCTGGGTGAGACCTGATGTTGATTAACACTGACAAAGGTCATGC	1216
Oy	1112	GCTTTCGTGTCAGCTCTGGGCACTGTTGAG---GACAAACGCGAGGTGCCCTCCACACTGCC	1168
Dd	1217	GATTCTGCTGTGATGAGAAAGTCTTGTAGTCCGCCGACACTTCTGASGTGGCTGCCAACCTCC	1276
Oy	1169	GTCACGTTTCTTTCC-----TCTCTCACAGGAAGGCCCCCGCACAAAC	1213
Dd	1277	GAGATGTTTCTTTTCCCGGAGGGCGGACACTGGGAGCCCCGCAAAACCCTGATGACGGA	1336
Oy	1214	ACTTCAGTTTGAACGACGACGACGACACTACCTGATCTCAAGCATGTGTGGCTTGGCGATG	1273
Dd	1337	CTTTCACCTTGGCCCGGCTAAATGAGACAGTACATCAAGGAGTTTACCTTCTTGGGATG	1396
Oy	1274	TCAATTGAGCGTGTCTTGGCCCAACCCGAGCTGGGCACTTGTAGGTGTGGGAGCTCGAGA	1333
Dd	1397	TCGAGAACCGTCTCTCCGGAATGTGCCCGGACACATGTGAGATCTGGGAGCTTGAGA	1456
Oy	1334	ACTCCTCTGGAAGCTGGAGCCACCCTGTCACATTCACCTTGTGACTTTCACATCTCTCA	1393
Dd	1457	ACAACCTCCAAAGGTTGGACATCAACCTGTTTCAATTCACCTCTTACCTTCCGAGACTCTTT	1516
Oy	1394	AGCACAATGAGGTGTCGGGCGGACGATGATGCCCTACGAGTCTCTGTCTTAAAGATGTGC	1453
Dd	1517	CTCGTTCACACTGCCCGTGG---AGTGGAGCCTTATGAGGCTCTGTCTCAAGATGTG	1573
Oy	1454	TCGTGTTGGGCAAGGGGTGAGACCCCTGACATCGAGGCCACTTACCAACCTGTGAC----	1508
Dd	1574	TCTGGCTGGCTCGTGGAGGTTGTCTATGTGAGGCCACATCAACCTCTTCCCGTAAG	1633
Oy	1509	-----TGGAGCCTTACAT	1520
Dd	1634	TTTCTGGCCTTTTACCTTACACTGATTTTTCACCTCATGCTAACATCTACAAAGTGTGCTACAT	1693
Oy	1521	GTTGCACTGTACAAACCTCATTCACGAGATTAACGACATGATGGCTGTATTCAACGTCAAC	1580
Dd	1694	GTTTCACCTGGCACAACTGTATCCACAGAGACACGACATGATGGCTGTTTCAATGTAC	1753
Oy	1581	CGCCATGGAGGAAGGGAATTTCTGAGGAGACTTTCAGAGACCCCATGAACCCCAAGTG	1640
Dd	1754	TGTTCTCGGTACTATGGCTTACACATCAACGAGATTCAATGTAGCCCAAGGAGGCTCTCTG	1813
Oy	1641	GGCGGCGGTTTCTTACAAACGCAACGACTTCATGCTGCGGTGGAAACTTCTCCGCGGA	1700
Dd	1814	GAGGCGCCGCGCTCTCTCTCTCGGANAAGTTCGAGAAATGCTCTGGGTGACTTTCACGAACT	1873
Oy	1701	GTCACATCACTGCCGAGTGCAGGAGCTGGCCGAGCAGGAGCCGTAACAACGCTTCGATGA	1760
Dd	1874	TGCCATCACTGACCGCAATTCAGGAGATGTGCTTACGTTCAACCCCTTACGCGCCAGGCTGATGA	1933

Oy	783	-----CAAGGACGACATGGCGTTTCCTTAAG	811
Db	857	AATTGTGATGCTCTTAACCAAGTCTTACAGACAGGTAAGCTTGGCCATGCTCAAG	916
Oy	812	TCACGCCCCCAGTACCGTTTCCGATTCCTCAACGCTGCGTGCTGGTGGCTCC	871
Db	917	TGCAGCCGCGCAGTAGTACCGGTTCTCGCTTCCCTCAACGCTCCGCTTCACGCTTTTTCGCTC	976
Oy	872	TCATACCTCGTCAGGACAGCTCTCCCAAGTGAATTCCTTCCAAAGCATTTGGCCCTG	931
Db	977	TGTATCTTGCTACCTCTGAGAGATTACAGACAGACTTCCCTTCAGATCATTTGCCCTG	1036
Oy	932	ATGCTGATCTTCCTCAAGCCCCGTTCAAGACCTTAACCTTACCTTGCTGTTGGCAGC	991

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RESULT 9
US-09-401-476-3
: Sequence 3, Application US/09401476
: Patent No. 6168936
: GENERAL INFORMATION:
: APPLICANT: Wang, Huaming
: TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
: FILE REFERENCE: GC584
: CURRENT APPLICATION NUMBER: US/09/401,476
: CURRENT FILING DATE: 1999-09-22
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 2095

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US-09-468-578-8

Query Match	10.5%;	Score 188.6;	DB 4;	Length 858;
Best Local Similarity	60.2%;	Pred. NO. 2.1e-42;		
Matches 434; Conservative	0;	Mismatches 254;	Indels 33;	Gaps 6

OY	586	ACGCTGAGAAATCCCTACTTGGTTCAGGGCTGGCGGCTACTATTATCAAGACAGAGCTGAG	645
Db	2	ACGCCGAGAGACCTTACTTTGGTCAAGCTGGCTTTTACATTCTGCACGACCCCGCTANA	61
OY	646	GATGCTCTCGGCTTCCTATGATGGCTATGGCGATTGCGATATCCCTGATCTGTGACGGCC	705
Db	62	GATGCAATGGGTGGCT-----TCGGCAGTATGATGATACCTCTTGCACTGTGCTCC	115
OY	706	AAGTACTATPACGCCGATGTACCTTGGCTTTGGACCGAGGGTGGAGACCAGGACTGTGG	765
Db	116	AAGCAGTACAAACGACGACGGTACCTTCCTTGACCCCAAGAGAGAAACGATCACTGTTC	175
OY	766	GGAGATGTCATGCATGCAACGAGACGCCATGGCCCTTTCCTTAAGCTCCAGCCCGGCAAG	825
Db	176	GGGAGTGTATTCACGTCACAGCACAACGACGCCATGGCCCTTATTAAGCTCGAGCTGCAAG	235
OY	826	TACCGTTTCGATTCCTCAACGCTGGCGGTGTGCGTCTGGCTCTCTACTCCCTCGAG	885
Db	236	TACCGTTCGGCTTCTCTCAATGGTGTATCAGCCGGC-----CTTCAAGCTACT	286
OY	886	ACCAAGCTTCCCAACGTCAGAAATTCCTTTCAAGTCAATTGCCCTGATGCTGGTCCCT	945
Db	287	TTTGAGAGCTGATGGCAAGAGTACACTTTCCTGTCATCGGTGGCGGATACCTGTCTTGG	346
OY	946	CAGGCCCGGCTGAGACCTCTAACCTCTACCTTGTGCTGGCGGACGCTTACGAAATCAT	1005
Db	347	ACCAAGCTGTGTAGACAAAGCAACTTGTGATCTCTATGGCCGACGCGTGGAGGATATT	406
OY	1006	ATTGACTTTCACCAACTTGTGCTGGCGAGACTCTTGACCTCGGCAAGTTGCTGAGACCAAC	1065
Db	407	TTTGACTTTCAGCAATTTTCCGGGAAGAACGTACCCCTCAAAACAGGTG-----C	457
OY	1066	GATGTGGGCGACGAGATGATGCTGTGCACTCTTGAGAGTATGCGGCTGTGTCAGC	1125
Db	458	GATGTGCGACGACGATGAGGACTACAACTCCACCGACAAGTGCATGCTAGTTGTTTGGC	517
OY	1126	TCGTGGCACTGT-----GAGGACAAACAGCAGAGTCCCTCCACACTCTCCGTAGCTTCT	1179
Db	518	AAGGATTTACGAGCCAGGCTGTATATGGCAACCTTCCGCGTCTCTGGCACTGTCC	577
OY	1180	TTCCCTCTTACAGGAAGGCCCCCGGACGACAGCACTTCAACTT--TGAACGCGACAGCG	1238
Db	578	TTCCCTCTTAAGAGG--GGCGGAGTGCACAGAGAGCTTAATTTGGCAGGGACCGGTTG	635
OY	1239	ACACTACCTGATCAACGATGTGGCTTTGCGGATGTCAATGACGCTGTCTGGCCAACG	1298
Db	636	CCAGTGACTGTTAATGGCTTGACCTTGCCTGATGTCAACAAACCCGATCTGGTAAGC	695
OY	1299	C	1299
Db	696	C	696

RESULT 11
 US-08-232-463-14
 : Sequence 14, Application US/08232463
 : Patent No. 5670367
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: DORNER, F.
 : APPLICANT: SCHEIFLINGER, F.
 : TITLE OF INVENTION: FALKNER, F. G.
 : TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 : NUMBER OF SEQUENCES: 52
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Foley & Lardner
 : STREET: 1800 Diagonal Road, Suite 500
 : CITY: Alexandria

```

1  STATE: VA
2  COUNTRY: USA
3  ZIP: 22313-0299
4
5  COMPUTER READABLE FORM:
6  MEDIUM TYPE: Floppy disk
7  COMPUTER: IBM PC compatible
8  OPERATING SYSTEM: PC-DOS/MS-DOS
9  SOFTWARE: Patent In Release #1.0, Versid
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/232,463
12 FILING DATE:
13 CLASSIFICATION: 435
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US/07/935,313
16 FILING DATE:
17 APPLICATION NUMBER: EP 91 114 300,6
18 FILING DATE: 26-AUG-1991
19 ATTORNEY/AGENT INFORMATION:
20 NAME: BENT, Stephen A.
21 REGISTRATION NUMBER: 29,768
22 REFERENCE/DOCKET NUMBER: 304/72/114 IMM
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (703)836-9300
25 TELEFAX: (703)683-4109
26 TELEX: 899149
27 INFORMATION FOR SEQ. ID NO. 14:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 7218 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 IMMEDIATE SOURCE:
34 CLONE: PTZ9pt-Fls
35 US-08-232-463-14

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Query Match	3.0%;	Score 54.6;	DB 1;	Length 7218;
Best Local Similarity	5.2%;	Pred. No. 4.1e-05;		
Matches	21;	Conservative 218;	Mismatches 162;	Indels 0;
			Gaps	0;

[illegible]

RESULT 12
5183745-1/c
; Patent No. 5183745
; APPLICANT: DADCHIN, ANTOINE; GLASER, PHILIPPE; KRIN, EVELYN
; BARZU, OCTAVIEN; LADANT, DANIEL; ULLMAN, AGNES

TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
BIOLOGICAL USES
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,541
FILING DATE: 25-OCT-1989
SEQ ID NO:1:
LENGTH: 4649

Query Match 2.6%; Score 45.8; DB 6; Length 4649;
Best Local Similarity 48.0%; Pred. No.0.0088;
Matches 131; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 934 GCTGCTCTCCCTTCAGCCCCCGCTTACACCTCTACCTCTGCTGTCGCCAGCGT 993
Db 3372 GCCGCGCGCGCGCGATGACCGTGTGTTGGCCCTCGCCGCAACAGGAGTGTGTCGCCG 3313
Qy 994 TACGAGATCATTTATTTGACTTTCACCACTTTGCTGGCCAGACTCTTGACCTGGCAACGTT 1053
Db 3312 GCCGCCATTCAGACCTGTGCTGCCGCCGCCGCTAGGAAGTTGCTGTGGCATTTGCC 3253
Qy 1054 GCTGAGACCAACGATGTGGCGAGAGATGATAGTACGCTCGCCTCGAGGTATGGCG 1113
Db 3252 GGTGATTCGAATGTTGCCGGCCCCCGCATGATGTGCTGCACATGCTCGAGCGTTCGAC 3193
Qy 1114 TTGCTGTCAGCTCTGCGACTGTGTAGAGACACAGCAGTCCCTCCACTCTCCGTGAC 1173
Db 3192 CTCACCACTTGGCCCGACAGGGCGCATGCTGACATGGCGGTATTGACATTTCCGTGG 3133
Qy 1174 GTTCCTTTCCTCTCCCTCACAAGAGAGGCCCGCC 1206
Db 3132 CTGGCGTAGGGGTTGTCTGTGGTAGCCAGCC 3100

RESULT 13
US-08-669-785-1/c
Sequence 1, Application US/08669785
Patent No. 6309648
GENERAL INFORMATION:
APPLICANT: Betsou, Fotini
APPLICANT: Sebo, Peter
APPLICANT: Guiso, Nicole
TITLE OF INVENTION: Protective Epitopes Of Adenyl
TITLE OF INVENTION: Cyclase-haemolysin(AC-Hly), Their Application To
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinagan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,785
FILING DATE: 27-JUN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0072-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6441 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 979..6096
OTHER INFORMATION: /note= "AMINO ACID SEQUENCE
OTHER INFORMATION: CORRESPONDING TO THE NUCLEOTIDE SEQUENCE OF THE GENE
OTHER INFORMATION: CODING FOR THE B. Pertussis AC-Hly"
US-08-669-785-1

Query Match 2.6%; Score 45.8; DB 4; Length 6441;
Best Local Similarity 48.0%; Pred. No.0.01;
Matches 131; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 934 GCTGCTCTCCCTTCAGCCCCCGCTTACACCTCTACCTCTGCTGTCGCCAGCGT 993
Db 4167 GCCGCGCGCGCGCGATGACCGTGTGTTGGCCCTCGCCGCAACAGGAGTGTGTCGCCG 4108
Qy 994 TACGAGATCATTTATTTGACTTTCACCACTTTGCTGGCCAGACTCTTGACCTGGCAACGTT 1053
Db 4107 GCCGCCATTCAGACCTGTGCTGCCGCCGCCGCTAGGAAGTTGTGTCGCAATTGCC 4048
Qy 1054 GCTGAGACCAACGATGTGGCGAGAGATGATAGTACGCTCGCCTCTCGAGGTATGGCG 1113
Db 4047 GGTGATTCGAATGTTGCCGGCCCCCGCATGATGTGCTGCACATGCTCGAGCGTTCGAC 3988
Qy 1114 TTGCTGTCAGCTCTGCGACTGTGTAGAGACAAACAGTCCCTCCACTCTCCGTGAC 1173
Db 3987 CTCACCACTTGGCCCGACAGGGCGCATGCTGACATGGCGGTATTGACATTTCCGTGG 3928
Qy 1174 GTTCCTTTCCTCTCCCTCACAAGAGAGGCCCGCC 1206
Db 3927 CTGGCGTAGGGGTTGTCTGTGGTAGCCAGCC 3895

RESULT 14
5183745-5/c
Patent No. 5183745
APPLICANT: DANCHIN, ANTOINE;GLASER, PHILIPPE;KRIN, EVELYN;
BARU, OCTAVIEN;LADANT, DANIEL;ULMAN, AGNES
TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
BIOLOGICAL USES
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,541
FILING DATE: 25-OCT-1989
SEQ ID NO:5:
LENGTH: 6443

Query Match 2.6%; Score 45.8; DB 6; Length 6443;
Best Local Similarity 48.0%; Pred. No.0.01;
Matches 131; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 934 GCTGCTCTCCCTTCAGCCCCCGCTTACACCTCTACCTCTGCTGTCGCCAGCGT 993
Db 4169 GCCGCGCGCGCGCGATGACCGTGTGTTGGCCCTCGCCGCAACAGGAGTGTGTCGCCG 4110
Qy 994 TACGAGATCATTTATTTGACTTTCACCACTTTGCTGGCCAGACTCTTGACCTGGCAACGTT 1053
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Qy 1054 GCTGAGACCAACGATGTGGCGAGAGATGATAGTACGCTCGCCTCTCGAGGTATGGCG 1113
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Qy 1114 TTGCTGTCAGCTCTGCGACTGTGTAGAGACAAACAGGAGTCCCTCCACTCTCCGTGAC 1173
Db 3989 CTCACCACTTGGCCCGACAGGGCGCATGCTGACATGGCGGTATTGACATTTCCGTGG 3930
Qy 1174 GTTCCTTTCCTCTCCCTCACAAGAGAGGCCCGCC 1206

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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(without alignments)
11275.230 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 424239 seqs, 254661826 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications-NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1474	82.3	3677	12	US-10-080-233-3
7	1470	82.3	2067	12	US-10-080-233-5
8	503.4	28.1	2905	10	US-09-338-723A-3
9	503.4	28.1	2905	12	US-10-080-210-3
10	502.8	28.1	2063	12	US-10-080-210-6
11	460.4	25.7	1958	9	US-09-942-185-1
12	460.4	25.7	2095	9	US-09-942-185-3
13	188.6	10.5	1533	12	US-10-080-210-8
14	79.8	4.5	1533	9	US-09-738-626-1053
15	45.8	2.6	6442	9	US-09-950-335A-11
16	44.6	2.5	1470	10	US-09-974-300-2204
17	42.6	2.4	1082	10	US-09-822-830A-368
18	41.8	2.3	390	10	US-09-790-399-7
19	40.8	2.3	1707	9	US-09-938-842A-186

20	39.2	2.2	1467	10	US-09-981-900B-6	Sequence 6, Appl1
21	37.8	2.1	1872	10	US-09-452-599-17	Sequence 17, Appl
22	37.6	2.1	1512	9	US-10-124-800-31	Sequence 31, Appl
23	37.6	2.1	4509	9	US-10-124-800-5	Sequence 5, Appl1
24	37.6	2.1	4512	9	US-10-124-800-27	Sequence 27, Appl
25	37.4	2.1	615	9	US-10-125-815-4	Sequence 4, Appl1
26	35.8	2.0	1642	10	US-09-765-231A-25	Sequence 25, Appl
27	35.6	2.0	651	9	US-09-738-626-2385	Sequence 2385, Ap
28	35.6	2.0	2148	9	US-09-738-626-2384	Sequence 2384, Ap
29	35.4	2.0	698	9	US-09-764-668-156	Sequence 156, Ap
30	35.2	2.0	1002	9	US-09-738-626-1755	Sequence 1755, Ap
31	35.2	2.0	2748	9	US-09-738-626-2853	Sequence 2853, Ap
32	35	2.0	951	9	US-09-975-719-432	Sequence 432, Ap
33	35	2.0	1050	9	US-09-975-719-428	Sequence 428, Ap
34	35	2.0	1104	10	US-09-815-242-7676	Sequence 7676, Ap
35	35	2.0	42235	9	US-09-975-719-1	Sequence 1, Appl1
36	34.8	1.9	1185	10	US-09-887-576-784	Sequence 784, App
37	34.8	1.9	6442	9	US-09-950-335A-11	Sequence 11, Appl
38	34.6	1.9	2787	10	US-09-815-242-6320	Sequence 6320, Ap
39	34.4	1.9	927	9	US-10-029-180-97	Sequence 97, Appl
40	34.4	1.9	1494	9	US-09-738-626-1237	Sequence 1237, Ap
41	34.2	1.9	522	10	US-09-880-107-1314	Sequence 1314, Ap
42	34.2	1.9	2419	10	US-09-939-408A-12	Sequence 12, Appl
43	34.2	1.9	2741	10	US-09-939-408A-28	Sequence 28, Appl
44	34	1.9	1191	10	US-09-949-562-1	Sequence 1, Appl1
45	34	1.9	3945	10	US-09-747-835A-30	Sequence 30, Appl

ALIGNMENTS

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RESULT 1
US-09-338-723A-5
; Sequence 5, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Humming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338, 723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220, 871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-338-723A-5

Query Match      100.0%  Score 1791:  DB 10:  Length 1791:
Best Local Similarity 100.0%:  Pred. No. 0:
Matches 1791:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

OY      1  GTCAATATGCTGTTCAAGTATGCACTGACACCTCCGGGCTCCTGTGAGTC 60
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Db      1  GTCAATATGCTGTTCAAGTATGCACTGACACCTCCGGGCTCCTGTGAGTC 60

OY      61  CTCGCGATCCCGATGAGACACCGGACCCACCTTGAGGCTGTTGCCGAGTGAAG 120
      |||
Db      61  CTCGCGATCCCGATGAGACACCGGACCCACCTTGAGGCTGTTGCCGAGTGAAG 120

OY      121  ACTGAGCTCTTGCTGACTCCCTCTTGTCTGACAGGCGATGACGACTGGAGTCACT 180
      |||
Db      121  ACTGAGCTCTTGCTGACTCCCTCTTGTCTGACAGGCGATGACGACTGGAGTCACT 180

OY      181  CCAATACACTGCTTACAGGAATGCCCTGCCAATTCACCTGTCAGACCCCAATATG 240
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Db      181  CCAATACACTGCTTACAGGAATGCCCTGCCAATTCACCTGTCAGACCCCAATATG 240

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Db 721 GATGTACCTCGCTGTCGACCGAGGCTGAGAGACAGAGACCTGTGGGAGATGTATCAT 780
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RESULT 2
US-10-080-210-5
; Sequence 5, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bode, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA
US-10-080-210-5
Query Match 100.0%; Score 1791; DB 12; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-10-080-233-1
; Sequence 1, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1e1 Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Stachybotrys sp.
US-10-080-233-1

Query Match 100.0%; Score 1791; DB 12; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 CTGGGATCCGATGAGACACCGGACGCCACCCATTTGAGAGCTGTGATCCGAAGTGAAG 120
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Qy 261 CGGCAAGGACATTTGGTACTATAGATCGAGATCAAGCCATTTACAGAA----- 311
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RESULT 5
US-10-080-210-1
; Sequence 1, Application US/10080210
; Patent No. US2002014242A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO. 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-10-080-210-1

Query Match	82.3%	Score 1474	DB 12	Length 3677	
Best Local Similarity	87.0%	Pred. No. 0			
Matches 1791	Conservative 0	Indels 267	Gaps 5		
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Db	1038	GTCATATGCTGTTCACGATGGAACGCGGAGAGCCTCGGGGCTCCTGCTGGAGTC	1097		
OY	61	CTGGCATCCCATGATGGAGACACGGCAGCCACCCATTTGAGGCTGTTCATCCCAAGTGAA	120		
Db	1098	CTGGCATCCCATGATGGAGACACGGCAGCCACCCATTTGAGGCTGTTCATCCCAAGTGAA	1157		
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Db	1158	ACTGAGGCTTCTGCTGACTCCTCCTCTGTCGACAGAGCGGATGACGACTGGAGTCACCT	1217		
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Db	1278	TCTTATAGSAAAGCCCTGGCAATTCACCTTCAGACAGCCCAAGTGTATGCTTTGAT	1337		
OY	240	-----			
Db	1338	TTTTTCAGAGCACTCGGCCCGCAGCTATATGTATTTCTAGATCAATTACCAACCCCTGTAC	1397		
OY	261	CGGCAAGGACATTTGCTACTATGATGAGATCAAGCCATTTCAGCAAG-----	311		
Db	1398	CGGCAAGGACATTTGCTACTATGATGAGATCAAGCCATTTCAGCAAGGGGTGAGTTT	1457		
OY	312	-----GATTATCCCAACCTT	326		
Db	1458	GCTCAAGAAACCTGTGTAATTAATCAATTGTACGACCCCTTCAGATTTACCCACCTT	1517		
OY	327	GGCCCTGCGCACTGTCTGCGGTACGATGCGATGAGCCCTGTCTTCAATTCAATGTTC	386		
Db	1518	GGCCCTGCGCACTGTCTGCGGTACGATGCGGTGAGCCCTGTCTTCAATTCAATGTTC	1577		
OY	387	CAGAGAACAGAGACGTGATGAGTTGATCAACAATGCGACCGTGGAGCAACGCGTCA	446		
Db	1578	CAGAGAACAGAGACGTGATGAGTTGATCAACAATGCGACCGTGGAGCAACGCGTCA	1637		
OY	447	TCTGCACGGCTCCCATGCGCGCTTTCATGTTGGGCTGGAAGATGACCTTCCC	506		
Db	1638	TCTGCACGGCTCCCATGCGCGCTTTCATGTTGGGCTGGAAGATGACCTTCCC	1697		
OY	507	TGGGAGTACAGAGATTACTACTTTCACAATCCGCGCGCTTCTGTGTACCA	566		
Db	1698	TGGGAGTACAGAGATTACTACTTTCACAATCCGCGCGCTTCTGTGTACCA	1757		
OY	567	TGACCAAGCTTTCATGA-----	583		
Db	1758	TGACCAAGCTTTCATGAAGATATGCTACGAGCCTTATCTTTCCTGGCTACCTTGGCTA	1817		
OY	584	-----AGACTGCTAGAAATGGCTACTTTGGTCAGAGCTGGCCCTACATT	627		
Db	1818	AGCAACTTCCTTCTGTAAGACTCTAGAAATGGCTACTTTGGTCAGAGCTGGCCCTACATT	1877		
OY	628	ATCAACGACGAGGCTGAGAGTCTCGGCTTCTCTAGTGGCTATGGCGAGTTGCATATC	687		
Db	1878	ATCAACGACGAGGCTGAGAGTCTCGGCTTCTCTAGTGGCTATGGCGAGTTGCATATC	1937		
OY	688	CCTCTGATCTTACGCGCCCAAGTACTATAAGCGCGATGGTACCTTGGCTTCGACCGAGGT	747		
Db	1938	CCTCTGATCTTACGCGCCCAAGTACTATAAGCGCGATGGTACCTTGGCTTCGACCGAGGT	1997		
OY	748	GAGGACCAAGGACCTTGAGGAGATGCATCCATGTCACAGGACGACGACGATGGCTTTCCT	807		
Db	1998	GAGGACCAAGGACCTTGAGGAGATGCATCCATGTCACAGGACGACGACGATGGCTTTCCT	2057		
OY	808	AACGTCCAGCCCGCAAGTACCTTTCGATTTCATACGCTGCGGTGTCTGTCTCTGG	867		

Db	2058	AACTCCAGCCCCCAGATGACCGTTTCCGATTCCTCAACGTCGCGTGTCTGTCCTTGG	2117
QY	868	CTCCCTACCCCGTCAGACACAGTCGCCCAAGTCAGAAATTCCTTCCAACTCATTTGGC	927
Db	2118	CTCCTCTACTCGTCGACAGGACAGACTCTCCCAAGCTGAGAAATTCCTTTCCAACTCATTTGGC	2177
QY	928	TCGTATGCTGTCTCTCTCAAGCCCCCGTTCAGACCTCTAACCTCTACCTTCGCTTGGC	987
Db	2178	TCGTATGCTGTCTCTCTCAAGCCCCCGTTCAGACCTCTAACCTCTACCTTCGCTTGGC	2237
QY	988	GAGGTTTACGAGATCATTTATTT-----	1008
Db	2238	GAGGTTTACGAGATCATTTATTTGGTATGCCCCCTCCCTCTCAGAAATGATCAAGAACTCTA	2297
QY	1009	-----GACTTTCACCAACTTTTGTGGCGACAGCTCTTGACCTGGCGCAAGCTT	1053
Db	2298	AGACTAACACTTGTATGAGCTTCCACCAACTTTGCTGGCGAAGCTTTGACTGGCGCAAGCTT	2357
QY	1054	GCTGAGACCAACGATGTGCGCGACGAGAGATGATGATGCTGCGACCTCTCGAGGTATGCGC	1113
Db	2358	GCTGAGACCAACGATGTGCGCGACGAGAGATGATGATGCTGCGACCTCTCGAGGTATGCGC	2417
QY	1114	TTGCTGCGACGCTGTGGGCACTGTGTGAGAGCAAGGCAAGTCCCTCCACTCTCCGTAC	1173
Db	2418	TTGCTGCGACGCTGTGGGCACTGTGTGAGAGCAAGGCAAGTCCCTCCACTCTCCGTAC	2477
QY	1174	GTTCTCTTCCCTCTCTCAAGGAAAGGCCCCCGCGACAAACACTTTCAGTTTGAAGCGACG	1233
Db	2478	GTTCTCTTCCCTCTCTCAAGGAAAGGCCCCCGCGACAAACACTTTCAGTTTGAAGCGACG	2537
QY	1234	AACGACACTACTGATCAACGATGTTTGGCTTTCCGATGTCAATGACGCTGCTCGCC	1293
Db	2538	AACGACACTACTGATCAACGATGTTTGGCTTTCCGATGTCAATGAGGCTGCTCGCGCC	2597
QY	1294	AAGCGCAGGCTCGGCGACGTTTGAGGTCGTGGAGCTCGAACAATCCCTCGAGGCTGAGAG	1353
Db	2598	AAGCGCAGGCTCGGCGACGTTTGAGGTCGTGGAGCTCGAANAACCTCTCGAGGCTGAGAG	2657
QY	1354	CACCCGCTGCATTCATTCACCTTGTGTGACTTTCAGATCCTCAAGCGAACTGGTGTGTGCG	1413
Db	2658	CACCCGCTGCATTCATTCACCTTGTGTGACTTTCAGATCCTCAAGCGAACTGTGTGTGCG	2717
QY	1414	CAGGTCATGCCCCCTACAGGTCGTGCTTAAAGATGTCTGTGTTGGGCGAGGGGTAG	1473
Db	2718	CAGGTCATGCCCCCTACAGGTCGTGCTTAAAGATGTCTGTGTTGGGCGAGGGGTAG	2777
QY	1474	ACCGTGACATCGAGGGCCACTCCAAACCTCGAGCTGAGGCTTACATGTGCGACTGTAC	1533
Db	2778	ACCGTGACATCGAGGGCCACTCCAAACCTCGAGCTGAGGCTTACATGTGCGACTGTAC	2837
QY	1534	AACTCTATTCAGAGATTAACGACATGATGGCTGTATTAACGTCAACGCCATGAGAGAG	1593
Db	2838	AACTCTATTCAGAGATTAACGACATGATGGCTGTATTAACGCTCAACGCCATGAGAGAG	2897
QY	1594	AAGGATATCTTCAGAGAGACTTCGAGAGACCCCATGAAACCCCAAGTGGCGCGCTTCTCT	1653
Db	2898	AAGGATATCTTCAGAGAGACTTCGAGAGACCCCATGAAACCCCAAGTGGCGCGCTTCTCT	2957
QY	1654	TACAAACGCAACGACTTCATGTCGCGGGGTGGGAAATTCCTCGCGGAGGCAATCACTGCC	1713
Db	2958	TACAAACGCAACGACTTCATGTCGCGGGGTGGGAAATTCCTCGCGGAGGCAATCACTGCC	3017
QY	1714	CGAGTCGAGAGCTGGCGCGAGAGAGACCGTCAACCCGCTCGATGAGATCTCTGAGGAT	1773
Db	3018	CGAGTCGAGAGCTGGCGCGAGAGAGACCGTCAACCCGCTCGATGAGATCTCTGAGGAT	3077
QY	1774	CTTGGAAATCGAGGAGTAA 1791	
Db	3078	CTTGGAAATCGAGGAGTAA 3095	

RESULT 6


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|||||
Db 2898 AAGGATATCTTTCAGAGACTTTCAGAGACCCCATGAACCCCAAGTGGCGGCTTCT 2957
OY 1654 TACAACCCGAAGACTTTCATGCTCGCGTGGAAAATTCTCGCGAGTCCATCACTGCC 1713
Db 2958 TACAACCCGAAGACTTTCATGCTCGCGTGGAAAATTCTCGCGAGTCCATCACTGCC 3017
OY 1714 CGAGTGCAGAGAGCTGGCGGAGCAGAGCCGTACACCCGCTCGATGAATCTCGAGAT 1773
Db 3018 CGAGTGCAGAGAGCTGGCGGAGCAGAGCCGTACACCCGCTCGATGAATCTCGAGAT 3077
OY 1774 CTGGAGATCGAGAGTAA 1791
Db 3078 CTGGAGATCGAGAGTAA 3095

RESULT 7
US-10-080-233-5
; Sequence 5, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1el Phenol oxidizing Enzymes
; FILE REFERENCE: GCS67
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid
US-10-080-233-5

Query Match 82.1%; Score 1470; DB 12; Length 2067;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 187; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
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Db 487 CCCTGCCACTCTCTGCGGCTAGCATGGCATGACCCCTGGTCTCACTTTCATATGTTCCAG 546
OY 390 AGGAACAGAGACTGTAGTTAGTTTCATACAAATGCGCACCGTGGAGAACTGGTCCATCT 449
Db 547 AGGAACAGAGACTGTAGTTAGTTTCATACAAATGCGCACCGTGGAGAACTGGTCCATCT 606
OY 450 GCAGGCTCCCATGCGCTGGCCCTTTGATGTTGGGCTGAAGATGAGACTTCCCTGG 509
Db 607 GCAGGCTCCCATGCGCTGGCCCTTTGATGTTGGGCTGAAGATGAGACTTCCCTGG 666
OY 510 CGAGTACAGAGATTACTACTTTCACCACTACCAATCCGCGCTTCTGTGGTACATGA 569
Db 667 CGAGTACAGAGATTACTACTTTCACCACTACCAATCCGCGCTTCTGTGGTACATGA 726
OY 570 CCAGCTTTCATGA----- 583
Db 727 CCAGCTTTCATGAAGGATGCTAGCAGACCTTATCTTCTTGGCTACCTTGGCTAAC 786
OY 584 -----AGACTGTGAAGTCCATCTTGGTGGAGGCTGGCGCTACATATTC 630
Db 787 AACTTCTTTCGTAGACTGTGAGATGCTAGCTTGGTCAAGGCTGGCGCTACATATTC 846
OY 631 AACGACAGAGCTGAGATGCTCTCGGCTCTCTAGTGGCTATGGCGAGTTCGATATCCCT 690
Db 847 AACGACAGAGCTGAGATGCTCTCGGCTCTCTAGTGGCTATGGCGAGTTCGATATCCCT 906
OY 691 CTGATCTGAGGCGCCAGTACTATTAACGCCGATGGTACCCTGCGTTCCAGCAGAGGTGAG 750
Db 907 CTGATCTGAGGCGCCAGTACTATTAACGCCGATGGTACCCTGCGTTCCAGCAGAGGTGAG 966
OY 751 GACCAAGACCTGTGGGGAGATGTCATTCATCAACGGACAGCAGTGGGCTTCTCTTAC 810
Db 967 GACCAAGACCTGTGGGGAGATGTCATTCATCAACGGACAGCAGTGGGCTTCTCTTAC 1026
OY 811 GTCCAGCCCGCAAGTACCGTTCCGATTCCTCAACGCTGCGGTCTCGTCTGGCTC 870
Db 1027 GTCCAGCCCGCAAGTACCGTTCCGATTCCTCAACGCTGCGGTCTCGTCTGGCTC 1086
OY 871 CTCTACCTCTGTCAGACACGCTCTCCCAAGCTGACAGATTCCTTCCAGTCACTTGGCT 930
Db 1087 CTCTACCTCTGTCAGACACGCTCTCCCAAGCTGACAGATTCCTTCCAGTCACTTGGCT 1146
OY 931 GATGCGGTCTGCTTCAACCCCGGTCAGACCTGTAACCTGACCTTCTGTGGCGAG 990
Db 1147 GATGCGGTCTGCTTCAACCCCGGTCAGACCTGTAACCTGACCTTCTGTGGCGAG 1206
OY 991 CGTTACGAGATCAATAT----- 1008
Db 1207 CGTTACGAGATCAATATGCTCCCTCCCTCAGCATGAGTCAAGAACTAAGA 1266
OY 1009 -----GACTTCAACAACTTGTCTGGCGAGACTCTTGGACCTGGCAACGTTC 1056
Db 1267 CTAAACACTGTGAGACTTCAACAACTTGTCTGGCGAGACTCTTGGACCTGGCAACGTTC 1326
OY 1057 GAGACCAAGAGTGTGGGCGAGCAGAGATGATGAGTGGCGACTCTCGAGGTGATGGCTTC 1116
Db 1327 GAGACCAAGAGTGTGGGCGAGCAGAGATGATGAGTGGCGACTCTCGAGGTGATGGCTTC 1386
OY 1117 GTCTGAGCTGTGGCACTGTGGAGCAACAGCAGAGTCCCTCCACTCTCGGTGACGTT 1176
Db 1387 GTCTGAGCTGTGGCACTGTGGAGCAACAGCAGAGTCCCTCCACTCTCGGTGACGTT 1446
OY 1177 CCTTTCCTCTCACAAGAGGCCCCGCGACAGCACTTCAAGTTTAAAGCAGCAAC 1236
Db 1447 CCTTTCCTCTCACAAGAGGCCCCGCGACAGCACTTCAAGTTTAAAGCAGCAAC 1506
OY 1237 GAGCACTACTGATCAACAGATGTGGCTTGGCGAGTCAATGAGGCTGCTGGCGAAG 1296
Db 1507 GAGCACTACTGATCAACAGATGTGGCTTGGCGAGTCAATGAGGCTGCTGGCGAAG 1566
OY 1297 CCGGACCTCGGCACTGTGGAGTCTGAGAACTCCTCTGAGGCTGAGCCAC 1356
|||||
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Db 1567 CCCGAGCTCGCCACCCGTTGAGGCTGAGGAGCTCGAAGAACTCCCTGTGAGGCTGAGCCAC 1626
OY 1357 CCCGTCACATTCACCTGTTGACTTTCAGAGATCTCAAGCAGAACTGGTGGTGGCCAG 1416
Db 1627 CCCGTCACATTCACCTGTTGACTTTCAGAGATCTCAAGCAGAACTGGTGGTGGCCAG 1686
OY 1417 GTCATGCCCTACGAGTCTGCTGGTCTTAAGATGTCGTGCTGGTGGGAGGGGTGAGACC 1476
Db 1687 GTCATGCCCTACGAGTCTGCTGGTCTTAAGATGTCGTGCTGGTGGGAGGGGTGAGACC 1746
OY 1477 CTGACACATCGAGGCCACTACCAACCCCTGGAGCTGAGCTTACATGTGGCATCTCAAC 1536
Db 1747 CTGACACATCGAGGCCACTACCAACCCCTGGAGCTTACATGTGGCATCTCAAC 1806
OY 1537 CTCATTCAGAGGATACGACATGATGGCTGTATTCACGTCACCGCCATGGAGGAGAG 1596
Db 1807 CTCATTCAGAGGATACGACATGATGGCTGTATTCACGTCACCGCCATGGAGGAGAG 1866
OY 1597 GGATATCTTCAGAGAGACTTCGAGAGACCCCATGAACCCCAATGGAGCGCCGTTCTTAC 1656
Db 1867 GGATATCTTCAGAGAGACTTCGAGAGACCCCATGAACCCCAATGGAGCGCCGTTCTTAC 1926
OY 1657 AACCCGAACGACTTCATGCTGCTGCGCTGGAAACTTCTCCGCGAGTCCATCACTGCCGA 1716
Db 1927 AACCCGAACGACTTCATGCTGCTGCGCTGGAAACTTCTCCGCGAGTCCATCACTGCCGA 1986
OY 1717 GTGAGAGGCTGGCGGAGAGGAGCCGTACAAACGCGCTCGATGAGATCCTGAGAGATCT 1776
Db 1987 GTGAGAGGCTGGCGGAGAGGAGCCGTACAAACGCGCTCGATGAGATCCTGAGAGATCT 2046
OY 1777 GGAATCGAGAGTA 1790
Db 2047 GGAATCGAGAGTA 2060

RESULT 8
US-09-338-723A-3
: Sequence 3, Application US/09338723A
: Patent No. US20020019038A1
: GENERAL INFORMATION:
: APPLICANT: Humming, Wang
: TITLE OF INVENTION: Phenol Oxidizing Enzymes
: FILE REFERENCE: GC561-2
: CURRENT APPLICATION NUMBER: US/09/338,723A
: CURRENT FILING DATE: 1999-06-23
: PRIOR APPLICATION NUMBER: 09/220,871
: PRIOR FILING DATE: 1998-12-23
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 2905
: TYPE: DNA
: ORGANISM: Bipolaris spliciferae
US-09-338-723A-3

Query Match 28.1%; Score 503.4; DB 10; Length 2905;
Best Local Similarity 60.6%; Pred. No. 1,4e-133;
Matches 998; Conservative 0; Mismatches 511; Indels 138; Gaps 5;

OY 245 TTACCAACCTGTGCACGCGAAGACATTTGGTACTATGATCGATCAAGCCATTTC 304
Db 423 TCACGAATCTGTGCACAAAGAGATATGTACTACGAGATTGTCAAAACCTTCA 482
OY 305 AGCAAGAGATTACCCCACTTGGCCCTGCGACCTCTGCGGCTACGATGGCATGAGCC 364
Db 483 CCCAGACAGTGTATCGACGCTGCGCCCTGCTGCTTGTAGTACGATACGCGCATCTCC 542
OY 365 CTGCTCTACTTTCATATGTCACAGAGAACAGAGACTAGTATGTTAGTTCATCAATG 424
Db 543 CAGGTCTTACATCATATATGCGGAGAGAACAGAGACTGTTGTACGGTTTATTAACCAAG 602
OY 425 CCACGCTGAGAACTGGTTCATCTGACGCGCTCCCATCGCGTCCCTTTCGATGTT 484

Db 603 GTATACGCCAAAGCTTCATCATCTTCACAGGCTCCCTCCGCTGCCCCCTTTGAGGAT 662
OY 485 GGGCTGAAGATGTGACCTTCCCTGGCGAGTACA----- 518
Db 663 GGGCTGATGATATGATCATGAAGGGGAATCAAAAGTACGATAGCTGTGATCTACGC 722
OY 519 -----GATTACTACTTCCCACTA 539
Db 723 ATCAGGAAGCCTTATCATACTACAGAGACTTCTTCTCAGACTACTACTACCCGACAA 782
OY 540 CCAATCCGCCGCTTCTGTGTACCATGACAGCGTTTCA----- 580
Db 783 CCAAGCTGCCAGATTTTGTGTACACGATCATGCTATGATGTTGAAGTCTTACCG 842
OY 581 -----TGAAGACTGCTGAGATG 598
Db 843 ACTTTTCATGTAGTGAAGAGAGATTAACTTAACATCTGTGAGAGCCGAGAAAAG 902
OY 599 CCTACTTTGTCAGGCTGGCGCTACATTAATCAGAGAGGCTGAGATGCTCTCGCTC 658
Db 903 CCTATTTTGGGGCAAGCCGGCGCTTACCTGATACAGACCCGCTGAGATGCTTCGGCC 962
OY 659 TTCTAGTGGCTATGGCGAGTTGATATCCCTGATCTGACGGCCAAATGACTATAAG 718
Db 963 TTCTAGTGGCTATGGCGAGAAATACAGACATTCCGCTGCTCAGTTTCAAGTACTAAG 1022
OY 719 CCGATGATCCCTTGGCTTGACCGAGGTGAGAGACGACTGTGGGAGATGTCATC 778
Db 1023 CCGATGGAATCTTAAAGACATGTGGGAGAGAAAGTGTGTTGGGCGCATCATCC 1082
OY 779 ATGCAACGAGACGATGCGCTTCTTAAGCTTCAGCTCAGCCCGCAAGTACGTTCCGAT 838
Db 1083 ATGTCACGATGAGCGCCCTGCTTCTTAATGTGAGCTCGGAAGATGCTCTTCGAT 1142
OY 839 TCCCTAAGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 898
Db 1143 TCCCTAAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1202
OY 899 AGCTGAGATTCCTTTCACAGTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 958
Db 1203 CCAGTAGCTTCTTTCAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1262
OY 959 AGACCTTACCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1018
Db 1263 AAACCTCAGATATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1322
OY 1019 ACTTGTGCGGCAAGCTTGAAGCTGCGCAAGTGTGAGACAGATGTGCGCGAG 1078
Db 1323 CCTATGCGGCGCAAGCGTGTGATGTGCGCAACTGCGCAAGTGTGATGTGCGTACCG 1382
OY 1079 AGGATGAGTACGCTGCGACTCTGAGAGTGTATGCGCTGCTGCTGCTGCTGCTGCTGCT 1138
Db 1383 AGGAGACTACGCAAAACATGACAAAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1442
OY 1139 AGCAACAGCCAGGTCCTCCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1198
Db 1443 TCGATTAATCCGTGTGATACCGGACAGCTATCTCAATCAGTATCCCGCGGACA---AAA 1499
OY 1199 GCCCGCGCAGCAAGCACTTCAAGTTTGAACGCGCAAGCGACATCTGATCAACGATG 1258
Db 1500 CCGACATATGACATCATCTTCCGTTTCAATGTCAGAGGCGAGTGGCGATCGGCA 1559
OY 1259 TTGGCTTTGGCGATGCTCAATGAGCTGTCTGCGCAAGCCGAGTGGCAGCTTGTAGG 1318
Db 1560 TCGGGTTTGGCAAGCTCGGAAGCCGTGTTTGGCCAAAGTACCGCGGTACTGTGAGC 1619
OY 1319 TCTGGAGCTCGAAGCTCTGAGAGCTGAGAGCCCGCTGACATTCATCACTTGTG 1378
Db 1620 TTTGGGAATGTGAAGACAGCTCGCGCGCTGTCAACCCCTTCCAGCTCCAGTATAG 1679
OY 1379 ACTTCAAGATCTCAAGCAAGCTG-----TGATGTCGCGAGGCTATGCTCAGAGT 1432
Db 1680 ACTTCCAGATGTGTCGCGCTACGCGGCGAGCAAGGCAAGTACGCGCGCTCATGCGCTATGAG 1739

QY	1701	GTTCATCACTGCCCGAGTGCAGGAGCTGGCGGAGCAGGAGCGGTACAACCGGCTCGATGA	1760
Db	1938	TGCCATCACTGACCGCATTCAGGAGATGGCTAGCTTCAACCCCTACGCCCAAGGCTGATGA	1997

RESULT 13

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US-10-080-210-8
Sequence 8, Application US/10080210
Patent No. US20020142423A1
GENERAL INFORMATION:
APPLICANT: Wang, Huang
APPLICANT: Bodie, Elizabeth A.
TITLE OF INVENTION: Phenol oxidizing Enzymes
FILE REFERENCE: GC561-3
CURRENT APPLICATION NUMBER: US/10/080,210
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/220, 871
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 09/338, 723
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 858
TYPE: DNA
ORGANISM: Amorospodium atrum
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(858)
OTHER INFORMATION: n = A,T,C or G
US-10-080-210-8

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Query Match	10.5%;	Score 188.6;	DB 12;	Length 858;
Best Local Similarity	60.2%;	Pred. No. 5.6e-44;		
Matches 434;	Conservative 0;	Mismatches 254;	Indels 33;	Gaps 6;

QY	586	ACTGCTGAGAAATGCTCTACTTTGGTCAGAGCTGGCGCCCTACATTAATATACAGACAGAGCTGAG	645
Db	2	ACCGCGCGAAGAACGGCTCTACTTTGGTCAGAGCTGGCGCTTTTACATTTCTGCGACACCCCGCTCA	61
QY	646	GATGCTCGCGGTTCCTAGTGGCTATGGGAGCTTGATATCCCTGTATTCGTGACGGCC	705
Db	62	GATGCTATTTGGCTGTGCGCT-----TCTGGCAAGTATGATGTACTCTTCTGCACTGTCTCC	115
QY	706	AAGTACTATTAACGGCGGATGAGTACCTGCTCTTCACCGAGAGGTGAGAGACCGAGCACTGTGG	765
Db	116	AAGCAGTACAAACACCGACGAGTACCTCTTGAGCCCAAGAGACGAGACCATTTACTGTTCC	175
QY	766	GGAGATGTCAATCATGTCTCAACGCGACGCCATGGGCTCTTCTTAAGCTTCAGCCCGCCGCAAG	825
Db	176	GGCGATGTCAATCCAGTCAACGCGACGCCATGGGCTCTTAAAGTGTGAGCGCTCGCAAG	235
QY	826	TACCGTTTCGCATTTCTTCACACGCTGGCGGTGTCTGTGCTTGGCTCCTTACTACTCGTCAAG	885
Db	236	TACCGTCTTCGCTTCTCTTCCAAAGCTGCTATCAGCGCTGC-----CTTCAAGCTCACT	286
QY	886	ACCACCTCTCCCAACGTACAGAAATCCTTCCCAAGTATGTGCTCTGATAGTCTGTGCCCTT	945
Db	287	TTTCGAGGCTGATGGCAAACTGATTAACCTTCTGTCTATGAGTGTGCGATACTGGTCTCTTGG	346
QY	946	CAAGCGCCCGTTTCAGACCTTAACCTCTTACTCTGTGCTGCTTCCGACAGCTTACAGATCAAT	1005
Db	347	ACCAAGCGCTGTTCAGACAGAAACCTTGAATCTCTATATGGCCGACGGCTGGGAGGTGTGT	406
QY	1006	ATTGACTTACCAACATTTGTGTGGCGAGACTCTTGACCTGCGCAACGTTGCTGAGACCAAC	1065
Db	407	TTTGTACTTCAGACAATTTTCCGGGAAGAAGTATACCTCTCAAGAACGCTGG-----C	457
QY	1066	GATGTTCGCGAGAGAGATGAGTACGCTGCACATCTCGAGGTGATGCGGCTTTCGTCTCAAC	1122
Db	458	GATGTTCGAGACAGATGAGAGATCAATCACTCAACGCAACCACTCACTGTGAGTTCTGTGTTGGC	517

QY	1126	TCTGGCACTGTT-----GAGGACAAACGCAAGTCCCTCCACATCTCGTAGCTTCT	1129
Db	518	AAGGATGTTACGAGCCAGGCGTGTGAATGGCAACCTTCGCGCTCTGCGCACTGTTC	577
QY	1180	TTCCCTCTCTACAGGAAGGCCCGCCGACCAACCTTCACAGTT--TGAACGAGCAGACGG	1238
Db	578	TTCCCTCTTAAGAAGG--GGCGGAGTGCACAGGAGCTTCAAGTTGCGGACGAGGACGGT	635
QY	1239	ACACTAACCTGATCAACAGATGTGGCTTTGGCATGTCAATGAGACGCTGCTTGCCCAAGCC	1298
Db	636	CCAGTGGACATGTTAATGAGCTTGACCTTCGCGTATGTCACAAACCGGATCTTGCTAAAGCC	695
QY	1299	C	1299
Db	696	C	696

RESULT 14
US-09-738-626-1053

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1  Sequence 1053, Application US/09738626
2  Publication No. US20020197605A1
3  GENERAL INFORMATION:
4  APPLICANT: NAKAGAWA, SATOSHI
5  APPLICANT: MIZOGUCHI, HIROSHI
6  APPLICANT: ANDO, SEIKO
7  APPLICANT: HAYASHI, MUKIRO
8  APPLICANT: OCHIAI, KETKO
9  APPLICANT: YOKOI, HARUHIKO
10 APPLICANT: TATEISHI, NAKKO
11 APPLICANT: SENOH, AKIHITO
12 APPLICANT: IKEBA, MASATO
13 APPLICANT: OZAI, AKIO
14 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
15 FILE REFERENCE: 249-125
16 CURRENT APPLICATION NUMBER: US/09/738, 626
17 CURRENT FILING DATE: 2000-12-18
18 PRIOR APPLICATION NUMBER: JP 99/377484
19 PRIOR FILING DATE: 1999-12-16
20 PRIOR APPLICATION NUMBER: JP 00/159162
21 PRIOR FILING DATE: 2000-04-07
22 PRIOR APPLICATION NUMBER: JP 00/280988
23 PRIOR FILING DATE: 2000-08-03
24 NUMBER OF SEQ ID NOS: 7059
25 SOFTWARE: PatentIn ver. 3.0
26 SEQ ID NO 1053
27 LENGTH: 1533
28 TYPE: DNA
29 ORGANISM: Corynebacterium glutamicum
30 US-09-738-626-1053

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Query Match	4.5%	Score 79.8;	DB 9;	Length 1533;
Best Local Similarity	47.3%	Pred. No. 8.5e-13;		
Matches 240; Conservative	0;	Mismatches 267;	Indels 0;	Gaps 0;

[illegible]

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OY 646 GATGCTCTGCTCTTCTAGTGGCTATGGGAGTTGCATATCCCTGATCTGACGGC 705
    || || || || || || || || || || || || || || || || || || || ||
Db 544 GACAACGTGGATCTGCGACGGGATGCGATGATATTCGGCTGTTTAAATGAT 603
OY 706 AAGTACTATAAGCGCGGATGACCTGCGCTGACCGAGGATGAGAACGACCTGTGG 765
    || || || || || || || || || || || || || || || || || || || ||
Db 604 CACCGCTTCTTAGAAGACGGTTCCCTTGATGAGGAAGACCTCCCGATCTTGGCTGTTG 663
OY 766 GGAGATGTCATCATGTCACGAGCAGCATGCGCTTTCCTTAAGCTCCAGCCCGCAAG 825
    || || || || || || || || || || || || || || || || || || || ||
Db 664 GCGGATACCCCGCATGCGCATTTACCAATGCGCACTTGTGATGCGACACGCGCGG 723
OY 826 TACCGTTTCCGATTCCTCAACGCTGCC 852
    || || || || || || || || || || || || || || || || || || || ||
Db 724 GTTCGGTTCCGGGTGCTCAACGGCTCC 750
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RESULT 15
US-09-950-335A-11/c
; Sequence 11, Application US/09950335A
; Publication No. US20020193330A1
; GENERAL INFORMATION:
; APPLICANT: HONE, DAVID M.
; TITLE OF INVENTION: GENETICALLY ENGINEERED CO-EXPRESSION DNA VACCINES, CONSTRUCTION M
; FILE REFERENCE: 4115-128
; CURRENT APPLICATION NUMBER: US/09/950,335A
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6442
; TYPE: DNA
; ORGANISM: Bordetella pertussis
US-09-950-335A-11
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Query Match 2.6%; Score 45.8; DB 9; Length 6442;
Best Local Similarity 48.0%; Pred. No. 0.0091;
Matches 131; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
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OY 934 GCTGCTCTCTTCAAGCCCCGTTGAGACCTCTAACCTTACTGCTGTGGCGAGCGT 993
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Db 4169 GCCGCGCGCGCGGATGACCGGTGTTGGCCCTGCGCCGCAACGAGGCTGCTTGGCGGG 4110
OY 994 TAGAGATCATATATGACTTCAACCACTTGTGTGGCAGACTCTTGACCTGGCAACGTT 1053
    || || || || || || || || || || || || || || || || || || || ||
Db 4109 GCCGCCATCCACCTGTGCTGCGCCGACCCGCGGCTAGGAAGTTGCTGCGCATTTGCC 4050
OY 1054 GCTGAGACCAAGATGTGCGAGAGATGATGAGTCACTCTCGACCTCGAGGTGATGGCG 1113
    || || || || || || || || || || || || || || || || || || || ||
Db 4049 GGTGATCGAATGCTTGCGGCGCCCGCGATGATGCTGACATGCTCGAGCGTGTGAC 3990
OY 1114 TTGCTGTCAGCTGTGGCACTTTGAGACAACAGCAGTCCCTCCACTCTCCGTGAC 1173
    || || || || || || || || || || || || || || || || || || || ||
Db 3989 CTCCACCACTTCCCGAGCGAGCGGCGAGCTCGAGATGCGGTAATTGACATTTCCGTGG 3930
OY 1174 GTTCCTTTCCTCTCTCACAAGAGAGCCCGCC 1206
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Db 3929 CTTGGCGTAGGCGGTTGCTGGGTAGCCACGCGC 3897
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Search completed: February 13, 2003, 05:15:01
Job time : 105.903 secs

This Page Blank (uspio)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 18:21:11 ; Search time 2415.3 Seconds
(without alignments)
12009.347 Million cell updates/sec

Title: US-09-218-702-1

Perfect score: 1791

Sequence: 1 gtcaatacgtctcaagtc.....atcttgatcgagagatga 1791

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
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27: em_estba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112.4	6.3	600	10	BE188240 M7ATIG In
2	112.4	6.3	700	10	BE187716 B10X In
3	78.8	4.4	664	10	BE188099 CFC377-R
4	51.8	2.9	580	13	BUI59802 BUI59802
5	48.6	2.7	599	12	BF258534 HVSMEF001
6	48.4	2.7	465	12	BC053739 RH122_9_B

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	8	47.4	2.6	848	10	BE216983	BE216983
	9	46.2	2.6	608	14	B0094667	B0094667
	10	44.6	2.5	463	12	BF059036	BF059036
	11	44.6	2.5	481	9	AI394530	AI394530
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	13	44.2	2.5	541	9	AI432408	AI432408
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	15	43.8	2.4	552	17	AZ302933	AZ302933
	16	43.8	2.4	584	12	BF258684	BF258684
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	19	43.6	2.4	640	13	BM585335	BM585335
	20	43.6	2.4	646	13	BM635882	BM635882
	21	43.6	2.4	662	13	BM626865	BM626865
	22	43.6	2.4	670	13	BM637091	BM637091
	23	43.6	2.4	682	13	BM652511	BM652511
	24	43.6	2.4	694	13	BM637162	BM637162
	25	43.2	2.4	467	14	W15474	W15474
	26	43.2	2.4	337	9	AA788842	AA788842
	27	43.2	2.4	409	9	AA731500	AA731500
	28	43.2	2.4	426	9	AA807669	AA807669
	29	43.2	2.4	442	9	AA687287	AA687287
	30	43.2	2.4	451	9	AI189014	AI189014
	31	43.2	2.4	463	10	AA576243	AA576243
	32	43.2	2.4	500	9	AI126707	AI126707
	33	43.2	2.4	507	9	AA977691	AA977691
	34	43.2	2.4	538	10	BE379236	BE379236
	35	43.2	2.4	571	10	AA007209	AA007209
	36	43.2	2.4	646	14	BM794003	BM794003
	37	43.2	2.4	777	12	BG744974	BG744974
	38	42.6	2.4	435	10	AA575077	AA575077
	39	42.6	2.4	463	12	BF446871	BF446871
	40	42.6	2.4	480	9	AA481991	AA481991
	41	42.6	2.4	486	9	AA825413	AA825413
	42	42.6	2.4	496	9	AI606612	AI606612
	43	42.6	2.4	497	9	AI187025	AI187025
	44	42.6	2.4	505	9	AA411507	AA411507
	45	42.6	2.4	508	9	AI200611	AI200611

ALIGNMENTS

RESULT 1
LOCUS BE188240 600 bp mRNA linear EST 25-SEP-2000
DEFINITION M7ATIG In vitro expressed cDNAs Cladosporium fulvum CDNA similar to
Bilirubin oxidase precursor, mRNA sequence.
ACCESSION BE188240
VERSION BE188240.1 GI:8667479
KEYWORDS
SOURCE
ORGANISM Cladosporium fulvum.
Cladosporium fulvum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothyriomycetes incertae sedis; Mycosphaerellaceae; mitosporic
Mycosphaerellaceae; Cladosporium.
REFERENCE
1 (bases 1 to 600)
AUTHORS Clark,A.J., Rasmussen,S.W. and Oliver,R.P.
TITLE In vitro expressed genes of Cladosporium fulvum
JOURNAL Unpublished (2000)
COMMENT Contact: R.P. Oliver
Necrotrophic Phytopathology Research Centre
Murdoch University
SABC, Perth 6150, Western Australia
Tel: +61-8-9360-7404
Fax: +61-8-9360-6303
Email: roliver@central.murdoch.edu.au
High quality sequence stop: 600
POLYA-No.
location/Qualifiers
1..600
/organism="Cladosporium fulvum"

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/strain="Race 4"
/db_xref="taxon:5499"
/clone_lib="In vitro expressed cDNAs"
/tissue_type="Mycelium"
/note="Vector: Lambda bluescript: A mixture of mycelial
cultures grown in liquid B5 for 48 hours and transferred
for 24 hours to media lacking carbon, nitrogen or
supplemented with hydrogen peroxide"
BASE COUNT      131 a      176 c      162 g      128 t      3 others
ORIGIN

Query Match      6.3%; Score 112.4; DB 10; Length 600;
Best Local Similarity 55.9%; Pred. No. 1.8e-17;
Matches 313; Conservative 0; Mismatches 238; Indels 9; Gaps 5;

OY 1062 CAACGATGTCGGGAGGAGATGATGACCTGCGACTGCGAGGTGATGCGCTGCTGCT 1121
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DB 42 CAACAGGGGGGACAAACACGNGNCATATACACCGACAGATCATAGAGTTGCTGCT 101
OY 1122 CAG--CTCTGGCACTGTGGAGACAACAGCCAGGTCCCTCCACTCTCCGTGACGTTCC 1178
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 102 TGGAGACAGGTCACCGAGAGTCAACAACAGTACCATCACTTGAGCGGTCCAT 161
OY 1179 TTTCCTCTCTCACAGGAAGGCCCGCCGACAAGCACTTCAAGTTTGAACGCAACGG 1238
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 162 CGAGTGGCGAGCGACGACGACACTATTGACAAGACCTTCAACTTCCAGATGGCGCGC 221
OY 1239 ACACACTGCTGA---TCAGAGATGTTGGCTTTCGCGATGTCATGAGCGGTGCTGCCAA 1295
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 222 GGAAGCTGTGAGACCGCTCAATAGCGGTGATTTACGCGACCCGAATCCGCTGTGCTAG 281
OY 1296 GCCGAGCTCGGACCGTGTGAGGTCTGGAGACTCGAGAACTCCTCTGGAAGCTGAGCCA 1355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 282 GCGGCCACAAGGACACTGTGAGGCTTGGCGCTCGTGACACTGGGGGCTCGGCTGCCA 341
OY 1356 CCCCCTCCATTCACACTTGTGTACTCAAGATCCTCAAGCACTGCTGCTGCTGCCA 1415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 342 CCCAGTACATATCCATCTGTCAACATGCAAGGTCTCTGCGACTGCTGCTGCCGCTG 401
OY 1416 GGTCAATGCCCTAGAGTCTGCTGCTTTAAGATGTCGTCGTGTTGGGAGGGGCTGAGAC 1475
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 402 CCTCATGCCATATAGAGCTGTGCTGTGAAGAAGCTGCTTATCTGCTGCTGCGACAT 461
OY 1476 CCTGACCATGAGGCCCATACCAACCTGAGCTGAGCTTACATGTGCACTGTGCACA 1535
    ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 462 TGTGACAGTGTGCTTTTACGCTCTTGAACGG-CTTGACATGTTTCATTGTGCAC-A 519
OY 1536 CCTCATTCACAGAGATACGACATGATGG-CTGTATTCAACGTCACCGCATGGAGAGA 1594
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 520 CCTTGTACAGGAAGATCACACCATGATGGCCGCTTCAACAGACACCCCTTGAACGCTG 579
OY 1595 AGGATATCTTCAGAGGAC 1614
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 580 GGCTACGACTTCAACAGCAC 599

RESULT 2
LOCUS      BE187716      700 bp      mRNA      linear      EST 25-SEP-2000
DEFINITION Billrubin in vitro expressed cDNAs Cladosporium fulvum cDNA similar to
ACCESSION      BE187716
VERSION      BE187716.1 GI:8666955
KEYWORDS      EST.
SOURCE      Cladosporium fulvum.
ORGANISM      Cladosporium fulvum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothyrionmycelis incertae sedis; Mycosphaerellaceae; mitosporic
Mycosphaerellaceae; Cladosporium.
REFERENCE      Clark,A.J., Rasmussen,S.W. and Oliver,R.P.
AUTHORS      Clark,A.J., Rasmussen,S.W. and Oliver,R.P.
TITLE      In vitro expressed genes of Cladosporium fulvum
JOURNAL      Unpublished (2000)
```

```
COMMENT
Contact: R.P.Oliver
Necrotrophic Phytopathology Research Centre
Murdoch University
SABC, Perth 6150, Western Australia
Tel: +61-8-9360-7404
Fax: +61-8-9360-6303
Email: roliver@central.murdoch.edu.au
High quality sequence stop: 700
POLYA-No.

FEATURES
source
location/Qualifiers
1..700
/organism="Cladosporium fulvum"
/strain="Race 4"
/db_xref="taxon:5499"
/clone_lib="In vitro expressed cDNAs"
/note="Vector: Lambda bluescript: A mixture of mycelial
cultures grown in liquid B5 for 48 hours and transferred
for 24 hours to media lacking carbon, nitrogen or
supplemented with hydrogen peroxide"
BASE COUNT      158 a      206 c      183 g      146 t      7 others
ORIGIN

Query Match      6.3%; Score 112.4; DB 10; Length 700;
Best Local Similarity 55.9%; Pred. No. 2e-17;
Matches 313; Conservative 0; Mismatches 238; Indels 9; Gaps 5;

OY 1062 CAACGATGTCGGGAGGAGATGATGACCTGCGACTGCGAGGTGATGCGCTGCTGCT 1121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 42 CAACAGGGGGGACAAACACGNGNCATATACACCGACAGATCATAGAGTTGCTGCT 101
OY 1122 CAG--CTCTGGCACTGTGGAGACAACAGCCAGGTCCCTCCACTCTCCGTGACGTTCC 1178
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 102 TGGAGACAGGTCACCGAGAGTCAACAACAGTACCATCACTTGAAGGTCAT 161
OY 1179 TTTCCTCTCTCACAGGAAGGCCCGCCGACAAGCACTTCAAGTTTGAACGCAACGG 1238
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 162 CGAGTGGCGAGCGACGACGACACTATTGACAAGACCTTCAACTTCCAGATGGCGCGC 221
OY 1239 ACACACTGCTGA---TCAGAGATGTTGGCTTTCGCGATGTCATGAGCGGTGCTGCCAA 1295
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 222 GGAAGCTGTGAGACCGCTCAATAGCGGTGATTTACGCGACCCGAATCCGCTGTGCTAG 281
OY 1296 GCCGAGCTCGGACCGTGTGAGGTCTGGAGACTCGAAGAACTCCTCTGGAAGCTGAGCCA 1355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 282 GCGGCCACAAGGACACTGTGAGGCTTGGCGCTCGTGACACTGGGGGCTCGGCTGCCA 341
OY 1356 CCCCCTCCATTCACACTTGTGTACTCAAGATCCTCAAGCACTGCTGCTGCTGCCA 1415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 342 CCCAGTACATATCCATCTGTCAACATGCAAGGTCTCTGCGACTGCTGCTGCCGCTG 401
OY 1416 GGTCAATGCCCTAGAGTCTGCTGCTTTAAGATGTCGTCGTGTTGGGAGGGGCTGAGAC 1475
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 402 CCTCATGCCATATAGAGCTGTGCTGTGAAGAAGCTGTTATGCTGCTGCTGCGACAT 461
OY 1476 CCTGACCATGAGGCCCATACCAACCTGAGCTGAGCTTACATGTGCACTGTGCACA 1535
    ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 462 TGTGACAGTGTGCTTTTACGCTCTTGAACGG-CTTGACATGTTTCATTGTGCAC-A 519
OY 1536 CCTCATTCACAGAGATACGACATGATGG-CTGTATTCAACGTCACCGCATGGAGAGA 1594
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 520 CCTTGTACAGGAAGATCACACCATGATGGCCGCTTCAACAGACACCCCTTGAACGCTG 579
OY 1595 AGGATATCTTCAGAGGAC 1614
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 580 GGCTACGACTTCAACAGCAC 599

RESULT 3
LOCUS      BE188099      664 bp      mRNA      linear      EST 25-SEP-2000
DEFINITION CFC377-R In vitro expressed cDNAs Cladosporium fulvum cDNA similar
to Billrubin in vitro expressed precursor, mRNA sequence.
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ACCESSION BE188099
 VERSION BE188099.1 GI:8667338
 KEYWORDS EST
 SOURCE Cladosporium fulvum.
 ORGANISM Cladosporium fulvum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et Chaetochytriomycetes incertae sedis; Mycosphaerellaceae; mitosporic Mycosphaerellaceae; Cladosporium.
 1 (bases 1 to 664)
 REFERENCE Clark,A.J., Rasmussen,S.W. and Oliver,R.P.
 AUTHORS In vitro expressed genes of Cladosporium fulvum
 TITLE Unpublished (2000)
 JOURNAL Contact: R.P. Oliver
 COMMENT Necrotrophic Phytopathology Research Centre
 Murdoch University
 SABC, Perth 6150, Western Australia
 Tel: +61-8-9360-7404
 Fax: +61-8-9360-6303
 Email: roliver@central.murdoch.edu.au
 High quality sequence stop: 664
 POLY(A)-No.
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 /organism="Cladosporium fulvum"
 /strain="Race 4"
 /db_xref="taxon:5499"
 /clone_lib="In vitro expressed cDNAs"
 /tissue_type="Mycelium"
 /note="Vector: Lambda bluescript; A mixture of mycelial cultures grown in liquid B5 for 48 hours and transferred for 24 hours to media lacking carbon, nitrogen or supplemented with hydrogen peroxide"
 BASE COUNT 149 a 174 c 174 g 140 t 27 others
 ORIGIN
 Query Match 4.4%; Score 78.8; DB 10; Length 664;
 Best Local Similarity 58.1%; Pred. No. 6e-09;
 Matches 176; Conservative 0; Mismatches 120; Indels 7; Gaps 2;
 QY 758 ACCTGGGAGATGTCATGCATGTCAGCAGCAGCCATGCGCTTTCCTTAAGTCGACG 817
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 DB 32 ACTTCTTCGCGCATACGATGAGTGATCGAGCCATGCGCATTCGTAACGTCGACG 91
 11
 QY 818 CCGGCAAGTACGGTTCCGATTCCTCAAGCGCGCTGCTGCTGCTGCTCTTACC 877
 11
 DB 92 CTGCGAAGTACCGATTCACACTCTT-----TGATATGCTCTAAGCAGATCTTACGACA 145
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 QY 878 TCGTCAGACCAAGCTCTCCCAAGCTCAGAAATTCCTTCCAAAGTCATGGCTGATGCTG 937
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 DB 146 TCTACTTGTCTGATGAGAACACAAACCAATTCATTCAGATCATTTGGCTCAGACTCGG 205
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 QY 938 GTCTCTTCAGAGCCCGCTTCAGAGCTTCAACCTTACCTTGGCTGTGGCGAGCGTTACG 997
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 DB 206 GCGTATTCGCCCGCTTCGAGAGCGAGTGTCTTCCATGAGGAGAGCGCT-TG 264
 11
 QY 998 AGATCATTTTGAAGTACCAACTTGGCGCAGACTTGAACGCCCAAGCTTGCTG 1057
 11
 DB 265 AGATCATTTTGAAGTACCAACTTGGCGCAGACTTGAACGCCCAAGCTTGCTG 324
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 QY 1058 AGA 1060
 11
 DB 325 AGA 327
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 RESULT 4
 BUI59802 580 bp mRNA linear EST 24-JAN-2002
 LOCUS BUI59802 full length cDNA library, chloronemata and young
 DEFINITION gametophores Physcomitrella patens subsp. patens cDNA clone
 pp1h7c15 5', mRNA sequence.
 ACCESSION BUI59802
 VERSION BUI59802.1 GI:18327798
 KEYWORDS EST.

SOURCE Physcomitrella patens subsp. patens.
 ORGANISM Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariaceae; Physcomitrella.
 1 (bases 1 to 580)
 REFERENCE Fujita,T., Shin-I,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.,
 AUTHORS Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
 M.
 TITLE Comparison of the moss Physcomitrella patens genome with flowering
 Plants genome
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasu Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescript(KS), that
 was in vivo excised from a modified lps phage vector (Mo bi Rec,
 Germany). 5' end of the cDNA that was digested with XhoI was
 ligated to SalI site of the vector and the 3' end including polyA
 tail was ligated to BamHI site of the vector. cDNA insert could be
 amplified with conventional T7 and T3 primers. This full-length
 cDNA library was generated basically according to the method
 described in The Plant J 15, 707-720 (1998) Seki M. et al.
 Protonemata were blended by the POLYTRON, and then cultivated on
 the BCDATG medium for 13-14 days under the continuous light.
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 source Location/Qualifiers
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 /organism="Physcomitrella patens subsp. patens"
 /db_xref="taxon:145481"
 /clone_lib="full length cDNA library, chloronemata and
 young gametophores"
 /tissue_type="mixture of chloronemata and young
 gametophores with 2 to 5 leaves"
 BASE COUNT 124 a 138 c 170 g 148 t
 ORIGIN
 Query Match 2.9%; Score 51.8; DB 13; Length 580;
 Best Local Similarity 56.9%; Pred. No. 0.037;
 Matches 95; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
 QY 753 CCAGGACCTGTGGGAGATGATTCATGTCAGCAGCAGCCATGCGCTTCCCTTAAGCT 812
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 DB 475 CCGGAGATTTTCGGCGAGTGTCTCTCGTAACGCAAGCAGCTTACTCTGCT 416
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 QY 813 CCAGCCCGCAGTACCGTTCGATTCCTCAACGCTGCGCTGCTGCTGCTGCT 872
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 DB 415 CAAGCTTCGCAAGTACCGCTTCGCTCGTAAGTGTGCAATGCGAGAGTTTTCAGACT 356
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 QY 873 CTACTCGTCAGGACCAAGCTCCCAAGCTCAGAAATTCCTTCCAAG 919
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 DB 355 TTCTCTGAGACCAACCAAAACGCGTTTCATTCAAATGTTACCGACG 309
 11
 RESULT 5
 BF258534 599 bp mRNA linear EST 22-OCT-2001
 LOCUS HVSMEF0015P21f Hordeum vulgare seedling root EST library HVC0DM0007
 DEFINITION (Etisolated and unstressed) Hordeum vulgare cDNA clone
 HVSMEF0015P21f, mRNA sequence.
 ACCESSION BF258534
 VERSION BF258534.2 GI:13119477
 KEYWORDS EST.
 SOURCE Hordeum vulgare.
 ORGANISM Hordeum vulgare.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae
 ; Trilicaceae; Hordeum.
 REFERENCE Wing,R., Close,T.J., Kleinof,A., Wise,R., Begum,D., Frisch,D., Yu
 1 (bases 1 to 599)

TITLE
JOURNAL
COMMENT

R., Rittner E., Kohn, S., Shu, T., Jackson, Y., Cardenas, M., McCann
R., Materoso, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact: cu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 423.

FEATURES

BASE COUNT	131 a	241 c	105 g	131 t
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Query Match	2.68;	Score 46.2;	DB 14;	Length 608;
Best Local Similarity	51.28;	Pred. No. 0.98;		
Matches 108; Conservative	0;	Mismatches 103;	Indels 0;	Gaps 0

RESULT	10
BF059036	
LOCUS	
DEFINITION	BF059036 463 bp mRNA linear EST 16-OCT-2000
	7K6d11.x1 NCI-GAP Ov18 Homo sapiens cDNA clone IMAGE:3776621 3'
	similar to TR:O63928 O63928 HORMONA RELATED PROTEIN 1 ; , mRNA
ACCESSION	BF059036

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE

1 (bases 1 to 463)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute. Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: csabbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop:341.

FEATURES
source

BASE COUNT	133 a	127 c	128 g	75 t
ORIGIN				

Query Match	2.58;	Score 44.6;	DB 12;	Length 463;
Best Local Similarity	45.98;	Pred. No. 2.1;		
Matches 152;	Conservative 0;	Mismatches 179;	Indels 0;	Gaps 0;

RESULT 11

LOCUS	AL1394530	481 bp	mRNA	linear	EST 30-MAR-1999
DEFINITION	U77b06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105267 3'				
ACCESSION	U77b06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105267 3'				
VERSION	similar to SW:SN23_HUMAN P51332 POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L3 ;, mRNA sequence.				
KEYWORDS	AL1394530				
ORGANISM	AL1394530.1 GI:4224077				
SOURCE	EST.				
REFERENCE	human.				
AUTHORS	Homo sapiens				
TITLE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.				
JOURNAL	NCI/NINDS_CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
COMMENT	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGA), Tumor Gene Index				
	Unpublished (1998)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgaps-remail.nih.gov				
	Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.				
	CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.				
	CDNA Library Arrayed by: Greg Lennon, Ph.D.				
	DNA Sequencing by: Washington University Genome Sequencing Center				
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html				
	Insert length: 905 Std Error: 0.00				
	Seq primer: -400P from Gibco				
	High quality sequence stop: 452.				
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SOURCE	1. 481				
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	/db_xref="taxon:9606"				
	/clone="IMAGE:2105267"				
	/clone_id="NCI_CGAP_Brn23"				
	/issue_type="gliblastoma (pooled)"				
	/lab_host="DH108"				
	/note="Organ: brain; Vector: pT7AD-Pac (Pharmacia) with a modified polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCCAACTGTGAAGTGGAGGCGCCGCAATCTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."				
BASE COUNT	138 a 128 c 141 g 74 t				
ORIGIN					
Query Match	2.5%: Score 44.6; DB 9; Length 481;				
Best Local Similarity	45.9%: Pred. No. 2.1;				
Matches 152:	Conservative 0; Mismatches 179; Indels 0; Gaps 0;				
QY	1461 GGGCAGGGGTGAGACCCCTGACCATCGAGCCCACTACCAACCTGAGACTGAGCTTACAT	1520			
DB	70 GCACAGCAGTGTGACGTGACGTGACGACGAGGCTTCATCCAGCTGCCTCGGAAAGGACT	129			
QY	1521 GTGGCACTGTATCAACAACCTCATTCACGAGATACGACATGATGGCTGATTCAACGTCAC	1580			
DB	130 GCCCGAGTACTACGACGTCCGCCAAGCCCGTGGACTTCAAGAAAGATMAAGAGCGCAT	189			
QY	1581 CGCCATGGAGGAGAAAGGATATCTTCAGGAGACACTGACGAGACCCCATGAMCCCAATG	1640			
DB	190 TCGCAACCAACAAGTACCGCAACCTCAAGACCTTATAGAAAGACGTCAATGCTCTGTGCCA	249			
QY	1641 GCGGCGCGTCTCTTCAACAACCGCAACGACTTCATGCTGCGCCTGGAAATCTCTCGCCGA	1700			
DB	250 GAACGACACAGACCTTCAACCTCGAAGGCGTCCCTGATATATGAAGACATCATGCTTTGCA	309			
QY	1701 GTCCATCACTGCCCCGAGTGACGAGACTGGCCGACGAGAGACCGTACCAACCGCTTGATGA	1760			

Db	310	GTCCGCTTTTACACCGCGCGCAGAAAATGACGAAGAGATGACACTGAAGCGGAGGA	369
QY	1761	GATCCTGGAGCATCTTGCATCGAGGAGCTAA	1791
Db	370	GAGTACGACGACGAGGAAGGCGCGAGGAGGA	400
RESULT 12			
LOCUS	BF115462		
DEFINITION	7083303.x1 NCI-CGAP OY18 Homo sapiens CDNA clone IMAGE:3571229 3'		
ACCESSION	BF115462		
VERSION	BF115462.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 475)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Christina Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLT, send email to: info@image.lnlnl.gov Seq primer: -400p from Glbco High quality sequence stop: 334. Location/Qualifiers		
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	/clone_image="3571229"		
	/clone_id="NCI-CGAP_OY18"		
	/tissue_type="fibrocyte"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: ovary; Vector: p7f3D-pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAAGTGGAGCGCGCGCGACATATTTTATTTTATTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7f3D vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	133 a 132 c 136 g 74 t		
ORIGIN			
Query Match	2.5%: Score 44.2; DB 12; Length 475;		
Best Local Similarity	45.9%: Pred. No. 2.7;		
Matches 151: Conservative 0; Mismatches 178; Indels 0; Gaps 0;			
QY	1463	GCAGGGGTGAGACCCCTGACATGACGCGCCACTACGACACCTCGACCTGACCTTACATGT	1522
Db	93	GCAGCAGTGGAGCGTACGCTCAGCGAGCGTCTTACATCCAGCTCCCTCGGAAAGAGAGCTGC	152
QY	1523	GGCAGCTGTGACACACCTCTATTCACGAGGATTAACGACATGATGGCTGTATTAACGTCACCG	1582
Db	153	CCGAGTACTACGAGCTCATCCGCAAGCCCGTGGACTTCAAGATTAAGAGAGCGCATTC	212
QY	1583	CCATGAGGAGAAAGGATATTTTCAAGAGAGACTTCGAGAGACCCCATGAACCCCAAGTGC	1642
Db	213	GCAACCAAAATACCGCAGCTCAACGACCTAGAGAAAGAGATGCTATGCTGTGCCAGA	272

QY	1643	GGGCGCTTCTTACAAACCCGACGACTTCCATGCTGCGCTGGAACCTTCTCCGCCAGT	1702
	1111	1111	1111
Db	273	AGCAGACAGACTTTTCAACCTGGAGGGCTCCCTGATCTATGTAACATCTCCATCTTGCACT	332
QY	1703	CCATCTACTCCCGAGTGGAGAGCTGGCCGACGAGGCGCTTACAAACCCCTCGATGAGA	1762
	1111	1111	1111
Db	333	CGGTCTTCCACACGCGCGGGGCAAAAATGTGACAAAGGAGATGACATGTAAACGATGAGA	392
QY	1763	TCCGTGGAGATCTTGGATCGAGAGTAA	1791
	11111111	11111111	11111111
Db	393	GTGAGGAGAGGAAGAGGCGCGAGAGAGA	421
RESULT 13			
AI432408			
LOCUS	AI432408	541 bp	mRNA linear
DEFINITION	tg73c04.x1 Soares.NHMPu.S1 Homo sapiens cDNA clone IMAGE:2114406		EST 30-MAR-1999
	3, similar to SM:SN3 HUMAN P51532 POSSIBLE GLOBAL TRANSCRIPTION		
ACTIVATOR	SNF2L3 ; mRNA sequence.		
ACCESSION	AI432408		
VERSION	AI432408.1	GI:4281458	
SOURCE	EST.		
ORGANISM	human.		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 541)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	This clone is available royalty-free through INLNL ; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
	Insert Length: 861 Std Error: 0.00		
	Seq primer: -40up from Gibco		
	High quality sequence stop: 499.		
FEATURES			
source	location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:2114406"		
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	/tissue_type="Pooled human melanocyte, fetal heart, and		
	pregnant uterus"		
	/lab_host="DH10B"		
	/note="Organ: mixed (see below) ; Vector: p77T3D-Pac		
	(Pharmacia) with a modified polylinker; Site.1: Not I;		
	Site.2: Eco RI; Equal amounts of plasmid DNA from three		
	normalized libraries (melanocyte 2NBH, pregnant uterus		
	NBHPu, and fetal heart NBH19W) were mixed, and ss circles		
	were made in vitro. Following HAP purification, this DNA		
	was used as tracer in a subtractive hybridization		
	reaction. The driver was PCR-amplified cDNAs from pools of		
	5,000 clones made from the same 3 libraries. The pools		
	consisted of T.M.A.G.E. clones 260232-265223,		
	340488-345479, and 484486-489479."		
BASE COUNT	148 a 150 c 167 g 76 t		
ORIGIN			
Query Match	2.5%: Score 44.2; DB 9; Length 541;		
Best Local Similarity	45.9%: Pred No. 2.9; Indels 0; Gaps 0;		
Matches 151; Conservative	0; Mismatches 178;		
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Db	93	GCAGCAGTGAGAGCTGACGTCAGGAGAGCTTCATCCAGCTGCCCGCAAGAGAGCTGC	152
QY	1523	GGCAGCTGTACAACTCATTTACAGAGAGATACGACATGATGCGTGTATTTCACAGTCACCG	1582
	11111111	11111111	11111111
Db	153	CCGAGTACATACGAGCTATCCGCAACCCGCTGTGACTTCAAGAAGATAAAGGAGCGCATTC	212

OY	1583	CCATGAGAGAGAAGGATATCTTTCAGAGAGACTTGAGAGACCAACCATTGAACCCCAACTGGC	1642
Db	213	GCACCCACAAAGTACCGCACCTCAAGAGACCTTAGAGAAAGGACGTATGCTCTGTGGACA	272
OY	1643	GGGCCGTTCTTACAAACGCCAAGACTTTCATGTCGCCCTGGAACACTTCGCCGGACT	1702
Db	273	ACGCACAGACCTTCAACCTCGAGAGGCTTCTCTATCATATAAGATTCATGCTTTGGCACT	332
OY	1703	CCATACACTCCCGAGTCAGAGACTGTGGCCAGCAGAGAGCCGTAACAACGCCCTCGATGACA	1762
Db	333	CAGTCTTTCACCAAGCGTGGCGGCAAAAATGAGAGAGAGATGACAGTAAAGCGAGAGAA	392
OY	1763	TCTTGAGGATCTTGGATCGAGAGTAA	1791
Db	393	GTTGAGAGAGAGAGAGAGCGCGAGAGAGAA	421
 RESULT 14 BG321313			
LOCUS	BG321313	700 bp	mRNA
DEFINITION	Zm04_04d06_R Zm04_AAFRC_ECORC_cold_stressed_maize_seedlings Zea mays	linear	EST 27-FEB-2001
ACCESSION	CDNA clone Zm04_04d06, mRNA sequence.		
VERSION	BG321313		
KEYWORDS	BG321313.1 GI:13150991		
SOURCE	EST.		
ORGANISM	Zea mays.		
REFERENCE	Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea. 1 (bases 1 to 700) Singh,J.A., Wakui,K., Couroux,P., De Moors,A., Harris,L.J., Hattorih, .J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A. Expressed Sequence Tags from Cold-Stressed Maize Seedlings Unpublished (2001) Contact: Singh,J.A. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada KW Neaby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA OC6, Canada Tel.: (613) 759-1662 Fax: (613) 759-1701 Email: singha@em.agr.ca		
TITLE	Location/Qualifiers		
JOURNAL	1..700		
COMMENT	/organism="Zea mays" /cultivar="CO328" /db_xref="taxon:4577" /clone="Zm04_04d06" /clone_lib="Zm04_AAFRC_ECORC_cold_stressed_maize_seedlings /tissue_type="Leaf, crown" /note="Vector: Bluescript SR-/XhoI-EcoRI; Site_1: Eco RI; Site_2: Xho I; Lower temperature 50 C / hour from 22 to 120C, bring to 50 in 1 hour from 120C. Leave at 50C 2 days , photoperiod 16 hours. Light intensity was 125 uE-1. library prepared by in vivo mass excision from amplified library."		
 FEATURES			
source	103 a	283 c	158 g 102 t 54 others
 BASE COUNT			
ORIGIN			
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OY	862	GCTTGCTCTCTACCTCGTCAAGAGACCACTTCGCCAACGTCTTTCGAAGTC	921
Db	192	GCGGCGCCCTGTACGCGCGTGTCTTKTMACCGCCGCTTCGTGGCBGCGGAGATGTC	251
OY	922	ATTGCGCTCTGATGTGGTCTTCTTCAAGCCCCCGTTCAAGACTCTTAACCTTACCTTGCT	981
Db	252	ATTCGCGCGCGCGTCAATCCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC	311

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OY 982 GTTCCGAGCTTACGAGATCATTTAGTCTACCACTTTGCTGGCCAGACTCTTGAC 1041
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Db 312 GCGCGCTGCTCTACTCCACACACACCGCTGCGCTGTTTCTTCGAGCCGCCAC 371
OY 1042 CTGGCCACGCTGTGACACACACATCTGCGGACGAGGATGATGACTCTGCACTTTC 1101
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Db 372 CACCCSACGCTGCGACCGGACCTTCTGCGGACGAGTCCCGCGGCTCAAGARG 431
OY 1102 GAGGTGATGCGCTTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 432 AMRGCTCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 491
OY 1162 ACTCTCCGT 1170
    | | | | |
Db 492 CBCTCCCT 500
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RESULT 15

A2302933

LOCUS

DEFINITION GSSBru1874 Brucella abortus random genomic library Brucella

mellitensis biovar Abortus genomic clone U01874, DNA sequence.

ACCESSION A2302933.1 GI:10129144

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

CONTACT

DEPARTMENT

TELEPHONE

FAX

EMAIL

SEQUENCES

CROSSMATCH

SEQUENCES

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Db 339 TCGTTCACACTGCTTCATCCGATCTGATGCGCACACTGCGGTCAGGACATATGAGC 398
OY 610 CAGGCTGGCGCTTACATATATCAACGACGAGGCTGAGGATGCTCTGCTCTGAGTGGC 669
Db 399 ATTGCGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 458
OY 670 TATGCGGCTGATATATATATATATATATATATATATATATATATATATATATATATAT 729
Db 459 TACGCGGTGACGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 518
OY 730 CTGCTTGCACCGAGGCTGAGGACGAG 756
Db 519 GTCTATGCGCGGATATATATATATATATATATATATATATATATATATATATATATAT 545
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Job time : 2428.3 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 21:13:53 : Search time 61 seconds
(without alignments)
1297.555 Million cell updates/sec

Title: US-09-218-702-2

Perfect score: 3189

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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3189	100.0	594	20	AAV45222
2	3189	100.0	594	20	AAV39992
3	3189	100.0	594	21	AAV95537
4	3189	100.0	594	21	AAV96761
5	3189	100.0	594	23	AAO18210
6	1954.5	61.3	627	21	AAV95538
7	1954.5	61.3	627	21	AAV96762
8	1954.5	61.3	627	23	AAO18211
9	1929.5	60.5	627	21	AAV95539
10	1929.5	60.5	627	21	AAV96763

11	1929.5	60.5	627	23	AAO18212	C pallenscens pheno
12	1735.5	54.4	583	23	AAU97312	Phenol oxidising e
13	1731.5	54.3	583	23	AAU97316	Phenol oxidising e
14	1731.5	54.3	583	23	AAU97318	Phenol oxidising e
15	1731.5	54.3	583	23	ABB75770	Phenol oxidising e
16	1731.5	54.3	583	23	ABB75772	Phenol oxidase B v
17	1730.5	54.3	583	23	AAU97321	Phenol oxidising e
18	1730.5	54.3	583	23	AAU97324	Phenol oxidising e
19	1730.5	54.3	583	23	AAU97352	Phenol oxidising e
20	1730.5	54.3	583	23	ABB75775	Phenol oxidase B v
21	1730.5	54.3	583	23	ABB75778	Phenol oxidase B v
22	1729.5	54.2	583	23	ABB75807	Phenol oxidase B v
23	1729.5	54.2	583	23	AAU97329	Phenol oxidising e
24	1729.5	54.2	583	23	AAU97334	Phenol oxidising e
25	1729.5	54.2	583	23	AAU97336	Phenol oxidising e
26	1729.5	54.2	583	23	ABB75766	Phenol oxidising e
27	1729.5	54.2	583	23	ABB75783	Phenol oxidase B v
28	1729.5	54.2	583	23	ABB75788	Phenol oxidase B v
29	1729.5	54.2	583	23	ABB75790	Phenol oxidase B v
30	1728.5	54.2	583	23	AAU97323	Phenol oxidising e
31	1728.5	54.2	583	23	AAU97337	Phenol oxidising e
32	1728.5	54.2	583	23	AAU97338	Phenol oxidising e
33	1728.5	54.2	583	23	AAU97356	Phenol oxidising e
34	1728.5	54.2	583	23	AAU97378	Phenol oxidising e
35	1728.5	54.2	583	23	ABB75777	Phenol oxidising e
36	1728.5	54.2	583	23	ABB75781	Phenol oxidase B v
37	1728.5	54.2	583	23	ABB75791	Phenol oxidase B v
38	1728.5	54.2	583	23	ABB75792	Phenol oxidase B v
39	1728.5	54.2	583	23	ABB75810	Phenol oxidase B v
40	1728.5	54.2	583	23	ABB75832	Phenol oxidase B v
41	1727.5	54.2	583	23	AAU97320	Phenol oxidising e
42	1727.5	54.2	583	23	AAU97326	Phenol oxidising e
43	1727.5	54.2	583	23	AAU97333	Phenol oxidising e
44	1727.5	54.2	583	23	AAU97335	Phenol oxidising e
45	1727.5	54.2	583	23	ABB75774	Phenol oxidase B v

ALIGNMENTS

RESULT 1
AAV45222
ID AAV45222 standard: Protein: 594 AA.
XX
AC AAV45222:
XX
DT 05-JAN-2000 (first entry)
XX
XX Stachybotrys chartarum phenol oxidising enzyme.
DE Stachybotrys chartarum phenol oxidising enzyme.
XX Stachybotrys chartarum phenol oxidising enzyme: colour; dye:
KW detergent; anti-dye transfer; stain removal; bleaching.
XX
XX Stachybotrys chartarum.
OS
PN WO9949010-A2.
XX
PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-EP02042.
XX
PR 24-MAR-1998; 98US-0046969.
XX
PR 22-DEC-1996; 98US-0218702.
PA (UNITL) UNILEVER NV.
PA (UNITL) UNILEVER PLC.
PI Convents D, Amory A, Wang H, Dhasee P, Lambrechts-Rongvaux A;
PI Wang C;
DR WPI; 1999-601211/51.
XX N-PSDB; AA25727.
XX

PT Detergent composition containing phenol oxidase from *Stachybotrys*, used
PT to bleach stains and prevent dye transfer
XX
XX
PS Claim 16; Fig 5; 56pp; English.
XX
CC The present invention describes a detergent composition containing a
CC pulled phenol oxidising enzyme derived from *Stachybotrys*. The present
CC sequence represents *Stachybotrys chartarum* phenol oxidising enzyme. The
CC enzyme can be used to modify the colour of dyes and other coloured
CC compounds (e.g. for use in pulp and paper bleaching also for removing
CC stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
CC transfer during fabric washing.
XX
XX
SQ Sequence 594 AA:
Query Match 100.0%; Score 3189; DB 20; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLFKSMQLAAASGLISGLVGIIPMDTGSHPLEAVDPEVKTEVPADSLAAAGDDMESPPY 60
DB 1 MLFKSMQLAAASGLISGLVGIIPMDTGSHPLEAVDPEVKTEVPADSLAAAGDDMESPPY 60
QY 61 NLTYRNALPIPPVKPKMIITNPVTGKDIWYEIEIKPQQRITPPLRATLVGDGMS 120
DB 61 NLTYRNALPIPPVKPKMIITNPVTGKDIWYEIEIKPQQRITPPLRATLVGDGMS 120
QY 121 GPTFNVPRGTETVVRFINNATVENSVHLHSGSPRAPFDGMADVYFPGGYKXYPPNYQS 180
DB 121 GPTFNVPRGTETVVRFINNATVENSVHLHSGSPRAPFDGMADVYFPGGYKXYPPNYQS 180
QY 121 GPTFNVPRGTETVVRFINNATVENSVHLHSGSPRAPFDGMADVYFPGGYKXYPPNYQS 180
DB 121 GPTFNVPRGTETVVRFINNATVENSVHLHSGSPRAPFDGMADVYFPGGYKXYPPNYQS 180
QY 181 ARLLWYHDAFMKTAENAYFGGAGAYIINDEADALGLPSYGEFDIPILITAKYYNADG 240
DB 181 ARLLWYHDAFMKTAENAYFGGAGAYIINDEADALGLPSYGEFDIPILITAKYYNADG 240
QY 241 TLRSTEGEDODLMGVDVHNNGOPWPLNVPKRYRFRFLNAVSRAMLVYRTSSPNVR 300
DB 241 TLRSTEGEDODLMGVDVHNNGOPWPLNVPKRYRFRFLNAVSRAMLVYRTSSPNVR 300
QY 301 IFFOVIASDAGLQAPVOTSNLYLAVEREYELIIDFTNAGOTLDRNVAETNDVGDEDE 360
DB 301 IFFOVIASDAGLQAPVOTSNLYLAVEREYELIIDFTNAGOTLDRNVAETNDVGDEDE 360
QY 361 YARTLEVMRFVVSSTGVEDNSOVPTSLRDVPRPRHKEGPADKHFKFERNNGHYLLINDVGF 420
DB 361 YARTLEVMRFVVSSTGVEDNSOVPTSLRDVPRPRHKEGPADKHFKFERNNGHYLLINDVGF 420
QY 421 ADVNERVLAKPELGTVEVWELNENSSGGMSHPVHILVDFKILKRTGGRGQVMPYESAGLK 480
DB 421 ADVNERVLAKPELGTVEVWELNENSSGGMSHPVHILVDFKILKRTGGRGQVMPYESAGLK 480
QY 481 DVVWILGRGETLTIEAHYQPTGAYMWHCHNLIHEDNDMAVFNVTAMEKGYLQEDFEDP 540
DB 481 DVVWILGRGETLTIEAHYQPTGAYMWHCHNLIHEDNDMAVFNVTAMEKGYLQEDFEDP 540
QY 541 MNPKRAVYNNRNDFHARAGNFSABESTARVOELAEQEPYNNRLDELLEDLGIEE 594
DB 541 MNPKRAVYNNRNDFHARAGNFSABESTARVOELAEQEPYNNRLDELLEDLGIEE 594

RESULT 2
AAY39992
ID AAY39992 standard; Protein: 594 AA.
XX
XX AAY39992;
AC
XX
XX 16-DEC-1999 (first entry)
DT
XX
XX
XX Stachybotrys phenol oxidase protein sequence.
DE
XX
XX Phenol oxidase: enzyme; coloured compound; dye transfer prevention;
KW fabric washing; stain bleaching; anti-dye transfer; detergent.
XX

OS *Stachybotrys chartarum*.
XX
XX WO9949020-A2.
XX
XX
XX 30-SEP-1999.
XX
XX 23-MAR-1999; 99WO-US06327.
XX
XX 24-MAR-1998; 98US-0046969.
XX 22-DEC-1998; 98US-0218702.
XX 22-MAR-1999; 99US-0273957.
XX
XX (GEMV) GENENCOR INT INC.
XX
XX Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;
XX
XX WPI: 1999-591088/50.
XX
XX N-PSDB: AA227601, AA227602.
XX
XX Novel enzyme for modifying coloured compounds used to prevent
XX dye-transfer -
XX
XX Claim 16; Fig 5; 64pp; English.
XX
XX This sequence is the *Stachybotrys chartarum* phenol oxidase enzyme
XX of the invention. The invention is used to modify a coloured compound and
XX prevent dye transfer during fabric washing, or for stain bleaching or
XX anti-dye transfer. It is useful in the detergent, paper and pulp, textile
XX and food industries.
XX
XX
SQ Sequence 594 AA:
Query Match 100.0%; Score 3189; DB 20; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLFKSMQLAAASGLISGLVGIIPMDTGSHPLEAVDPEVKTEVPADSLAAAGDDMESPPY 60
DB 1 MLFKSMQLAAASGLISGLVGIIPMDTGSHPLEAVDPEVKTEVPADSLAAAGDDMESPPY 60
QY 61 NLTYRNALPIPPVKPKMIITNPVTGKDIWYEIEIKPQQRITPPLRATLVGDGMS 120
DB 61 NLTYRNALPIPPVKPKMIITNPVTGKDIWYEIEIKPQQRITPPLRATLVGDGMS 120
QY 121 GPTFNVPRGTETVVRFINNATVENSVHLHSGSPRAPFDGMADVYFPGGYKXYPPNYQS 180
DB 121 GPTFNVPRGTETVVRFINNATVENSVHLHSGSPRAPFDGMADVYFPGGYKXYPPNYQS 180
QY 121 GPTFNVPRGTETVVRFINNATVENSVHLHSGSPRAPFDGMADVYFPGGYKXYPPNYQS 180
DB 121 GPTFNVPRGTETVVRFINNATVENSVHLHSGSPRAPFDGMADVYFPGGYKXYPPNYQS 180
QY 181 ARLLWYHDAFMKTAENAYFGGAGAYIINDEADALGLPSYGEFDIPILITAKYYNADG 240
DB 181 ARLLWYHDAFMKTAENAYFGGAGAYIINDEADALGLPSYGEFDIPILITAKYYNADG 240
QY 241 TLRSTEGEDODLMGVDVHNNGOPWPLNVPKRYRFRFLNAVSRAMLVYRTSSPNVR 300
DB 241 TLRSTEGEDODLMGVDVHNNGOPWPLNVPKRYRFRFLNAVSRAMLVYRTSSPNVR 300
QY 301 IFFOVIASDAGLQAPVOTSNLYLAVEREYELIIDFTNAGOTLDRNVAETNDVGDEDE 360
DB 301 IFFOVIASDAGLQAPVOTSNLYLAVEREYELIIDFTNAGOTLDRNVAETNDVGDEDE 360
QY 361 YARTLEVMRFVVSSTGVEDNSOVPTSLRDVPRPRHKEGPADKHFKFERNNGHYLLINDVGF 420
DB 361 YARTLEVMRFVVSSTGVEDNSOVPTSLRDVPRPRHKEGPADKHFKFERNNGHYLLINDVGF 420
QY 421 ADVNERVLAKPELGTVEVWELNENSSGGMSHPVHILVDFKILKRTGGRGQVMPYESAGLK 480
DB 421 ADVNERVLAKPELGTVEVWELNENSSGGMSHPVHILVDFKILKRTGGRGQVMPYESAGLK 480
QY 481 DVVWILGRGETLTIEAHYQPTGAYMWHCHNLIHEDNDMAVFNVTAMEKGYLQEDFEDP 540
DB 481 DVVWILGRGETLTIEAHYQPTGAYMWHCHNLIHEDNDMAVFNVTAMEKGYLQEDFEDP 540
QY 541 MNPKRAVYNNRNDFHARAGNFSABESTARVOELAEQEPYNNRLDELLEDLGIEE 594

Db 541 MNPKRAVPYNNDFHARAGNFSAESITARVOELAEQEPYNNRDLDELIDGIEE 594

RESULT 3

AAV9537

ID AAV95537 standard; Protein: 594 AA.

AC AAV95537;

DT 10-OCT-2000 (first entry)

DE Stachybotrys chartarum phenol oxidizing enzyme.

KW phenol oxidizing enzyme; detergent; bleaching.

OS Stachybotrys chartarum.

PN WO200039306-A2.

PD 06-JUL-2000.

PF 20-DEC-1999: 99WO-EP10287.

PR 23-DEC-1998: 98US-0220871.

PR 23-JUN-1999: 99US-0338723.

XX (UNIT) UNILEVER NV.

PA (UNIT) UNILEVER PLC.

PA (HIND-) HINDUSTAN LEVER LTD.

PI Bodie EA, Van Der Velden S, De Vries CH, Wang H;

DR WPI: 2000-514528/46.

DR N-PSDB: AAA50018; AAA50019.

PT Detergent composition comprising novel phenol oxidizing enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition

XX Claim 2: Fig 5A-B; 45pp: English.

XX The present sequence is that of a phenol oxidizing enzyme of Stachybotrys chartarum MUC1 38898. A claimed detergent composition comprises a phenol oxidizing enzyme having at least 60% identity to the present sequence, and preferably obtained from a bacterium, yeast or non-Stachybotrys fungus, especially Bipolaris spicifera, Curvularia pallescens or Amersporium atrum (see AAY9538-40). The phenol oxidizing enzyme is capable of modifying the colour associated with dyes or coloured compounds, and can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. It may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidizing enzyme, methods for producing the phenol oxidizing enzyme, and methods for constructing expression hosts are provided.

XX Sequence 594 AA:

Query Match 100.0%; Score 3189; DB 21; Length 594;

Best Local Similarity 100.0%; Pred. No. 2,9e-299;

Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLEKSMQLAASGLISGLVIGIPMDTGSHPREAVDEPVKTEVFADSLAAAGDDMESPPY 60

Db 1 MLEKSMQLAASGLISGLVIGIPMDTGSHPREAVDEPVKTEVFADSLAAAGDDMESPPY 60

OY 61 NLLYNNALPIPPYKPKMTITNPYTGKDIWYEIEIKPQOQIYTLRPATLVGTGMS 120

Db 61 NLLYNNALPIPPYKPKMTITNPYTGKDIWYEIEIKPQOQIYTLRPATLVGTGMS 120

OY 121 GPTFNVPRTETVVRFINNATVENSVLHGSPSRAPFDGMADVFPPGPKYKXYFPNQS 180

Db 121 GPTFNVPRTETVVRFINNATVENSVLHGSPSRAPFDGMADVFPPGPKYKXYFPNQS 180

OY 181 ARLLWYHDAFMKTAENAVFGAGAYIINDEADALGSPGGEFDIPILITAKYNNADG 240

Db 181 ARLLWYHDAFMKTAENAVFGAGAYIINDEADALGSPGGEFDIPILITAKYNNADG 240

OY 241 TLIRSTEGEDQDLMDGVIHVNGQPMPLNVPKRYRFRFLNAVSRAMLTYLVRTSSPNR 300

Db 241 TLIRSTEGEDQDLMDGVIHVNGQPMPLNVPKRYRFRFLNAVSRAMLTYLVRTSSPNR 300

OY 301 IPFOVIASDAGLLOAPVQTSNLYLVAERYELIIDFTNAGOTLDLRNVAETNDGDEDE 360

Db 301 IPFOVIASDAGLLOAPVQTSNLYLVAERYELIIDFTNAGOTLDLRNVAETNDGDEDE 360

OY 361 YARTLEVMRFVSSGTVEDNSQVPTLRDVPKPKGEPADKHFFERSNGHYLINDVGE 420

Db 361 YARTLEVMRFVSSGTVEDNSQVPTLRDVPKPKGEPADKHFFERSNGHYLINDVGE 420

OY 421 ADVNERVLAKPELGTVEVWELENSSGWSPVHILVDFKILKRTGGQVMPYESAGLK 480

Db 421 ADVNERVLAKPELGTVEVWELENSSGWSPVHILVDFKILKRTGGQVMPYESAGLK 480

OY 481 DVMWLGRCETLTIEAHYQPMTCAYMMHCHNLIHEDNDMAVFNTAMEEKGYLQEDFEDP 540

Db 481 DVMWLGRCETLTIEAHYQPMTCAYMMHCHNLIHEDNDMAVFNTAMEEKGYLQEDFEDP 540

OY 541 MNPKRAVPYNNDFHARAGNFSAESITARVOELAEQEPYNNRDLDELIDGIEE 594

Db 541 MNPKRAVPYNNDFHARAGNFSAESITARVOELAEQEPYNNRDLDELIDGIEE 594

RESULT 4

AAV96761

ID AAV96761 standard; Protein: 594 AA.

AC AAV96761;

DT 09-OCT-2000 (first entry)

DE Stachybotrys chartarum phenol oxidizing enzyme.

KW phenol oxidizing enzyme; colour; dye; modification; detergent; stain; pulp; paper bleaching.

OS Stachybotrys chartarum.

PN WO200037654-A2.

PD 29-JUN-2000.

PF 20-DEC-1999: 99WO-US31009.

PR 23-DEC-1998: 98US-0220871.

PR 23-JUN-1999: 99US-0338723.

PA (GENV) GENENCOR INT INC.

PI Wang H, Bodie EA;

DR WPI: 2000-452191/39.

DR N-PSDB: AAA51313; AAA51314.

PT New phenol oxidizing enzyme for modifying colors associated with dyes or colored compounds, is obtained from fungus and is encoded by a nucleic acid comprising a specific nucleotide sequence

PS Claim 1: Fig 5A-B; 45pp: English.

XX This is the sequence of Stachybotrys chartarum phenol oxidizing enzyme. CC Phenol oxidizing enzymes encoded by nucleic acid sequences which hybridize to the coding DNA are claimed, as long as the enzyme is capable of modifying the colour associated with dyes or coloured compounds. The

CC enzymes are useful in detergent compositions and for modifying colors
CC associated with dyes or colored compounds which occur in stains in a
CC sample. The enzymes are also useful for pulp and paper bleaching,
CC anti-dye transfer in detergent and other textile applications.

XX
SO Sequence 594 AA;

Query Match 100.0%; Score 3189; DB 21; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLFKSWQLAASGLISGLVGIPTMTGSHPIEAVDPEVKTEVFADSLAAGDDMESPPY 60
DB 1 MLFKSWQLAASGLISGLVGIPTMTGSHPIEAVDPEVKTEVFADSLAAGDDMESPPY 60
QY 61 NLTYNALPIPPVKOPKMITNPVTGKDIWYEIETKPEQORITPTLRPATLVGDGMS 120
DB 61 NLTYNALPIPPVKOPKMITNPVTGKDIWYEIETKPEQORITPTLRPATLVGDGMS 120
QY 121 GPTFNVPRTETVVFRIINNAIVENSVLHSGSPRAPFDGMADVTFFPGYKDYPPNYQS 180
DB 121 GPTFNVPRTETVVFRIINNAIVENSVLHSGSPRAPFDGMADVTFFPGYKDYPPNYQS 180
QY 181 ARLLWYHDAHFEMKTAENAYFGQAGAYIINDEAEDALGLPSGGEEDIPLLITAKYYNADG 240
DB 181 ARLLWYHDAHFEMKTAENAYFGQAGAYIINDEAEDALGLPSGGEEDIPLLITAKYYNADG 240
QY 241 TLRTSGEDDOLMGVIVHNGOPWFLNVPKRYFRFLNAVSRAMLIVRTSSPNVR 300
DB 241 TLRTSGEDDOLMGVIVHNGOPWFLNVPKRYFRFLNAVSRAMLIVRTSSPNVR 300
QY 301 IPFOYIASDAGLLQAPVOTSNLTYLAVEREYELIIDFTNAGOTLDRNVAETNDVGDEDE 360
DB 301 IPFOYIASDAGLLQAPVOTSNLTYLAVEREYELIIDFTNAGOTLDRNVAETNDVGDEDE 360
QY 361 YARTLEVNRFFVSSGTVEDNSQVSTLRDVPKPRKEGPADKHFFERSNGHYLLINDVGF 420
DB 361 YARTLEVNRFFVSSGTVEDNSQVSTLRDVPKPRKEGPADKHFFERSNGHYLLINDVGF 420
QY 421 ADVNERVLAKPELGTVEWELENSSGGSHRPHILVDFKILKRTGGKQOVVPYSAGLK 480
DB 421 ADVNERVLAKPELGTVEWELENSSGGSHRPHILVDFKILKRTGGKQOVVPYSAGLK 480
QY 481 DVMVLGRGETTLTIEAHYQWPTGAYMMHCHNLIHEDNDMAAVFNVTAMEBKGYLQEDFEDP 540
DB 481 DVMVLGRGETTLTIEAHYQWPTGAYMMHCHNLIHEDNDMAAVFNVTAMEBKGYLQEDFEDP 540
QY 541 MNPKRAVPYNNDFHARAGNFSASITARVOELAEQEBYRNLDLELDGIEE 594
DB 541 MNPKRAVPYNNDFHARAGNFSASITARVOELAEQEBYRNLDLELDGIEE 594

RESULT 5
AA018210

ID AA018210 standard; Protein: 594 AA.

XX AC AA018210;

XX DT 13-SEP-2002 (first entry)

XX DE S chartarum phenol oxidizing enzyme.

XX KW Phenol oxidizing enzyme; fungus; redox reaction; detergent;

XX KW paper industry; pulp industry; textile; food industry.

XX OS Stachybotrys chartarum.

XX PN US6399329-B1.

XX PD 04-JUN-2002.

XX PF 21-DEC-1999; 99US-0468578.

XX

PR 12-DEC-1998; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.

XX (GENV) GENENCOR INT INC.

XX PI Wang H, Bodie EA;

XX WI; 2002-496835/53.

DR N-PSDB; AAL47582, AAL47584.

PT New polynucleotides encoding phenol oxidizing enzymes, useful for
PT preventing the transfer of dyes in solution from one textile to another
PT during detergent washing -

PS Example 5; Fig 4; 37pp; English.

CC The present invention provides the protein and coding sequences of phenol
CC oxidizing enzymes from Stachybotrys chartarum, Bipolaris spicifera and
CC Curvularia pallescens. These enzymes are useful in the textiles, paper,
CC pulp, detergent and food industries. In particular they are useful for
CC preventing the transfer of dyes in solution from one textile to another
CC during detergent washing (dye transfer inhibition). The present sequence
CC is the S. chartarum phenol oxidizing enzyme.

XX
SO Sequence 594 AA;

Query Match 100.0%; Score 3189; DB 23; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLFKSWQLAASGLISGLVGIPTMTGSHPIEAVDPEVKTEVFADSLAAGDDMESPPY 60

DB 1 MLFKSWQLAASGLISGLVGIPTMTGSHPIEAVDPEVKTEVFADSLAAGDDMESPPY 60

QY 61 NLTYNALPIPPVKOPKMITNPVTGKDIWYEIETKPEQORITPTLRPATLVGDGMS 120

DB 61 NLTYNALPIPPVKOPKMITNPVTGKDIWYEIETKPEQORITPTLRPATLVGDGMS 120

QY 121 GPTFNVPRTETVVFRIINNAIVENSVLHSGSPRAPFDGMADVTFFPGYKDYPPNYQS 180

DB 121 GPTFNVPRTETVVFRIINNAIVENSVLHSGSPRAPFDGMADVTFFPGYKDYPPNYQS 180

QY 181 ARLLWYHDAHFEMKTAENAYFGQAGAYIINDEAEDALGLPSGGEEDIPLLITAKYYNADG 240

DB 181 ARLLWYHDAHFEMKTAENAYFGQAGAYIINDEAEDALGLPSGGEEDIPLLITAKYYNADG 240

QY 241 TLRTSGEDDOLMGVIVHNGOPWFLNVPKRYFRFLNAVSRAMLIVRTSSPNVR 300

DB 241 TLRTSGEDDOLMGVIVHNGOPWFLNVPKRYFRFLNAVSRAMLIVRTSSPNVR 300

QY 301 IPFOYIASDAGLLQAPVOTSNLTYLAVEREYELIIDFTNAGOTLDRNVAETNDVGDEDE 360

DB 301 IPFOYIASDAGLLQAPVOTSNLTYLAVEREYELIIDFTNAGOTLDRNVAETNDVGDEDE 360

QY 361 YARTLEVNRFFVSSGTVEDNSQVSTLRDVPKPRKEGPADKHFFERSNGHYLLINDVGF 420

DB 361 YARTLEVNRFFVSSGTVEDNSQVSTLRDVPKPRKEGPADKHFFERSNGHYLLINDVGF 420

QY 421 ADVNERVLAKPELGTVEWELENSSGGSHRPHILVDFKILKRTGGKQOVVPYSAGLK 480

DB 421 ADVNERVLAKPELGTVEWELENSSGGSHRPHILVDFKILKRTGGKQOVVPYSAGLK 480

QY 481 DVMVLGRGETTLTIEAHYQWPTGAYMMHCHNLIHEDNDMAAVFNVTAMEBKGYLQEDFEDP 540

DB 481 DVMVLGRGETTLTIEAHYQWPTGAYMMHCHNLIHEDNDMAAVFNVTAMEBKGYLQEDFEDP 540

QY 541 MNPKRAVPYNNDFHARAGNFSASITARVOELAEQEBYRNLDLELDGIEE 594

DB 541 MNPKRAVPYNNDFHARAGNFSASITARVOELAEQEBYRNLDLELDGIEE 594

RESULT 6

AAV95538

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ID  AAY9538 standard: Protein; 627 AA.
XX
XX  AAY9538;
AC
XX  10-OCT-2000 (first entry)
DT
XX  Bipolaris spicifera phenol oxidizing enzyme.
DE
XX  Bipolaris spicifera phenol oxidizing enzyme.
KM  Phenol oxidizing enzyme; detergent; bleaching.
XX
OS  Bipolaris spicifera.
PN  WO200039306-A2.
XX
XX  06-JUL-2000.
PD
XX  20-DEC-1999; 99WO-EP10287.
PF
XX  23-DEC-1998; 98US-0220871.
PR  23-JUN-1999; 99US-0338723.
XX
XX  (UNIL ) UNILEVER NV.
PA  (UNIL ) UNILEVER PLC.
XX  (HIND-) HINDUSTAN LEYER LTD.
PI  Bodle EA, Van Der Velden S, De Vries CH, Wang H;
XX  WPI. 2000-514528/46.
DR  N-PSDB: AAY50020.
XX
XX  Detergent composition comprising novel phenol oxidizing enzyme obtained
PT  from fungus or bacteria, useful for pulp and paper bleaching, bleaching
PT  color of stains on fabric and for anti-dye redeposition -
XX
XX  Claim 8, Fig 3; 45pp; English.
XX
XX  The present sequence is that of the Bipolaris spicifera
CC  phenol oxidizing enzyme. The invention relates to detergent
CC  compositions comprising novel phenol oxidizing enzymes that have at
CC  least 60% identity with the phenol oxidizing enzyme of Stachybotrys
CC  chartarum (see AAY9537), and which are obtained from a bacterium,
CC  yeast or non-stachybotrys fungus, especially B. spicifera,
CC  Curvularia pallescens (see AAY9539) and Amoratorium atrum (see
CC  AAY95540). The phenol oxidizing enzyme is capable of modifying the
CC  colour associated with dyes or coloured compounds, and can be used
CC  for pulp and paper bleaching, for bleaching the colour of stains on
CC  fabric and for anti-dye transfer in detergent and textile
CC  applications. It may also be capable of modifying the colour in
CC  the absence or presence of an enhancer. Expression vectors and
CC  host cells comprising a nucleic acid encoding a phenol oxidizing
CC  enzyme, methods for producing the phenol oxidizing enzyme, and
CC  methods for constructing expression hosts are provided.
XX
XX  Sequence 627 AA:
SQ

```

Query Match 61.3%; Score 1954.5; DB 21; Length 627;
 Best Local Similarity 61.1%; Pred. No. 1e-179;
 Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

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OY  2 LFKSQQLAASAGLSGLGIPMDTGSHPRIEAVDPKTEVFADSLAAGDD----- 53
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB  6 LFSALQIVS---IAKGIYVAL--SERPAKFVDNTPDEKKA--LASIYEDDPADVNNML 58
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY  54 -DWSEPPYLLYRNALPIPPVKQPKMITNPVTGKDIWYEIEIKPQGRIPPTLRPATL 112
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB  59 KDWOSPEYPLIRFOPLPPIPAKEPNK-LTNPTNKEIWIYEIYIKPFTQOVPPLSPAPRL 117
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY  113 VGYDGSPPGPTNVNPGCTVVRFTINNATVENSYHLHSGSPRAPFGMGADMTFFPEXYD 172
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB  118 VYDGISPEPTTIIVPRGTEAVVRFINQGDRESSIHGHGSPSRPFMGADMDIMKGEYKD 177
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY  173 YVFPNYSARLMLYHDHAFMKTAENAYFGQAGAYIINDAEDALGLPSCYGEFDIPLILT 232
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

```

```

DB  178 YVYPPNNOAARFLWYHDHAMVHTAENAYFGQAGAYLITDPAEDALGLPSCYGYDIPVLVS 237
OY  233 AKYNNADGTLRSTEGEDODIMGDVHIVNGQPPFPLVVOFRKTRFRFLNAAVSRAMLITLY 292
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB  238 SKYYNADGTLKTSVGEDKSYWGDIIHVNGQPPFPLVVEBRKYRLRLNAAVSRNFALYEV 297
OY  293 RTSSPNVRIPFQVIASDAGLLOAPVOTSNLYLAVAREYIITDFTNPAOCTLDLRVAET 352
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB  298 KQDNTATRLPFOVIASDAGLITHPVOTSDMYVAAAAREYIIVDFEFAFYACOTLDLRNFAPA 357
OY  353 NDVDEDEYAKRTLEVNRFPVSSGTVEDNSQVPSLTLDVPEPPKEGPADKHKFEKRSNGH 412
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB  358 NGIGTDDDYANFDKVMRPFVHSSQTVVDNSVPEQLSQIOFPADKT-DIDHHPFRHTNDE 416
OY  413 YLINDVGFADVNERVLAKEBELGVEVWELENSSGGSHPEVYHILHDFKLKRTGCGQ-- 470
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB  417 WRINGIGFADVNERVLAKEPRGTVELMELENSGGSHPEVYHILHDFRVARAGDGTGEG 476
OY  471 VMPYESAGLKDVYWLGRGFTLTTEAHYOPMTGAYVMHCHNLHEDNDMAVFNVTAMEEK 530
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB  477 VMPEYAGLKDVYWLGRHETVLEAHYAPMDGYVMHCHNLHEDNDMAVFNVTAMEEK 536
OY  531 GYLQ-EDFEDPMNPKRAVPYNRNDPFHARAGNFSASITARVOELAEQPPYRLDEILED 589
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB  537 GYNETTDFHDPEDPRKWSARPFATGDLTARSGIFSEESIRARVNELALRQPSFLAQVTA 596
OY  590 L 590
DB  597 L 597

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Result 7
 AAY96762
 ID AAY96762 standard: Protein; 627 AA.
 AC AAY96762;
 XX
 XX 09-OCT-2000 (first entry)
 DT
 XX Bipolaris spicifera phenol oxidizing enzyme.
 DE
 XX Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
 KM pulp; paper bleaching.
 XX
 OS Bipolaris spicifera.
 PN WO200037654-A2.
 XX
 XX 29-JUN-2000.
 PD
 XX 20-DEC-1999; 99WO-US31009.
 PF
 XX 23-DEC-1998; 98US-0220871.
 PR 23-JUN-1999; 99US-0338723.
 XX
 PA (GENEV) GENENCOR INT INC.
 PI Wang H, Bodle EA;
 XX
 XX WPI: 2000-452191/39.
 DR N-PSDB: AAY51315.
 XX
 XX New phenol oxidizing enzyme for modifying colors associated with dyes
 PT or colored compounds, is obtained from fungus and is encoded by a
 PT nucleic acid comprising a specific nucleotide sequence
 XX
 PS Claim 8; Fig 3; 45pp; English.
 XX
 XX This sequence is the Bipolaris spicifera phenol oxidizing enzyme.
 CC Phenol oxidizing enzymes encoded by nucleic acid sequences which
 CC hybridize to the Stachybotrys chartarum DNA (AAY51313) are claimed, as
 CC long as the enzyme is capable of modifying the colour associated with
 CC dyes or coloured compounds. The enzymes are useful in detergent

[illegible]

Db	59	KMOSPPEPILFERALPLPRPAKEPKK -MTNPYTKKEIYYITVTKPRNOOYVPSLRPARL	117
QY	113	VGCDMSGQPTFFNNPBCGETVYVRFINATVENSYHLHGSSPRAFPDGMADVTPEGEYKD	172
Db	118	VGCDGISPPPTIIVBCGETEAVYRFFVNGQDRESSIHLHGSSPRAFPDGMADLIMKGGFKD	177
QY	173	YTFPNYQSARLLMTYHDHAFMKTAENATFGOGANITINDAEDALGDPSCGGEFDPIILT	232
Db	178	YTFPNNOQARFLMYHDHMHYTAENAYFGQAGAVLITDPADADALGDPSCGYKXIDPLVS	237
QY	223	AYYVADGTLRSTEGEGDDLMGDYIHVNGQPMPLNTQPRKYRFRFLNAAVSRAMLXYLV	292
Db	238	SAFYNSDGLTQTSVEDNSLMDGYIHNVGQPMPEFNPVPRKYRLFLNAAVSRMFALYEV	297
QY	293	RFSSTNNVPIPEOVIASDAGLLQAPQVQTSNLYLAVAERYEIIIDPTNFCOTLDRNVAET	352
Db	298	KQQAATATPLPFGVYIASDAGLLTHRPQTSDIYVAAAREIYFDPAPACQITDLRNFAKA	357
QY	353	NDVGEDEYARTLEVMRFVSSGTVEDNSQVPSFLRDYPPPPHKEGPADKHFKFERSNGH	412
Db	358	NGVYGDDEYANTDKMRFRHVSSQAAVVDNSVYPADLSQIQEPADTGT-IDHHFRHRTNSE	416
QY	413	YLINDVGPADVNERLAKPELGTVEYVWLENSSGGSWSHPVHILYDPRKILKRTGCG---RG	468
Db	417	WRINIGIPADVQNRILAVPGRGTVELMELENSSGGSWSHPVHILYDPRVYARVGDESTGTG	476
QY	470	QVMPESASGLKDVWVLGRGETLTLEAHYQPTGAYVMHCHNLIHEDDMMAVFNVTAMEE	529
Db	477	-VMPEASGLKDVWVLGRHEIVLYEAAHAPPDGYVMHCHNLIHEDDMMAEPVYTKLN	535
QY	530	KGYLD-EDFEDPMNKRAVHPYNNRNDFHARAGNFSASISTARVOELAEQEPYNRILILE	588
Db	536	FGYNETTDFHPDEDSRMSARPFATADLTARSGIFSEASIRARVNELAEQPYSELAQVTA	595
QY	589	DL 590	
Db	596	SL 597	
RESULT 10			
AA96763			
ID	AA96763 standard; Protein: 627 AA.		
XX	AA96763:		
AC			
XX			
DT	09-OCT-2000 (first entry)		
XX			
DE	Curvularia pallens phenol oxidizing enzyme.		
XX			
KM	Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;		
KW	pulp; paper bleaching.		
XX			
OS	Curvularia pallens.		
XX			
PN	MO200037654-A2.		
XX			
PD	29-JUN-2000.		
XX			
PE	20-DEC-1999; 99MO-US31009.		
XX			
PR	23-DEC-1998; 98US-0220871.		
PR	23-JUN-1999; 99US-0338723.		
XX			
PA	(GENV) GENENCOR INT INC.		
XX			
PL	Wang H, Bodie EA;		
XX			
DR	WPI: 2000-452191/39.		
XX			
XX	N-PSDB; AAA51316.		
PT	New phenol oxidizing enzyme for modifying colors associated with dyes		
PT	or colored compounds, is obtained from fungus and is encoded by a		
PT	nucleic acid comprising a specific nucleotide sequence		

QY	470	QVMPESAGLKVYVWLGRTGLTLEATQYOWTQATYMHCHNLIEDNDMAAFVNTAME	529
Db	477	-VMPESAGLKVYVWLGRTGLTLEATQYOWTQATYMHCHNLIEDNDMAAFVNTAME	535
OY	530	KGYLO-DEPEDPMPPKRRAPVYNNDENHARAGNFSSEITARYOEAEOPVNRDEILE	588
Db	536	FGYNETTDFHDPEDSRNSARPTFTADLTARSGLFSEASTARVNEALQOPISLAAQVTA	595
OY	589	DL 590	
Db	596	SL 597	
RESULT 12			
AAU97312			
ID	AAU97312	standard; Protein: 583 AA.	
AC	AAU97312:		
XX	30-JUL-2002	(first entry)	
DT	Phenol oxidising enzyme L76W/M254F mutant.		
DE	Phenol oxidising enzyme L76W/M254F mutant.		
XX	Phenol oxidising enzyme: colour modification: cleaning: textile:		
KW	denim treatment; decolouring indigo waste; fabric dyeing; bleaching;		
KW	fibre modification; leather industry; paper pulp manufacture;		
KW	fluff pulp manufacture; wood processing; pump bleaching; bio-glye;		
KW	linin activation; MDP manufacturing; ink removal; paper dyeing;		
KW	adhesives; feed additive; plant material processing; oxygen scavenger;		
KW	contact lens cleaning; bread improver; food preservation; personal care;		
KW	frangence; skin care; hair care; oral hygiene; deodorant; antiperspirant		
KW	hair dye; skin dye; surface modification; anti-microbial agent;		
KW	odour removal; teeth whitening; cleaning; waste water treatment;		
KW	decolorification of phenolic component; bio-remediation; bio-material;		
KW	bio-catalyst; biopolymer; surface modification; biosensor;		
XX	primary alcohol production; organic syntheses; enzyme; mutant; mutein.		
OS	Stachybotrys chartarum.		
OS	Synthetic.		
XX	Key	Location/Qualifiers	
FH	Misc-difference 76	/note- "Wild type Leu substituted by Trp"	
FT	Misc-difference 254	/note- "Wild type Met substituted by Phe"	
FT			
XX	W0200220755-A2.		
PN	14-MAR-2002.		
PD	30-AUG-2001; 2001WO-US27263.		
XX	07-SEP-2000; 2000US-0656640.		
PR	(GEMV) GENENCOR INT INC.		
XX			
PA	Wang H, Aehle W, Rodriguez AM, Toppozada A, Van Gastel FOC;		
PI	WPI: 2002-415728/44.		
XX			
XX			
DR			
XX			
PT	Novel enzymatically active variant of precursor phenol oxidising enzyme		
PT	derived from Stachybotrys species to modify colour associated with		
PT	coloured compounds such as in cleaning, e.g. for removing food stains on		
PT	fabric -		
XX			
XX			
PS	Claim 5; Page -: 54pp; English.		
CC	The invention describes an enzymatically active variant (I) of a		
CC	precursor phenol oxidising enzyme (EI) derived from a species of		
CC	Stachybotrys. (I) is useful in: modification of colour associated with		
CC	coloured compounds; cleaning; textiles. The enzyme variants are useful		
CC	in: denim treatment; decolouring indigo waste; fabric dyeing; textile		

Query Match	Best Local Similarity	Score	DB	Length	583:
Matches	332:	Conservative	67:	Mismatches	123:
				Indels	19:
				Gaps	9
57	SEPPNLLYNALRIPPYKOPKMITNPVTGKDIWYEIEIKRPOORITPTLRPATLVGCD	116			
Db	45	SEPPNLLYNALRIPPYKOPKMITNPVTGKDIWYEIEIKRPOORITPTLRPATLVGCD	116		
117	GMSPGTFNVPRTGTEVNVAFINNA--TVENSVHLHSPSRAPDDGAEDVTPGCEKDYV	174			
Db	103	GMSPGTFNVPRTGTEVNVAFINNA--TVENSVHLHSPSRAPDDGAEDVTPGCEKDYV	174		
175	PNVYSARLLWHDHAFMKTAEAAVFGCAAYIINDEADALGSPGYEFDIPLLTAK	234			
Db	163	PNVYSARLLWHDHAFMKTAEAAVFGCAAYIINDEADALGSPGYEFDIPLLTAK	234		
235	YNADGTLSTEGEDDLDGDIIVNGOPWPLNVQPRKRYRFRFLAAVSRAMLVYVPT	294			
Db	223	YNADGTLSTEGEDDLDGDIIVNGOPWPLNVQPRKRYRFRFLAAVSRAMLVYVPT	294		
295	SSPNVIRPVOVIALDAGLQAPVQSNLTLVAEREIITIDTNPAGOLFDIRNVAETND	354			
Db	283	SSPNVIRPVOVIALDAGLQAPVQSNLTLVAEREIITIDTNPAGOLFDIRNVAETND	354		
355	VQDEDEYATLLMRRFVVSSTGIVE--DNGQVSTLADVPFPKHKEG---PA---DKHF	404			
Db	343	VQDEDEYATLLMRRFVVSSTGIVE--DNGQVSTLADVPFPKHKEG---PA---DKHF	404		
405	KEERSNGHYLLINDVGFADNERYVLAKPBLGTVEVWELENSGGWSHPVHILVDFKILR	464			
Db	399	KEERSNGHYLLINDVGFADNERYVLAKPBLGTVEVWELENSGGWSHPVHILVDFKILR	464		
465	TGGRQVMPYESAGLKDYVWLGREGELTLEAHYQPTGTAYMMHCHNLIHEDNDMAVENV	524			
Db	459	TGGRQVMPYESAGLKDYVWLGREGELTLEAHYQPTGTAYMMHCHNLIHEDNDMAVENV	524		
525	TAMEEKGYLOEFDDEDMNKRWAPVPRNRDFAHARAGNFAESITARVOELAEDEPNRLD	584			
Db	518	TAMEEKGYLOEFDDEDMNKRWAPVPRNRDFAHARAGNFAESITARVOELAEDEPNRLD	584		
585	E 585				
Db	578	D 578			

XX AA097316;
AC 30-JUL-2002 (first entry)
DE Phenol oxidising enzyme L76W/M254F/E302V mutant.
XX
XX Phenol oxidising enzyme; colour modification; cleaning; textile;
XX denim treatment; decolouring indigo waste; fabric dyeing; bleaching;
KW fibre modification; leather industry; paper pulp manufacture;
KW fluff pulp manufacture; wood processing; pump bleaching; bio-glu-
KW lignin activation; MDF manufacturing; ink removal; paper dyeing;
KW adhesives; feed additive; plant material processing; oxygen scavenger;
KW contact lens cleaning; bread improver; food preservation; personal care;
KW fragrance; skin care; hair care; oral hygiene; deodorant; antiperspirant;
KW hair dye; skin dye; surface modification; anti-microbial agent;
KW odour removal; teeth whitening; cleaning; waste water treatment;
KW detoxification of phenolic component; bio-remediation; bio-material;
KW bio-catalyst; biopolymer; surface modification; biosensor;
KW primary alcohol production; organic syntheses; enzyme; mutant; mutein.
XX
XX Stachybotrys chartarum.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 76
FT Misc-difference /note= "Wild type Leu substituted by Trp"
FT Misc-difference 254
FT Misc-difference /note= "Wild type Met substituted by Phe"
FT Misc-difference 302 /note= "Wild type Glu substituted by Val"
XX
XX WO200220755-A2.
XX
XX 14-MAR-2002.
XX
XX 30-AUG-2001; 2001WO-US27263.
XX
XX 07-SEP-2000; 2000US-0656640.
XX
XX (GENEV) GENENCOR INT INC.
XX
XX Wang H, Aehle W, Rodriguez AM, Topozada A, Van Gastel FJC;
XX
XX WPI; 2002-415728/44.
XX
XX Novel enzymatically active variant of precursor phenol oxidising enzyme
XX derived from Stachybotrys species to modify colour associated with
XX coloured compounds such as in cleaning, e.g. for removing food stains on
XX fabric -
XX
XX Claim 5; Page -: 54pp; English. *

CC syntheses; and for reducing or eliminating the microbial load of various
CC foods, e.g. meats or feed. This is the amino acid sequence of a modified
CC Stachybotrys chartarum phenol oxidising enzyme, the properties of which
CC are discussed in the invention.
CC Note: This sequence does not appear in the specification but has been
CC created using the wild type sequence shown in AA097301 using Information
CC given in the invention.
XX
XX SQ Sequence 583 AA;
XX
XX Query Match 54.3%; Score 1731.5; DB 23; Length 583;
XX Best Local Similarity 61.4%; Pred. No. 3,4e-158;
XX Matches 332; Conservative 66; Mismatches 124; Indels 19; Gaps 9;
QY 57 SPPEYLRLNALPPIPVKOPKMIITNPYTKGDIWYEIEIKPQORIRYPTLRPATLVGYD 116
DB 45 SPPL-ALTEVPLPIPLKAPN-TVPNPTGEDIMYEMIEIRFSQIITPDLFPAMVGYD 102
QY 117 GMSPGPTNVPRGTEYVRFINNA--TVENSYHLGSPSRAPFDGMAEDYFPGCKDY 174
DB 103 GMSPGPTTIIVPRGTESVYRVFVNGSENTSPSVHLHGSPSRAPFDGMAEDYTPGCEYKDY 162
QY 175 PPNYOSARLWYHDHAFMKTAENATFGQAGAYIINDEADALGIPSGCEDPIPLITAK 234
DB 163 YPNRQAARLWYHDHAMSITAEANAYMGAGVYMIODPADADALNPSGYGEPDIPLVITAK 222
QY 235 YYNADGTLRSTEGEODLWGDVYHNGOPWPLANTOPKRYRFRFMAAVSRAMLTYLVT 294
DB 223 RYNADGTLFTSTGEVSRMGVDIYNGOPWPLANTOPKRYRFRFMAAVSRFALYLT 282
QY 295 SSPNVRIPEQVIASDAGLLQAPVQTSNLYLAVAREYEIITDFNAGOTGLDRNVAETND 354
DB 283 EDSERLRFQVYIAADGGLVCPVDTDTLYISAEKWEVVIDESTFAGQSIDIRNLPGADG 342
QY 355 VGDEDEYARTLEVMRPFVSSGTYE--DNSQVSTLRDVPFPHKRG---PA----DKHF 404
DB 343 LGVEPEPNTDKVMRPFVDE-VLESPTSEVPANLRDVPF--EGGMDPAPPTDDEF 398
QY 405 KPERSNGHYLINDGVADFVNERVLAKPELGTVEVMELESNGSGMSPHYHLVDFKIKR 464
DB 399 TTEGRANGQMTIYVFSDVENLRLNVPDLYETMRLENSNGWHPVPHILYDFRVL 458
QY 465 TGGRGQVMPESAGLKDVMVILGRGETLTIEAHYQPTGAYMHCHNLIHEDNMMAVFN 524
DB 459 STARG-VEPYEAGLKDVMVILARREYVYEAHYDFPGVYMLCHNLIHEDNMMAVFN 517
QY 525 TAMEKGYLQEDFEDPMPKRAVPYRNDFHARAGNSAESTIRVQELAQEPEYRNL 584
DB 518 TVLGDYGYNTETFDMPFLMRPRFLLEGFENGSGDSELAITDRIQEMASFNPAQAD 577
QY 585 E 585
DB 578 D 578
XX
XX RESULT 14
XX AA097318
XX ID AA097318 standard; Protein: 583 AA.
XX
XX AA097318;
XX
XX 30-JUL-2002 (first entry)
XX
XX Phenol oxidising enzyme L76W/M254F/E302V/D394N/V425M mutant.
XX
XX Phenol oxidising enzyme; colour modification; cleaning; textile;
XX denim treatment; decolouring indigo waste; fabric dyeing; bleaching;
KW fibre modification; leather industry; paper pulp manufacture;
KW fluff pulp manufacture; wood processing; pump bleaching; bio-glu-
KW lignin activation; MDF manufacturing; ink removal; paper dyeing;
KW adhesives; feed additive; plant material processing; oxygen scavenger;
KW contact lens cleaning; bread improver; food preservation; personal care;
KW fragrance; skin care; hair care; oral hygiene; deodorant; antiperspirant;
KW

XX (UNITL) UNILEVER NV.
PA (UNITL) UNILEVER PLC.
PA (UNITL) HINDUSTAN LEVER LTD.
XX
PI Aehle W, Convents D, Doornink M, Van Gastel F, Rodriguez AM.
PI Toppozada A, De Vries CH, Wang H;
XX WPI: 2002-339800/37.
XX

PT Detergent composition containing phenol-oxidizing enzyme, useful for
PT stain removal, derived from a precursor enzyme of Stachybotrys -
XX
XX Example 8; Page -: 52pp; English.

XX The present sequence is a L76W/M254F/E302V variant of Stachybotrys
CC chartarum Muctl 38898 phenol oxidase B. The variant was obtained
CC using site-directed mutagenesis. Claimed detergent compositions
CC of the invention comprise at least 1 surfactant and an enzymatically
CC active variant of the phenol oxidase B enzyme, which may include
CC the present amino acid substitutions. The compositions are useful
CC as laundry and dishwashing products, particularly for removing
CC stains from fabrics, or generally to oxidise coloured compounds.
CC They are also useful for bleaching paper and pulp, in personal care
CC products, foods, animal feeds, textiles, leather, contact lens
CC cleaners, for starch production, for deodourisation, sanitation or
CC waste-water treatment, as biocatalysts, in connection with
CC biopolymers, packaging, adhesives or biosensors, in surface
CC modification, in production of primary alcohols, and as
CC antimicrobials. Variant enzymes may have increased phenol-oxidising
CC activity at high pH compared with the parent enzyme, and especially
CC have an optimum pH of at least 9. They may also show increased
CC productivity, oxidative, thermal, alkaline, or proteolytic stability,
CC different substrate specificity or different catalytic activity.
CC The present variant has a specific activity for guaiacol of 1.65
CC deltaOD/min.mg protein (compared with 1.38 deltaOD/min.mg for the
CC parent enzyme).
CC Note: The present sequence is not shown in the specification, but
CC is derived from the Stachybotrys wild-type phenol oxidase B
CC sequence given in figure 2 (see ABB75754).
XX

SQ Sequence 583 AA:

Query Match 54.3%; Score 1731.5; DB 23; Length 583;
Best Local Similarity 61.4%; Pred. No. 3.4e-158;

Matches 332; Conservative 66; Mismatches 124; Indels 19; Gaps 9;

QY 57 SPPYLLLYRNALPIPPYKQPKMTITPVYTKGDIYIEIKPQQRITYPLRPATLVGYD 116
DB 45 SPPL-ALYEPPLPIPLKAPN-TVPNPNMGEDIMYEMETRPESHQIYPDLEPANMVGVD 102
QY 117 GMSPGPTFNVPRGTETVFRFINNA--TVENSYHLHGSPPSRAPFDGMAEDVTFPEYKDDY 174
DB 103 GMSPGPTTIIVPRGTESVFRVNSGENTSPNSVYHLHGSFSRAPFDGMAEDTTPQPEYKDDY 162
QY 175 FPNYQASRLMYDHAEMKTAENAYEFGAGAYLIINDEADALGPSYGEFDIPLITAK 234
DB 163 YPRQAARMLMYDHAEMKTAENAYEFGAGAYMIQDPAEDALNPSYGEFDIPLITAK 222
QY 235 YTNADGTLNSTEGEDODLMDGVHVGQPFELNVQPRKRYFRFLNAAVSRAMLIVRT 294
DB 223 RYNADGTLNSTEGEDVSSFWGDVIVNGQPPFELNVQPRKRYFRFLNAAVSRFALYATS 282
QY 295 SSPNVRIIPFOVIVASDGLQAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNVAETND 354
DB 283 EDESETRIPFOVIVADGGLGVPVDTLITSMERKEVVIDFTFAQOSTIDIRNLPGADG 342
QY 355 VGDEDEYARTLEVMRFVSSGTV--DNSQVPSLTDVPPPHKEG---PA---DKHF 404
DB 343 LGVEPEPFENDTKVMRFVDE-VLESPTSEVPANLRDVPFP---EGGNMPPANPTDETF 398
QY 405 KPEKRSNGHYLINDGVADVNERVLAKPELCTVEVMELENSGSGMHPVHILYDFEKLKR 464

DB 399 TFCRANGQWTINGVTFSDVENRLLRNVPDVEIWRLENNNSNGWHPYHILVDERSLR 458
QY 465 TCGRGQVMPYESAGLKDYVWLGREGTLLTIEAHYQWGTGATYMHCHNLHEDNDMAAVNV 524
DB 459 STARG-VEPYEAAAGLKDYVWLARREVYVEAHYAPPGYMLCHNLHEDNDMAAVNV 517
QY 525 TAMEEKGYLQEDFEDPMPKMRAPYNNRNDPHARAGNFSAESITARVOELARQEPYNRLD 584
DB 518 TVLGDYGYNTTEFIDPMEPLMRPRPFLGGEFENGSGDFSELATITRIDEMASFNRYAQAD 577
QY 585 E 585
DB 578 D 578

Search completed: February 13, 2003, 05:15:53
Job time : 62 secs

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OM protein - protein search, using sw model

Run on: February 13, 2003, 05:15:48 : Search time 21 seconds
(without alignments)
832.248 Million cell updates/sec

Title: US-09-218-702-2

Perfect score: 3189

Sequence: 1 MLFMSQMLAAASGLSGVLG.....ABQEPYRLDEILEDLGIEE 594

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3189	100.0	594	US-09-468-578-2	Sequence 2, Appl1
2	3189	100.0	594	US-09-218-702-2	Sequence 2, Appl1
3	1954.5	61.3	627	US-09-468-578-4	Sequence 4, Appl1
4	1929.5	60.5	627	US-09-468-578-7	Sequence 7, Appl1
5	1724.5	54.1	572	US-09-401-476-4	Sequence 4, Appl1
6	1716.5	53.8	583	US-09-401-476-2	Sequence 2, Appl1
7	1712.5	53.7	568	US-09-218-702-4	Sequence 4, Appl1
8	400.5	12.6	322	US-09-134-001C-2946	Sequence 2946, Ap
9	357.5	11.2	114	US-09-468-578-9	Sequence 9, Appl1
10	202	6.3	616	US-08-749-882A-2	Sequence 2, Appl1
11	202	6.3	616	US-08-539-134-2	Sequence 2, Appl1
12	202	6.3	616	US-08-991-531-2	Sequence 2, Appl1
13	202	6.3	616	US-09-032-315-9	Sequence 9, Appl1
14	202	6.3	616	US-08-993-318A-9	Sequence 9, Appl1
15	202	6.3	616	US-09-028-887-2	Sequence 2, Appl1
16	202	6.3	616	US-09-399-886-9	Sequence 9, Appl1
17	202	6.3	616	US-09-396-260-9	Sequence 9, Appl1
18	202	6.3	616	US-09-518-901-2	Sequence 2, Appl1
19	202	6.3	616	US-09-576-281-9	Sequence 9, Appl1
20	198.5	6.2	529	US-08-172-331B-14	Sequence 14, Appl1
21	198.5	6.2	529	US-08-706-037-25	Sequence 25, Appl1
22	198.5	6.2	529	US-09-005-397-25	Sequence 25, Appl1
23	198.5	6.2	529	US-09-032-315-5	Sequence 5, Appl1
24	198.5	6.2	529	US-08-993-318A-5	Sequence 5, Appl1
25	198.5	6.2	529	US-09-399-886-5	Sequence 5, Appl1
26	198.5	6.2	529	US-09-396-260-5	Sequence 5, Appl1
27	198.5	6.2	529	US-09-576-281-5	Sequence 5, Appl1

28	198	6.2	620	1	US-08-940-661A-2	Sequence 2, Appl1
29	198	6.2	620	2	US-09-083-485-2	Sequence 2, Appl1
30	198	6.2	620	2	US-08-939-218A-2	Sequence 2, Appl1
31	197	6.2	573	2	US-08-991-531-1	Sequence 1, Appl1
32	197	6.2	573	2	US-09-032-315-10	Sequence 10, Appl1
33	197	6.2	573	3	US-08-993-318A-10	Sequence 10, Appl1
34	197	6.2	573	3	US-09-028-887-1	Sequence 1, Appl1
35	197	6.2	573	4	US-09-399-886-10	Sequence 10, Appl1
36	197	6.2	573	4	US-09-396-260-10	Sequence 10, Appl1
37	197	6.2	573	4	US-09-518-901-1	Sequence 1, Appl1
38	197	6.2	573	4	US-09-576-281-10	Sequence 10, Appl1
39	197	6.2	616	5	PCT-US95-06816-2	Sequence 2, Appl1
40	197	6.2	620	1	US-08-706-037-27	Sequence 27, Appl1
41	197	6.2	620	2	US-09-005-397-27	Sequence 27, Appl1
42	197	6.2	620	5	PCT-US95-06815-2	Sequence 2, Appl1
43	194	6.1	511	1	US-08-462-484-8	Sequence 8, Appl1
44	194	6.1	511	1	US-08-441-147-8	Sequence 8, Appl1
45	194	6.1	511	5	PCT-US95-07536-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1									
US-09-468-578-2									
; Sequence 2, Application US/09468578									
; Patent No. 6399329									
; GENERAL INFORMATION:									
; APPLICANT: Wang, Huaming									
; APPLICANT: Bodie, Elizabeth A.									
; TITLE OF INVENTION: Phenol Oxidizing Enzymes									
; FILE REFERENCE: GC561-3									
; CURRENT APPLICATION NUMBER: US/09/468,578									
; CURRENT FILING DATE: 1999-12-21									
; PRIOR APPLICATION NUMBER: US 09/220,871									
; PRIOR FILING DATE: 1998-12-23									
; PRIOR APPLICATION NUMBER: US 09/338,723									
; PRIOR FILING DATE: 1999-06-23									
; NUMBER OF SEQ ID NOS: 17									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 594									
; TYPE: PRT									
; ORGANISM: Stachybotrys chartarum									
US-09-468-578-2									
Query Match									
Best Local Similarity 100.0%; Score 3189; DB 4; Length 594;									
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
OY	1	MLFMSQMLAAASGLSGVLGIPMDTGSHPLEAVDPVKTEVFADSLAAGDDWESP	60						
DB	1	MLFMSQMLAAASGLSGVLGIPMDTGSHPLEAVDPVKTEVFADSLAAGDDWESP	60						
OY	61	NLLRYNALPPEPKOKMIIITNVTGKDIWYIEIEIKPQORITPLRATLVGYGMS	120						
DB	61	NLLRYNALPPEPKOKMIIITNVTGKDIWYIEIEIKPQORITPLRATLVGYGMS	120						
OY	121	GPTFNVPRGTETVVRINNATVENSVHLGSPSRAPFDGMAEDVPEGCKDYFPN	180						
DB	121	GPTFNVPRGTETVVRINNATVENSVHLGSPSRAPFDGMAEDVPEGCKDYFPN	180						
OY	181	ARLWYHDAFMKTAENAFVGAAYIINDEADALGSPGGEFDIPLILAKKYNAD	240						
DB	181	ARLWYHDAFMKTAENAFVGAAYIINDEADALGSPGGEFDIPLILAKKYNAD	240						
OY	241	TLRSTGEGDODLGDVYIHVNGOPWPLNVOPRKYRFRPLNAVSRAMLIVRTSS	300						
DB	241	TLRSTGEGDODLGDVYIHVNGOPWPLNVOPRKYRFRPLNAVSRAMLIVRTSS	300						
OY	301	IPQVIAASDAGLLQAPVQTSNLYLAVEREITIDTFNAGOTLDLRNVAETNDV	360						
DB	301	IPQVIAASDAGLLQAPVQTSNLYLAVEREITIDTFNAGOTLDLRNVAETNDV	360						

```
OY      361 YARPLEVREYVSSGTYEDNSQVSTLRDVPFPPHKESPADKHKFKERSNGHYLINDVGF 420
      |||
Db      361 YARPLEVREYVSSGTYEDNSQVSTLRDVPFPPHKESPADKHKFKERSNGHYLINDVGF 420
OY      421 ADVNERVLAKRELGTVEVWELENSGGSHPVHILHVDFFKILKRTGGGOVMPYESAGLK 480
      |||
Db      421 ADVNERVLAKRELGTVEVWELENSGGSHPVHILHVDFFKILKRTGGGOVMPYESAGLK 480
OY      481 DVVWLGRETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAVENVYTAAMEKGYLQDEDFDP 540
      |||
Db      481 DVVWLGRETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAVENVYTAAMEKGYLQDEDFDP 540
OY      541 MNPKRAVPYRNDFHARAGNFSAESITARVOELAEQEPYRNDELIEDLGIEE 594
      |||
Db      541 MNPKRAVPYRNDFHARAGNFSAESITARVOELAEQEPYRNDELIEDLGIEE 594

RESULT 2
US-09-218-702-2
; Sequence 2, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218, 702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys sp.
US-09-218-702-2

Query Match      100.0%; Score 3189; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.5e-308;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MLEFKSMOLAAASGLSGVLGIPMDTGSHPTEAVDPEVTEVFADSLAAAGDDMESPPY 60
      |||
Db      1 MLEFKSMOLAAASGLSGVLGIPMDTGSHPTEAVDPEVTEVFADSLAAAGDDMESPPY 60
OY      61 NLLYRNALPPIPVKOPKMITNPVTGKDIWYEIEIKPQORITPTLRPATLVGDCGMS 120
      |||
Db      61 NLLYRNALPPIPVKOPKMITNPVTGKDIWYEIEIKPQORITPTLRPATLVGDCGMS 120
OY      121 GGTENVPRGTETVVRFINNATYVENSYHLHSGSPRAFDDGMADVPRGGYKDYPPNYQS 180
      |||
Db      121 GGTENVPRGTETVVRFINNATYVENSYHLHSGSPRAFDDGMADVPRGGYKDYPPNYQS 180
OY      121 GPTFVNPRTGETVVRFINNATYVENSYHLHSGSPRAFDDGMADVPRGGYKDYPPNYQS 180
      |||
Db      121 GPTFVNPRTGETVVRFINNATYVENSYHLHSGSPRAFDDGMADVPRGGYKDYPPNYQS 180
OY      181 ARLLVHDAHPFKTAENAFVGOAGAYIINDEADALGLPSGGEFDIPILITAKYYNADG 240
      |||
Db      181 ARLLVHDAHPFKTAENAFVGOAGAYIINDEADALGLPSGGEFDIPILITAKYYNADG 240
OY      181 ARLLVHDAHPFKTAENAFVGOAGAYIINDEADALGLPSGGEFDIPILITAKYYNADG 240
      |||
Db      181 ARLLVHDAHPFKTAENAFVGOAGAYIINDEADALGLPSGGEFDIPILITAKYYNADG 240
OY      241 TLRTSGEGDODLMDGVYIHVNGQPMPEFLANVOPRKYRFRFLNAAVSRAMLLYLVFTSSPNVR 300
      |||
Db      241 TLRTSGEGDODLMDGVYIHVNGQPMPEFLANVOPRKYRFRFLNAAVSRAMLLYLVFTSSPNVR 300
OY      301 IFFOVYASAGLLQAPVQTSNLYLAVEREYIITDFTNAGOTLDRNVAETNDVDEDE 360
      |||
Db      301 IFFOVYASAGLLQAPVQTSNLYLAVEREYIITDFTNAGOTLDRNVAETNDVDEDE 360
OY      361 YARTELVMPFVSSGTYEDNSQVSTLRDVPFPPHKESPADKHKFKERSNGHYLINDVGF 420
      |||
Db      361 YARTELVMPFVSSGTYEDNSQVSTLRDVPFPPHKESPADKHKFKERSNGHYLINDVGF 420
OY      421 ADVNERVLAKRELGTVEVWELENSGGSHPVHILHVDFFKILKRTGGGOVMPYESAGLK 480
      |||
Db      421 ADVNERVLAKRELGTVEVWELENSGGSHPVHILHVDFFKILKRTGGGOVMPYESAGLK 480
OY      481 DVVWLGRETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAVENVYTAAMEKGYLQDEDFDP 540
      |||
Db      481 DVVWLGRETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAVENVYTAAMEKGYLQDEDFDP 540
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Db      481 DVVWLGRETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAVENVYTAAMEKGYLQDEDFDP 540
OY      541 MNPKRAVPYRNDFHARAGNFSAESITARVOELAEQEPYRNDELIEDLGIEE 594
      |||
Db      541 MNPKRAVPYRNDFHARAGNFSAESITARVOELAEQEPYRNDELIEDLGIEE 594

RESULT 3
US-09-468-578-4
; Sequence 4, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468, 578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220, 871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338, 723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Bipolaris splicifera
US-09-468-578-4

Query Match      61.3%; Score 1954.5; DB 4; Length 627;
Best Local Similarity 61.1%; Pred. No. 1.3e-185;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

OY      2 LEFSWOLAAASGLSGVLGIPMDTGSHPTEAVDPEVTEVFADSLAAAGD----- 53
      |||
Db      6 LEFSALQVLS---IAGGIYVAL--SERPAKEVDNTPDEKKA--LASIVEDDPADVNNL 58
OY      54 -DMESPYNLLYRNALPPIPVKOPKMITNPVTGKDIWYEIEIKPQORITPTLRPATL 112
      |||
Db      59 KDMQSPREYLIROPRLPIPAKEPNK-LTNPTNKEIWIYEIVIRPFOQVYPSLRPALT 117
OY      113 VGYDGMSPGRTNPNRGPTVTVVRFINNATYVENSYHLHSGSPRAFDDGMADVPRGGYKDY 172
      |||
Db      118 VGYDGISSPGRTIIVRGTEAVVRFINQGDRESSIHLHSGSPRAFDDGMADVIMKGEYKD 177
OY      173 YFFPNQASARLLVHDAHPFKTAENAFVGOAGAYIINDEADALGLPSGGEFDIPILIT 232
      |||
Db      178 YFFPNQASARLLVHDAHPFKTAENAFVGOAGAYIITDPAEDALGLPSGYGAYDIPFLVS 237
OY      233 ARYYNADGTLRTSGEGDODLMDGVYIHVNGQPMPEFLANVOPRKYRFRFLNAAVSRAMLLYLV 292
      |||
Db      238 SKYYNADGTLKTSVGBDKSVMGDIHVNGQPMPEFLVBERKYLRLFLNAAVSRNFALYEV 297
OY      293 RTSSPNVRPIPOVIASDADLQAPVQTSNLYLAVEREYIITDFTNAGOTLDRNVAET 352
      |||
Db      298 KODNTRATRLPFOVIASDADLTHPVQTSNLYLAVEREYIITDFTNAGOTLDRNVAET 357
OY      353 NDVGDEDEYARTLEVARFVSSGTYEDNSQVSTLRDVPFPPHKESPADKHKFKERSNGH 412
      |||
Db      358 NGIGTDDVYANDDKVAKRFIVSSQTYVVDNSVPEQLSQIOFPADKT-DIDHNRFRHRTNE 416
OY      413 YLINDVGFADVNERVLAKRELGTVEVWELENSGGSHPVHILHVDFFKILKRTGGGO-- 470
      |||
Db      417 WRINGIGFADVNERVLAKVPGTVEVWELENSGGSHPIVHILVDFRVYARVGDEGTBG 476
OY      471 VMPYESAGLKDVVWLGRETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAVENVYTAAMEK 530
      |||
Db      477 VMPYEAAGKDVVWLGRETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAADVYTKLQNF 536
OY      531 GYIQQ-EDFEDPMNPKRAVPYRNDFHARAGNFSAESITARVOELAEQEPYRNDELIED 589
      |||
Db      531 GYIQQ-EDFEDPMNPKRAVPYRNDFHARAGNFSAESITARVOELAEQEPYRNDELIED 589
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Db 537 GYNETTDPHDPEDPKMSARPTAGDULANSKIFSEESIRARVNELALQOYSELAQVTAS 596
QY 590 L 590
Db 597 L 597

RESULT 4
US-09-468-578-7
; Sequence 7, Application US/09468578
; Patent No. 6393229
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Curvularia pallescens
US-09-468-578-7

Query Match 60.5%; Score 1929.5; DB 4; Length 627;
Best Local Similarity 60.5%; Pred. No. 3.9e-183;
Matches 364; Conservative 81; Mismatches 134; Indels 23; Gaps 9;

QY 2 LFSKQOLAASGLSGVIGIPMDTSGHPLEAVDPREKTEVPFDSLLAAGD----- 53
Db 6 LFSALQAS--IAKIGVAL--SERPAKYIDETPDEKAA--LAAIYEDDPADVFRIL 58
QY 54 -DMESPVLILYRNALIPRVKOPKMIINPVTKGDIWYIEIKPFOORITPTLRPATL 112
Db 59 KMOSPETIILREALPIPAKEPNK-KTNPVTKKEIWIYEIVIKFNOQVPSLPAPL 117
QY 113 VGYDMSGPPTFENPRGTETVVRFINNATVENSVLHSGSPRAPEDGMAEDVTFPEYKD 172
Db 118 VGYDGIISPTIIVRGTAAYRVFVNOGDRRESSIHLHSGSPRAPFGWAMEDLIMKQFND 177
QY 173 YFEPYQASRLIYHDHAFKTAENAYFGOAGAYIINDAEDALGLPSYGEEDIPLIIT 232
Db 178 YFPPNQAARFLMYHDHAFKTAENAYFGOAGAYLITDPAEDALGLPSYGYGRYDIPLVLS 237
QY 233 AKYUADGTLSTEGEDDLMGDIHVNGOPWPLNVORPKYRFRRLNAVSRAMLLYLV 292
Db 238 SFETYSDGLTQTSVEEDNSLMGDIHVNGOPWPFVNERPKTKRLRLNAVSRKNEALYLV 297
QY 293 RTSSPNVRIPEQVIASDAGLQAPVQTSNLYLAVEREYIIDFTFAGOTIDLRLVAET 352
Db 298 KQQAATATRLPEQVIASDAGLLTHPVQTSIYVAAERVITVDFEAPYAOITIDLRLFAKA 357
QY 333 NDVGEDEYARFLLEVYMRVYVSSGVIEDNSQVSTLRDVPFPPHKEGPADKHFEKRSNGH 412
Db 338 NGVGTDDDYANDKVMRFVSSQAAVVDNSVPAQLSQIDFPADKTG-IDHHRFRHTNSE 416
QY 413 YLINVGFAVDNERVLARPELGTVEVWELSSGGSHSVHILHYDFKTLKRTG---SG 469
Db 417 WHINIGFADVONRIIAKPRGTVELMELENSGGWSPHIIHVLDFRVARGDDESTRG 476
QY 470 QVMPYESAGLKDVNLGRGETLITIAHYOPTGAYMMCHNLIHEDNDMAVFNVTAMEE 529
Db 477 -VMPYESAGLKDVNLGRGETLITIAHYOPTGAYMMCHNLIHEDNDMAVFNVTAMEE 535
QY 530 KGYLO-EDFEDPMKRAVVPYRNDFHARAGNFSASSTIARVOELAEQEPYRNRLDEILE 588
Db 536 FGYNETTFHDEPDESRMSARPTADLTARSGIFSEASIRARVNELALQOYSELAQVTA 595

QY 589 DL 590
Db 596 SL 597

RESULT 5
US-09-401-476-4
; Sequence 4, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Stachybotrys charatum
US-09-401-476-4

Query Match 54.1%; Score 1724.5; DB 4; Length 572;
Best Local Similarity 60.3%; Pred. No. 8.6e-163;
Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;

QY 57 SPBYNLLYNALPIPVKOPKMIINPVTKGDIWYIEIKPFOORITPTLRPATLVGD 116
Db 43 SPQYP-MFTVPLPIPVKOPRLVTNPVNGQETIWEYIEIKFTHQVYDGLGADLVGD 101
QY 117 GMSPGPTFENPRGTETVVRFINNATVENSVLHSGSPRAPFGWMAEDVTFPEYKDYTP 176
Db 102 GMSPGPTFENPRGTETVVRFINNATVENSVLHSGSPRAPFGWMAEDVTFPEYKDYTP 161
QY 177 NYOSARLLYHDAEFKTAENAYFGOAGAYIINDAEDALGLPSYGEEDIPLIITAKY 236
Db 162 NQASARTLWYHDHAFKTAENAYFGOAGAYLITDPAEDALGLPSYGEEDIPLIITLSKY 221
QY 237 NADGTLSTEGEDDLMGDIHVNGOPWPLNVORPKYRFRRLNAVSRAMLLYLVTS 296
Db 222 TANGNLVTTNGELNSFWGDIHVNGOPWPEKKNVPRKRYRFRFLDAVSRSGFLYFADTDA 281
QY 297 PNVRILPEQVIASDAGLQAPVQTSNLYLAVEREYIIDFTFAGOTIDLRLV-ARTNDV 355
Db 282 IDRLPEKVIASDAGLQAPVQTSNLYLAVEREYIIDFTFAGOTIDLRLV-ARTNDV 341
QY 356 GDEDEYARFLLEVYMRVYVSSGVIE-DNSQVPSLTDVPP-PHKEGPADKHFEKRSNGH 413
Db 342 GDTDTVDNTDKVMRFVYVADDTQPDTSVVPANLRDVPFSPITNP--RQFRGRTGPTW 399
QY 414 LINDVGFADVNERVLAKPELGTVEVWELSSGGSHSVHILHYDFKTLKRTG---OV 471
Db 400 TINGVAFADVONRLLANVPGTVERWELINAGNGWTHPIHILYDVKVISRSGNARTV 459
QY 472 MPYESAGLKDVNLGRGETLITIAHYOPTGAYMMCHNLIHEDNDMAVFNVTAMEEG 531
Db 460 MPYES-GLKDVNLGRGETLITIAHYOPTGAYMMCHNLIHEDNDMAVFNVTAMEEG 518
QY 532 YLOEDEDPMKRAVVPYRNDFHARAGNFSASSTIARVOELAEQEPYRNRLDE 585
Db 519 YNATVVDMEELMOKARPIELGEFGQSQSFVQVATERTIQMAEYRPTAADE 572

RESULT 6
US-09-401-476-2
; Sequence 2, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584


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; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-401-476-2
```

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Query Match          53.8%; Score 1716.5; DB 4; Length 583;
Best Local Similarity 61.0%; Pred. No. 5,5e-162;
Matches 330; Conservative 67; Mismatches 125; Indels 19; Gaps 9;
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QY 57 SPPYLLRNALPIPPVKOPKMIITNPVTGKDIWYEIEIKFPQORIYPTLRPATLVGYD 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 45 SPPL-ALVEPLPIPLPKAPN--TVNPNTGEDIILYEMERIRFSSHQIYDLEPANVGYD 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 117 GMSPGPTFVPRGTETVYAFINNA--TVENSYHLGSPSRAPFDGMAEDVTFPGEKDY 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 103 GMSPGPTIIVPGTGVYAFVNSGENTSPNSVHLGFSFRAFDGMAEDTTPGEEKDY 162
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 175 FPNYSARLLWYHDAFMKTAENAYFGAGAYIINDEADALGPSYGEFDIPLITAK 234
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 163 YPNRQARMLWYHDAFMKTAENAYFGAGAYIINDEADALGPSYGEFDIPLITAK 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 235 YYNADGTLRSTEGEDODLMDGVIVHNGOPWFLVOPRRYFRFLNAVSRAMLLYVET 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 223 RYNAGDTLSTNGEVSSFFMGDIVIQNGQPMILNQPKYRRFLMAAVSRFALYATS 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 295 SSPNRRIPPOVIASDAGLLQAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNVAETND 354
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 EDSETRLPQVIASDAGLLQAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNVAETND 342
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 355 VGDEDEYARTLEVMFVYSSGTYE--DNSQVSTLRDVPFPHKEG---PA----DKHF 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 343 LGVEPEFDNTDKVMRFVDE-VLESFDTSEVPANLRDVFPP---EGGNMPPANPDDETF 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 405 KEERSNGHYLINDVGFADYNEVLAKEPGLTVEVWELNSSGSMHPVHILVDKILKR 464
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 399 TFGRANGQWITNGVTFSDVENRLLRVPRDTVEIMLENNNSMGTHPVHILHVDKILSR 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 465 TGGRCQVMEYESAGLKDVYVWLGRETITIEAHYQPTGAYMHCNHLIHEDNDMAVENV 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 459 STARG-VEVEYEAAGLKDVYVWLGRETITIEAHYQPTGAYMHCNHLIHEDNDMAVENV 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 525 TAMEEKGYLQEDFEDPMNPKRAVPYNRNDFHARAGNFSASITARVQELAEQEPYNRLD 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 518 TVLGQVGYVTFEIDPMERLMPRPFLGLGFENGSGDFSELATIDRIQDMASFNRYAQAD 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 585 E 585
    :
DB 578 D 578
```

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RESULT 7
US-09-218-702-4
; Sequence 4, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410e1 Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Bilirubin oxidase
US-09-218-702-4
```

```

Query Match          53.7%; Score 1712.5; DB 4; Length 568;
Best Local Similarity 59.7%; Pred. No. 1,3e-161;
Matches 318; Conservative 76; Mismatches 128; Indels 11; Gaps 6;
```

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QY 57 SPPYLLRNALPIPPVKOPKMIITNPVTGKDIWYEIEIKFPQORIYPTLRPATLVGYD 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 43 SPQYR-METVPLPIPPVKOPRLTNTNPVNGQETIWEYIEIKFTQVYDPLDGSALVGYD 101
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 117 GMSPGPTFVPRGTETVYAFINNAVENSYHLGSPSRAPFDGMAEDVTFPGEKDYFP 176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 102 GMSPGPTFQVPRGTETVYAFINNAEAPNSVHLGFSFRAFDGMAEDITEPSPFDYYP 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 NQOSARLLWYHDAFMKTAENAYFGQAGAYIINDEADALGPSYGEFDIPLITAKY 236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 162 NQOSARLLWYHDAFMKTAENAYFGQAGAYIINDEADALGPSYGEFDIPLITAKY 221
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 NADGTLRSTEGEDODLMDGVIVHNGOPWFLVOPRRYFRFLNAVSRAMLLYVETNS 296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 222 TANGMLVTTNGELNSFWGDVIVHNGOPWFLVOPRRYFRFLNAVSRFGLYADTDA 281
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 297 PNVRIPOVIASDAGLLQAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNV-AETNDV 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 282 IDTRLPFKVIASDAGLLQAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNV-AETNDV 341
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 356 GDEDEYARTLEVMFVYSSGTYE--DNSQVSTLRDVPFPHKEGADKHFKERSNGHYL 414
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 342 GDTDTYDNTDKVMRFVADDTTPPTSVVPAHLRDVFP--SPTNQFRGRGPTWT 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 415 INDVGFADYNEVLAKEPGLTVEVWELNSSGSMHPVHILVDKILKRTGGRC--QVM 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 399 INGVAFADYQNLNANVPRGTYERHLLINAGQWTHPHIHLHVDKIVISRTSGNARRYM 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 473 PYESAGLKDVYVWLGRETITIEAHYQPTGAYMHCNHLIHEDNDMAVENVYAMEEKY 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 459 PYES--KDVYVWLGRETITIEAHYQPTGAYMHCNHLIHEDNDMAVENVYAMEEKY 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 533 LQDEDEDDPMNPKRAVPYNRNDFHARAGNFSASITARVQELAEQEPYNRUDE 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 516 NATVEVDPMEELMQARPEYELGEFOAGSGFSVQAVETRIQTMAEYRYPAAADE 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 8
US-09-134-001C-2946
; Sequence 2946, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2946
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2946
```

```

Query Match          12.6%; Score 400.5; DB 4; Length 322;
Best Local Similarity 32.9%; Pred. No. 2e-31;
Matches 118; Conservative 43; Mismatches 151; Indels 47; Gaps 12;
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```

QY 171 KDYEPNYSARLLWYHDAFMKTAENAYFGQAGAYIINDEADALGPSYGEFDIPLI 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6 KTIKFEVNDASATLWYHNPSPNTARQVYVNGSLGIYIDSKN--NYPNSYGNKNDLPI 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 231 LTAKYINADGTLRSTEGEDOD-LMGDIVIVHNGOPWFLVOPRRYFRFLNAVSRAMLL 289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 64 IODKTF-VSKKLINYSKTEDEDTQGDVTLVNGIVNPKLTAKKEKIRLLRLNGSNARDNL 122
QY 290 YLVRTSSPNVRPRPOVIVASDAGLLQAPVQTSNLYLAVEREYIIIDFTFPAQOTDLNRV 349
Db 123 KLSNNOS-----FEYIASDGGQLNNAKLKEINLAPSRKEIVIDL SMKEXISL--- 173
QY 350 AETNDVGDDEDEARLEVMREFVSSGTVEDNSQVSTLRDVPFPKHEGPARKHFEERS 409
Db 174 -----VONDK-----TYLPI SNKESKSNKNTK-----VSKTKLEGM 208
QY 410 NGHYIINDVGADVNERVLAKPELCTVEWELEN--SSGWSHPVHILVDPEKILKRTG 466
Db 209 NDHYTINGNKF-DPN-RIDFTQKLNQKEWMEIENVKDKMGKHPFHIGTQFKVLSVD- 265
QY 467 GRGQVMPRESAGLKVWNLGRGETITLIEAHQVPMTGAYMHCHNLHEDNDMAAFNVT 525
Db 266 -GEKPPKDMRGKKDVISLEPGQAKIEVFPKN-TGYTFHCHLLEHEDNGMKGOIKVT 321

RESULT 9

US-09-468-578-9
: Sequence 9, Application US/09468578
: Patent No. 6393329
: GENERAL INFORMATION:
: APPLICANT: Wang, Huang
: APPLICANT: Bodle, Elizabeth A.
: TITLE OF INVENTION: Phenol Oxidizing Enzymes
: FILE REFERENCE: GC561-3
: CURRENT APPLICATION NUMBER: US/09/468, 578
: CURRENT FILING DATE: 1999-12-21
: PRIOR APPLICATION NUMBER: US 09/220, 871
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: US 09/338, 723
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 114
: TYPE: PRT
: ORGANISM: *Aerospirillum atrum*
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (1)...(114)
: OTHER INFORMATION: Xaa - space of unknown number of aa
US-09-468-578-9

Query Match 11.2%; Score 357.5; DB 4; Length 114;
Best Local Similarity 32.2%; Pred. No. 6.8e-28;
Matches 85; Conservative 13; Mismatches 15; Indels 151; Gaps 4;

QY 194 TAENAYFQOAGAYIINDAEDALGIPSGYGERDIPILITAKYNNADGTLRSTEGEDDILW 253
Db 1 TAENAYFQOAGFYIILHDAEDALGLPS--GKYDPLALSLKAYNSDGLTFDKDETDLSIF 58
QY 254 GDVIVNGQMPPELVOPKRYFRFRFLNAVASRAWLLVLRSSPNVRIPFOVIADAGLL 313
Db 59 GDVIVNGQMPPELVOPKRYFRFRFLNAVASRAWLLVLRSSPNVRIPFOVIADAGLL 313
QY 314 QAPVQTSNLYLAVEREYIIIDFTFPAQOTDLNRVAETNDVGDDEDEARLEVMREFVVS 373
Db 92 ----- 91
QY 374 SGTVEDNSQVSTLRDVPFPKHEGPARKHFEERSNGHYIINDVGADVNERVLAKPEL 433
Db 92 -----FK----- 93
QY 434 GTVEWELEN--SSGWSHPVHIL 456
Db 94 ---XWMELENTSSGWSHPVHIL 114

RESULT 10
US-08-749-882A-2

: Sequence 2, Application US/08749882A
: Patent No. 5750388
: GENERAL INFORMATION:
: APPLICANT: Berka, Randy
: APPLICANT: Thompson, Sheryl
: APPLICANT: Xu, Feng
: TITLE OF INVENTION: Purified *Scytalidium* laccases
: TITLE OF INVENTION: And Nucleic Acids Encoding Same
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 57503880 No. 5750388disk Of No. 5750388th America, Inc.
: STREET: 405 Lexington Avenue - 64th Fl.
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10174
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/749, 882A
: FILING DATE: 15-NOV-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias J
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4186, 020-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-878-9652
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 616 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: *Scytalidium thermophilum*
US-08-749-882A-2

Query Match 6.3%; Score 202; DB 1; Length 616;
Best Local Similarity 23.1%; Pred. No. 3.4e-11;
Matches 147; Conservative 77; Mismatches 237; Indels 174; Gaps 35;

QY 8 LAASGGL-SGVLGIPMDTGSHPICAVDPEVTEVFADSLAAAGDDMESPPVLLYRN 66
Db 9 LLLAGLNSGALAAP---STHP--RSNPDILLERDHSLSRSQG--SCHSPSNRACWS 61
QY 67 ALRPPVQPKMILITNPVYTKDVIWYEIEIKFOQRIYP--TLRPATLVGYDGMSPGTF 124
Db 62 GFDINTVDET-----TPMNGV--VRRYTFDITVDNRPPGPDVYIKKMLINDKLL-GFTV 115
QY 125 NVPRGTEIVVRITNN--ATVENSVLHGSPPSRAP--FDGMAEDVTF-----DEYKDYVFP 176
Db 116 FANWG-DTIEVTVNNHLERTNGTSIMHGHQKGTNYHNG-ANGVTECPILPGGSRYVSFR 173
QY 177 NYQASRLMYHDHAFMAKTAENAYFQOAGAYIINDAEDALGIPSGYGERDIPIL-ILTKV- 234
Db 174 ARQYG-TSNYHSH-FSAQYGN---GVSQAIQINGPA---SLP-----YDIDGLVLPLOD 219
QY 235 --YVNADGTLRSTEGEDDILMGDVIVNGO-----PMPFLNVOP-RKYRFRFLNAA 282
Db 220 WYKKSADQVLETTLAKGNAPFSDNVLLINGTAKHPTTGGGEVAVIKLTPDKRRLRLIMMS 279
QY 283 VSRAMLVLRVTSPPNVRIPFOVIVASDAGLLQAPVQTSNLYLAVEREYIIIDFT----- 337
Db 280 VENNFOVSLAKHT-----MTVIAADWVPVNA-MTVISLFWAGQRYDVITIDAQAVGN 331
QY 338 -----NFAGO-----TDLNRVAETN 353

Db 332 YWFNTFGGQKCGFSHPAPALIFRYEGAPDALPTDGAAPKDHQCLDTLIDLSPVYOKN 391
Qy 354 DVGDEDEYARTLEWRFVYSSGTVEDNSQVSTLRDVPFPFHKEGSPADKHFKERSNG-- 411
Db 392 -----VPVDGFYKEPG-----NTLPVTL-----HVDQAAAPHVFTWKINGS 428
Qy 412 -----HYLINDYGFADVNERVYLAKPELGTVEWELENSSGG--WSHPVHILV 457
Db 429 ADVMDRPLEYEVNMNDLSIPVKNNIVYVDGVNEMTYWLVENDEGRSLSPHMHHLGH 488
Qy 458 DFKILKRTGGRGOVVPYESAGL-----KDYVWL-GRGETLTTEAHYQ 498
Db 489 DFEVLGRS---PDVSPDSETRFVEPDPAVDLPRLRGHNFRYRDVYMLPARGWLILAFRTDN 545
Qy 499 PWTGAYMMHCHNLHEDNDMAVFNWTAMEEKGYL 533
Db 546 P--GAMLFHCHIAHWVSGLSVDFLERPDELRGOL 578

RESULT 11
US-08-539-134-2
; Sequence 2, Application US/08539134
; Patent No. 5843745
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy
; APPLICANT: Thompson, Sheryl
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: Purified Scytalidium Laccases
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 58437450 No. 5843745disk Of No. 5843745th America, Inc.
; STREET: 405 Lexington Avenue - 64th Fl.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,134
; FILING DATE: 04-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4186,010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-878-9652
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Scytalidium thermophilum
; US-08-539-134-2

Query March 6,34; Score 202; DB 2; Length 616;
Best Local Similarity 23.18; Pred. No.3.4e-11;
Matches 147; Conservative 77; Mismatches 237; Indels 174; Gaps 35;

Qy 8 LAASGGLTSGVLGIPMDTGSHPTEAVPEVTEVFAADSLAAAGDDWESPYYMLLYRN 66
Db 9 LLLLAGLNLNSGLAP---STHP--RSNPDLILERDHSLSRSG--SCHSRSNACMS 61
Qy 67 ALPIPPVKOPKMITNPVTGADIWYEIEIKPQORIP--TLRPATLVGIDGMSPGPTF 124

Db 62 GEDINTDYETK---TPMTGV-VRRYTFDITEVDNRPGPDGVIEKMLINDKLL-GETV 115
Qy 125 NVPRCTETVRFIN--ATVENSVHLGSPSRAP--FDGMAEDVTF---DGEYKDYFFP 176
Db 116 FANNG-DTIEYTVNNHLLFTNGTSHHMHGLHOKGTNYHNG-ANGYECETIPPGGSRVYFR 173
Qy 177 NYQARLLMYHDHAFEMKTAENAYFGQAGAVIINDAEADALPSPGGEFDIPL-ILTAK- 234
Db 174 AROYG-TSMYHSH-FSAQYGN--GVSQAIOINGPA---SLP-----YDIDLGLVPLQD 219
Qy 235 --YINADGTLSTEGEDDDINGDVIHNGQ-----PPFPLNVOP-RKYRFRFLNAA 282
Db 220 WYKSAQDLVIETLAKGNAPPSDNVLLNGTAKHPTTGEGEYAIYKLPDKRHLRLNMS 279
Qy 283 VSRAMLIVYRTSSPNVRIPECVIASDAGLLQAPVQTSNLVLAVEREITIIDFT----- 337
Db 280 VENHFOVSLAKHT-----MTVIAADNVPYNA-MTVISLMAVQQRVDYITDASQANGN 331
Qy 338 ----NFAQG-----TDLRNVAETN 353
Db 332 YWFNTFGGQKCGFSHPAPALIFRYEGAPDALPTDGAAPKDHQCLDTLIDLSPVYOKN 391
Qy 354 DVGDEDEYARTLEWRFVYSSGTVEDNSQVSTLRDVPFPFHKEGSPADKHFKERSNG-- 411
Db 392 -----VPVDGFYKEPG-----NTLPVTL-----HVDQAAAPHVFTWKINGS 428
Qy 412 -----HYLINDYGFADVNERVYLAKPELGTVEWELENSSGG--WSHPVHILV 457
Db 429 ADVMDRPLEYEVNMNDLSIPVKNNIVYVDGVNEMTYWLVENDEGRSLSPHMHHLGH 488
Qy 458 DFKILKRTGGRGOVVPYESAGL-----KDYVWL-GRGETLTTEAHYQ 498
Db 489 DFEVLGRS---PDVSPDSETRFVEPDPAVDLPRLRGHNFRYRDVYMLPARGWLILAFRTDN 545
Qy 499 PWTGAYMMHCHNLHEDNDMAVFNWTAMEEKGYL 533
Db 546 P--GAMLFHCHIAHWVSGLSVDFLERPDELRGOL 578

RESULT 12
US-08-991-531-2
; Sequence 2, Application US/08991531
; Patent No. 5925554
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; TITLE OF INVENTION: myceliophthora And scytalidium laccase
; TITLE OF INVENTION: Variants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 59255540 No. 5925554disk Of No. 5925554th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,531
; FILING DATE: 16-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5125,200-US

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 616 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-531-2

Query Match      6.3%; Score 202; DB 2; Length 616;
Best Local Similarity 23.0%; Pred. No. 3.4e-11;
Matches 146; Conservative 76; Mismatches 239; Indels 174; Gaps 34;

OY 8 LAAASGLL-SGVLGIPMDTGSHPTEAVDEPKTEVFADSLAAAGDDMESPPYLLRYN 66
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9 LLLLAGLLNSGALAAP---STHP--RSNPDLILERDHSILTSRQG--SCHSPSNRACWS 61

OY 67 ALPIPVKQPKMITNPVTKGKDIWYEIEIKRQORITP--TLRPATLVGYGMSGPTF 124
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 62 GEDINTDYTK-----TPNPGV--VRRTPDITEVDNRPDGVYKELMLINDKL-GPTV 115

OY 125 NVPRGTEFVRFIN--ATVENSVLHSGSPSRAP--FDGMAEDVTF---PGEYKDYFP 176
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 116 FANWG-DTIEVYNNHLRLRTNGSIHHGHLKQKTNHDG-ANGVTCPRLPGSGRYYSFR 173

OY 177 NQASARLLYHDAEMFKTLEMAVFGQAGAYIINDEAEDALGSPSGYGERDIPL---ILT 232
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 174 ARQYG-TSWYHSH-FSAQYGN--GVSGAIQINGPA---SLP-----YDIDGLVPLXD 219

OY 233 AKYUNADGTLRSTEGDDQLMGDVHIVNGO-----PWPLNYPQ-RKYRFRFLNA 282
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 220 WYKKSADQLVITLTKGNAPFSDNVLINGTAKHPPTGEGEYAIKLTLPKRRRLRLNMS 279

OY 283 VSRAMLVLVLTSSPNVRIIPQVIASDAGLLQAPVQTSNLYLAVERYEIITDFT----- 337
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 280 VENHFGVSLAKHT-----MTVIADMYPVNA-MTVDSLPAVAGQRYVYTTDASQAVGN 331

OY 338 -----NFAQO-----TLDLRNVAETN 353
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 332 YWFNITFGGQOKCGFSHNPAAPAFREYEGAPDALPTDGAAPKDHQCLDTLDSLPAVQKN 391

OY 354 DVGDEDEVARTLEVRFVYSSGTVEDNSOVPTSLRDVPRPKKEGADNHFKEFSNG--- 411
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 392 -----VPVDEGVKPERG-----MTLPVTL-----HYDDAADAAPHVFTWKINGSA 428

OY 412 -----HYLINDVGFADVNERVLAKPELGTVEVWELENSSG---WSHPVHIHLV 457
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 429 ADVDMDRPYLEVVMNNDLSSIPVKNIVAVDGVNEMTYLVLENDPGRSLSLPHPHLHGH 488

OY 458 DKILKRTGRCQVMPYESAGL-----KDVVWL-GRGETLTTEAHYQ 498
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 489 DEFVLGRS---PDVSPDSETRFVFPDPAVDLPRLRGHNPRVRDVTMLPARGMILLAFRTDN 545

OY 499 PWTGAYVMHCHNLHEDNDMAVFNVTAMEEKGYL 533
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 546 P--GAWLFHCHIAHXVSGLSYDFLERPEDELRGOL 578

RESULT 13
US-09-032-315-9
Sequence 9, Application US/09032315
Patent No. 5985818
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 59858180 No. 5985818disk of No. 5985818th America, Inc.
STREET: 405 Lexington Avenue
```

```
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,315
FILING DATE: 27-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 616 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-032-315-9

Query Match      6.3%; Score 202; DB 2; Length 616;
Best Local Similarity 23.0%; Pred. No. 3.4e-11;
Matches 146; Conservative 76; Mismatches 239; Indels 174; Gaps 34;

OY 8 LAAASGLL-SGVLGIPMDTGSHPTEAVDEPKTEVFADSLAAAGDDMESPPYLLRYN 66
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9 LLLLAGLLNSGALAAP---STHP--RSNPDLILERDHSILTSRQG--SCHSPSNRACWS 61

OY 67 ALPIPVKQPKMITNPVTKGKDIWYEIEIKRQORITP--TLRPATLVGYGMSGPTF 124
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 62 GEDINTDYTK-----TPNPGV--VRRTPDITEVDNRPDGVYKELMLINDKL-GPTV 115

OY 125 NVPRGTEFVRFIN--ATVENSVLHSGSPSRAP--FDGMAEDVTF---PGEYKDYFP 176
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 116 FANWG-DTIEVYNNHLRLRTNGSIHHGHLKQKTNHDG-ANGVTCPRLPGSGRYYSFR 173

OY 177 NQASARLLYHDAEMFKTLEMAVFGQAGAYIINDEAEDALGSPSGYGERDIPL---ILT 232
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 174 ARQYG-TSWYHSH-FSAQYGN--GVSGAIQINGPA---SLP-----YDIDGLVPLXD 219

OY 233 AKYUNADGTLRSTEGDDQLMGDVHIVNGO-----PWPLNYPQ-RKYRFRFLNA 282
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 220 WYKKSADQLVITLTKGNAPFSDNVLINGTAKHPPTGEGEYAIKLTLPKRRRLRLNMS 279

OY 283 VSRAMLVLVLTSSPNVRIIPQVIASDAGLLQAPVQTSNLYLAVERYEIITDFT----- 337
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 280 VENHFGVSLAKHT-----MTVIADMYPVNA-MTVDSLPAVAGQRYVYTTDASQAVGN 331

OY 338 -----NFAQO-----TLDLRNVAETN 353
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 332 YWFNITFGGQOKCGFSHNPAAPAFREYEGAPDALPTDGAAPKDHQCLDTLDSLPAVQKN 391

OY 354 DVGDEDEVARTLEVRFVYSSGTVEDNSOVPTSLRDVPRPKKEGADNHFKEFSNG--- 411
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 392 -----VPVDEGVKPERG-----MTLPVTL-----HYDDAADAAPHVFTWKINGSA 428

OY 412 -----HYLINDVGFADVNERVLAKPELGTVEVWELENSSG---WSHPVHIHLV 457
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 429 ADVDMDRPYLEVVMNNDLSSIPVKNIVAVDGVNEMTYLVLENDPGRSLSLPHPHLHGH 488

OY 458 DKILKRTGRCQVMPYESAGL-----KDVVWL-GRGETLTTEAHYQ 498
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 489 DEFVLGRS---PDVSPDSETRFVFPDPAVDLPRLRGHNPRVRDVTMLPARGMILLAFRTDN 545
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QY 499 PWTGAYMMHCHNLHEDNDMAVENVTAMEEKGYL 533
+ + + + +
Db 546 P--GAWLFHCHIXHVSGLSVDFLERPDELRGOL 578

RESULT 14
US-08-993-318A-9

; Sequence 9, Application US/08993318A
; Patent No. 5998353
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Anders
; APPLICANT: Pedersen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 59983530 No. 5998353disk of No. 5998353th America
; STREET: 405 Lexington Avenue
; CITY: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,318A
; FILING DATE: December 18, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valera A.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 5032.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; MOLECULE TYPE: protein
; US-08-993-318A-9

Query Match 6.3%; Score 202; DB 2; Length 616;
Best Local Similarity 23.0%; Pred. No. 3.4e-11;
Matches 146; Conservative 76; Mismatches 239; Indels 174; Gaps 34;

QY 8 LAAASGLL-SGVIGTMDGSHPIEAVDEPVKTEVFADSLAAAGDDMESPPYNNLLYN 66
+ + + + +
Db 9 LLLAAGLNSGALAP--STHP--RSNPDLLEERDHSLSRQG--SCHSPSNRAKWS 61
+ + + + +
QY 67 ALPIPVKOPKMITTPVNGKDIWYEIEIKPQORIVP--TLRPATLVGDGMSGPTF 124
+ + + + +
Db 62 GPDINDIYEK-----TPNIGV-VRRITFDITEVDNRPGDGVKIKELMLINKLL-GPIV 115
+ + + + +
QY 125 NVPRGTETVVRFLTN--ATVENSVHLHGSFRAP--FDGMAEDVT---PGEYKDYYP 176
+ + + + +
Db 116 FAWMG-DTIEVYVNNHLRTNGTISHHGLHOKGTNYHDG-ANGVTECPPIPPGSSRYVSFR 173
+ + + + +
QY 177 NQSALLWTHDAFMKTAENAFGQAGAYIINDEADALGLSGGEPDIPL-----ILT 232
+ + + + +
Db 174 ARQYG-TSMVHSH-FSAQYGN--GVSGAIOINGPA---SLP-----XDIDLGVLPLXD 219
+ + + + +
QY 233 AKYVNDGTLRSTEGEDODLMDGVINHNGO-----PMPLNVOP-RKYFRFLNAA 282
+ + + + +
Db 220 WYKSDQVLYETFLXKGNAPFSDNVLINGTAKAPTTGEGEYAIYKLTLPDKRHLRLINMS 279
+ + + + +

QY 283 VSRAMLXLYVTSSPNVRLIPQVLTASDAGLLQAPVQTSNLYLAVEREIIIDFT----- 337
+ + + + +
Db 280 VENNFOVSLAKHT-----MTVITADWVPVNA-MTVDSLFAVAGQKRDVYITDASQANG 331
+ + + + +
QY 338 ----NFAGQ-----TDLRNVAEFN 353
+ + + + +
Db 332 YWENTTFGGQKCGFSHPAPALIFRYEGAPDALPTDGAAPKDHQCJDTLDLSFVYQKN 391
+ + + + +
QY 354 DVGDEDEYAKTLEVKRFVYVSSGTVEDNSQVSTLADVFPFRPKKEPRAKHKEFEKSN-- 411
+ + + + +
Db 392 -----VPVDFVKEPQ-----NTLPVYTL-----HVDQAAAPHFTWKINSGA 428
+ + + + +
QY 412 -----HYLNDGFAVDYNERVLAKPELGVEVWELENSSGG---MSHPVHILV 457
+ + + + +
Db 429 ADVMDRPLEYVMNNNDLSSTIPVKNVIVKVGCVNEMTYWLVNDEGRSLSPHMHILGH 488
+ + + + +
QY 458 DEKILKRTGRCQVMPYESAGL-----KDVWL-GRGETLTTEAHYQ 498
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Db 489 DEFLVIGRS---PDVSPDSTRFVFPDPAVDLPRLRGNPVRDVTMLPARGWLILAFRTDN 545
+ + + + +
QY 499 PWTGAYMMHCHNLHEDNDMAVENVTAMEEKGYL 533
+ + + + +
Db 546 P--GAWLFHCHIXHVSGLSVDFLERPDELRGOL 578

RESULT 15
US-09-028-887-2

; Sequence 2, Application US/09028887
; Patent No. 6060442
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 60604420 No. 6060442disk of No. 6060442th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,887
; FILING DATE: 24-February-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valera A.
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 5201.200-US
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-028-887-2

Query Match 6.3%; Score 202; DB 3; Length 616;
Best Local Similarity 23.0%; Pred. No. 3.4e-11;
Matches 146; Conservative 76; Mismatches 239; Indels 174; Gaps 34;

QY 8 LAAASGLL-SGVIGTMDGSHPIEAVDEPVKTEVFADSLAAAGDDMESPPYNNLLYN 66
+ + + + +
Db 9 LLLAAGLNSGALAP--STHP--RSNPDLLEERDHSLSRQG--SCHSPSNRAKWS 61
+ + + + +
QY 67 ALPIPVKOPKMITTPVNGKDIWYEIEIKPQORIVP--TLRPATLVGDGMSGPTF 124
+ + + + +
Db 62 GPDINDIYEK-----TPNIGV-VRRITFDITEVDNRPGDGVKIKELMLINKLL-GPIV 115
+ + + + +

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 05:15:58 ; Search time 46 Seconds
(without alignments)
329.914 Million cell updates/sec

Title: US-09-218-702-2

Perfect score: 3189
Sequence: 1 MLFSWQLAASGLSLGVIG.....AEQEPYNRLEDELDGIEE 594

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 2554876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3189	100.0	594	10 US-09-338-723A-2	Sequence 2, Appli
2	3189	100.0	594	12 US-10-080-210-2	Sequence 2, Appli
3	3189	100.0	594	12 US-10-080-233-2	Sequence 2, Appli
4	1954.5	61.3	627	10 US-09-338-723A-4	Sequence 4, Appli
5	1954.5	61.3	627	12 US-10-080-210-4	Sequence 4, Appli
6	1929.5	60.5	627	12 US-10-080-210-7	Sequence 4, Appli
7	1724.5	54.1	572	9 US-09-942-185-4	Sequence 7, Appli
8	1716.5	53.8	583	9 US-09-942-185-2	Sequence 2, Appli
9	1712.5	53.7	568	12 US-10-080-233-4	Sequence 4, Appli
10	500	15.7	511	9 US-09-738-626-4553	Sequence 4553, Ap
11	357.5	11.2	614	12 US-10-080-210-9	Sequence 9, Appli
12	202	6.3	616	9 US-09-869-877-9	Sequence 9, Appli
13	202	6.3	616	10 US-09-732-350-9	Sequence 9, Appli
14	198.5	6.2	529	9 US-09-869-877-5	Sequence 5, Appli
15	198.5	6.2	529	10 US-09-732-350-5	Sequence 5, Appli
16	197	6.2	573	9 US-09-869-877-10	Sequence 10, Appli
17	197	6.2	573	10 US-09-732-350-10	Sequence 10, Appli
18	192.5	6.0	499	9 US-09-869-877-2	Sequence 2, Appli
19	192.5	6.0	499	10 US-09-732-350-2	Sequence 2, Appli

20	187.5	5.9	539	9 US-09-869-877-1	Sequence 1, Appli
21	187.5	5.9	539	10 US-09-732-350-1	Sequence 1, Appli
22	179	5.6	548	9 US-09-869-877-4	Sequence 4, Appli
23	179	5.6	548	10 US-09-732-350-4	Sequence 4, Appli
24	174.5	5.5	499	9 US-09-869-877-3	Sequence 3, Appli
25	174.5	5.5	499	10 US-09-732-350-3	Sequence 3, Appli
26	162	5.1	564	9 US-09-944-160-12	Sequence 12, Appli
27	147	4.6	493	9 US-09-738-626-6780	Sequence 6780, Ap
28	126.5	4.0	572	9 US-09-869-877-7	Sequence 7, Appli
29	126.5	4.0	572	10 US-09-732-350-7	Sequence 7, Appli
30	121.5	3.8	886	9 US-10-002-3098-2	Sequence 2, Appli
31	119.5	3.7	575	9 US-09-869-877-8	Sequence 8, Appli
32	119.5	3.7	575	10 US-09-732-350-8	Sequence 8, Appli
33	111	3.5	599	9 US-09-869-877-6	Sequence 6, Appli
34	111	3.5	599	10 US-09-732-350-6	Sequence 6, Appli
35	105	3.3	2764	9 US-09-808-602-80	Sequence 80, Appli
36	104.5	3.3	1938	9 US-10-014-436-2	Sequence 2, Appli
37	103	3.2	19	10 US-09-338-723A-6	Sequence 6, Appli
38	103	3.2	19	12 US-10-080-210-10	Sequence 10, Appli
39	100.5	3.2	1600	9 US-09-738-626-4310	Sequence 4310, Ap
40	100.5	3.2	1653	10 US-09-741-669-402	Sequence 402, App
41	100	3.1	2765	9 US-09-808-602-84	Sequence 84, Appli
42	99	3.1	1092	9 US-09-423-126-5	Sequence 5, Appli
43	97.5	3.1	1198	9 US-09-975-719-405	Sequence 405, App
44	97.5	3.1	2724	9 US-09-808-602-13	Sequence 13, Appli
45	97.5	3.1	2733	9 US-09-808-602-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-338-723A-2
; Sequence 2, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huaming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-338-723A-2

Query Match 100.0%; Score 3189; DB 10; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.2e-256;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLFSWQLAASGLSLGVIGIPMDTGSHPRIEAVDPVKTEVFADSLAAGDDMESPPY	60
DB	1	MLFSWQLAASGLSLGVIGIPMDTGSHPRIEAVDPVKTEVFADSLAAGDDMESPPY	60
QY	61	NLLYRALPIPPKOPKMITNPVTGKDIWYEIEIKPPOQRIYPLRPATLVGDGMSF	120
DB	61	NLLYRALPIPPKOPKMITNPVTGKDIWYEIEIKPPOQRIYPLRPATLVGDGMSF	120
QY	121	GPTFNPVPGTETVYRFINNATVENSYHLGSPSRADFQMAEDVTFPGCYKDYFPNVS	180
DB	121	GPTFNPVPGTETVYRFINNATVENSYHLGSPSRADFQMAEDVTFPGCYKDYFPNVS	180
QY	181	ARLWYHDAFAFKMTANAFQGAATITNDEADALGSPGGEPIPLILAKYYNADG	240
DB	181	ARLWYHDAFAFKMTANAFQGAATITNDEADALGSPGGEPIPLILAKYYNADG	240
QY	241	TURSTGEODLMDGVDIYHNGOPWPLNQPRKYRFRFLNAVSRAMLTYLVRTSSPNR	300
DB	241	TURSTGEODLMDGVDIYHNGOPWPLNQPRKYRFRFLNAVSRAMLTYLVRTSSPNR	300

Db 241 TLRSTEGEDDLMGDVIAHNGQPWPFLLNVQPRKRYRFLNAAVSRAWLLYLVRTSSPNVR 300
QY 301 IFFOVIASDAGLLQAPVQTSNLYLVAERYEIIIDFTNAGOTLDRNVAETNDVDEDE 360
Db 301 IFFOVIASDAGLLQAPVQTSNLYLVAERYEIIIDFTNAGOTLDRNVAETNDVDEDE 360
QY 361 YARTLEVMRFVYVSSGTVEDNSQVPSLTDVPPPPHKEGPADKHFKFERSNGHYLLINDVGF 420
Db 361 YARTLEVMRFVYVSSGTVEDNSQVPSLTDVPPPPHKEGPADKHFKFERSNGHYLLINDVGF 420
QY 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
Db 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
QY 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAVENVTAMEKGYLOEDFEDP 540
Db 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAVENVTAMEKGYLOEDFEDP 540
QY 541 MNPKNRAVPYNNDFPHARAGNFSAESITARVOELAEQEPYNNLDEILDGIEE 594
Db 541 MNPKNRAVPYNNDFPHARAGNFSAESITARVOELAEQEPYNNLDEILDGIEE 594

RESULT 2
US-10-080-210-2
; Sequence 2, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-10-080-210-2

Query Match 100.0%; Score 3189; DB 12; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.2e-256;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 NLLYRNALPIPPYKOPKMITNPVTGKDIWYIEIKPQORITPTLRPATLVGDGMS 120
QY 61 NLLYRNALPIPPYKOPKMITNPVTGKDIWYIEIKPQORITPTLRPATLVGDGMS 120
Db 61 NLLYRNALPIPPYKOPKMITNPVTGKDIWYIEIKPQORITPTLRPATLVGDGMS 120
QY 121 GPTFNVPRTGETVVRFINNATVENSYHLHGSPSRAPFDGMAEDVTFPGEEKDYEPFNYS 180
Db 121 GPTFNVPRTGETVVRFINNATVENSYHLHGSPSRAPFDGMAEDVTFPGEEKDYEPFNYS 180
QY 181 ARLLWYHDAEFKKTAEANAFGQAGATIIINDEADALGSPSGEEDIPILITAKYYNAG 240
Db 181 ARLLWYHDAEFKKTAEANAFGQAGATIIINDEADALGSPSGEEDIPILITAKYYNAG 240
QY 241 TLRSTEGEDDLMGDVIAHNGQPWPFLLNVQPRKRYRFLNAAVSRAWLLYLVRTSSPNVR 300
Db 241 TLRSTEGEDDLMGDVIAHNGQPWPFLLNVQPRKRYRFLNAAVSRAWLLYLVRTSSPNVR 300
QY 301 IFFOVIASDAGLLQAPVQTSNLYLVAERYEIIIDFTNAGOTLDRNVAETNDVDEDE 360
Db 301 IFFOVIASDAGLLQAPVQTSNLYLVAERYEIIIDFTNAGOTLDRNVAETNDVDEDE 360

QY 361 YARTLEVMRFVYVSSGTVEDNSQVPSLTDVPPPPHKEGPADKHFKFERSNGHYLLINDVGF 420
Db 361 YARTLEVMRFVYVSSGTVEDNSQVPSLTDVPPPPHKEGPADKHFKFERSNGHYLLINDVGF 420
QY 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
Db 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
QY 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAVENVTAMEKGYLOEDFEDP 540
Db 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAVENVTAMEKGYLOEDFEDP 540
QY 541 MNPKNRAVPYNNDFPHARAGNFSAESITARVOELAEQEPYNNLDEILDGIEE 594
Db 541 MNPKNRAVPYNNDFPHARAGNFSAESITARVOELAEQEPYNNLDEILDGIEE 594

RESULT 3
US-10-080-233-2
; Sequence 2, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1 Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys sp.
US-10-080-233-2

Query Match 100.0%; Score 3189; DB 12; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.2e-256;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLEFSWQLAAAGLLSGVIGIPMDTGSHP IEAVDPEVKTVEFADSLAAAGDDMESPPY 60
Db 1 MLEFSWQLAAAGLLSGVIGIPMDTGSHP IEAVDPEVKTVEFADSLAAAGDDMESPPY 60
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Db 121 GPTFNVPRTGETVVRFINNATVENSYHLHGSPSRAPFDGMAEDVTFPGEEKDYEPFNYS 180
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Db 241 TLRSTEGEDDLMGDVIAHNGQPWPFLLNVQPRKRYRFLNAAVSRAWLLYLVRTSSPNVR 300
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Db 301 IFFOVIASDAGLLQAPVQTSNLYLVAERYEIIIDFTNAGOTLDRNVAETNDVDEDE 360
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Db 361 YARTLEVMRFVYVSSGTVEDNSQVPSLTDVPPPPHKEGPADKHFKFERSNGHYLLINDVGF 420
QY 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
Db 421 ADVNERVLAKPELGTVEWELENSSGGSHPVHILVDFKILKRTGGRCQVMPYESAGLK 480
QY 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAVENVTAMEKGYLOEDFEDP 540
Db 481 DVVWLGREGTLLTEAHYQPTGAYMMHCHNLJHEDNDMAVENVTAMEKGYLOEDFEDP 540

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Qy 541 MNPKNRAVYNRNDPFHARAGNFSAESITARVOELAEQEPYNRDLDELIDGIE 594
Db 541 MNPKNRAVYNRNDPFHARAGNFSAESITARVOELAEQEPYNRDLDELIDGIE 594

RESULT 4
US-09-338-723A-4
; Sequence 4, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huangming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Bipolaris spicifera
US-09-338-723A-4

Query Match 61.3%; Score 1954.5; DB 10; Length 627;
Best Local Similarity 61.1%; Pred. No. 4.7e-154;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

Qy 2 LFKSMQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTEVPFDSLLAAGDD----- 53
Db 6 LFSALQVLS---IAKGIYVAL--SERPAKEVDNTPDEEKA--LASTIVEDDPADVNMKL 58
Qy 54 -DMESPPYNNLYRNALPIPPVKQPKMIITNPYTGKDIWYEIEIKPFOQRIYPTLRPATL 112
Db 59 KMWQSEYELIRQPLPIPAKEPNK-LTNPYTNKEIWIYELIVKFTQGVYPSLRPAL 117
Qy 113 VGIDGMSPEPTNPVPGTIVVRFINMATVENSVLHSGSPRAPDGMADVTFFGEYKD 172
Db 118 VGYDGISPGPTIIVPGCTAVVRFINQGDRESSIHLSGSPRAPDGMADDMIMKEYKD 177
Qy 173 YEPNYSARLWYHDHAKMTAENAYFGQAGAYIINDAEALGLPSGYGEFDPILIT 232
Db 178 YTPPNQAARFLMYHDHAKMTAENAYFGQAGAYLITDPAEDALGLPSGYGYDIPVLVS 237
Qy 233 AKYNNADGTLRSTEGEDDQDLMGDVHVNQOPWPFNLVQPRKYRFRFLNAVASRAMLLYLV 292
Db 238 SKYYNADGTLKTSVGEDKSVMGDIIHVNQOPWPFNLVBERKTRRLFLNAVASRNFALYFV 297
Qy 293 RTSSPNVRILPFOVIASDAGLLQAPVQTSNLYLAVEREYIIIDFTNFACQTLDLRNAVET 352
Db 298 KQDNATATRLPFOVIASDAGLLTHPVQTSMDYVAAERYEIVDFAPYAGQOTDLRNFAPA 357
Qy 353 NDVGDEDEARLLEVMRFVSSGTVEDNSQVSTLRDVFPPRHKESPRADKHKFEKRSNH 412
Db 358 NGIGTDDDTAANDKVMRFVSSQTVVANSVPEQLSQIQFPAQKT-DIDHNRFRHRTNGE 416
Qy 413 YLINDVGFADVNERVYLAKPDELCTVEVMELENSSGMSHSHVHILVDKFLIKRTGGRGQ-- 470
Db 417 WRINGGFADVNERVYLAKPRTVELMELENSSGMSHSHIHVLVDFRVAVYAGDGSTRG 476
Qy 471 VMPYESAGLKDVYVWLGSGTLLTEAHYQPTWGTAYMWHCHNLHEDNDMAVENVVTAMEEK 530
Db 477 VMPYESAGLKDVYVWLGSRHETVLEAHYAPWDGVYMFHCHNLHEDODMAAFDVTKLQNF 536
Qy 531 GYLQ--EDFEDPMNPKRAVPYRNDFHARAGNFSAESITARVOELAEQEPYNRDLDELID 589
Db 537 GYNETTDHFDPEDPMNSAPRTAGDLTARSGLFSEESIRARVNELALQEPYSELAQVYAS 596
Qy 590 L 590
```

```
Db 597 L 597

RESULT 5
US-10-080-210-4
; Sequence 4, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huangming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Bipolaris spicifera
US-10-080-210-4

Query Match 61.3%; Score 1954.5; DB 12; Length 627;
Best Local Similarity 61.1%; Pred. No. 4.7e-154;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

Qy 2 LFKSMQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTEVPFDSLLAAGDD----- 53
Db 6 LFSALQVLS---IAKGIYVAL--SERPAKEVDNTPDEEKA--LASTIVEDDPADVNMKL 58
Qy 54 -DMESPPYNNLYRNALPIPPVKQPKMIITNPYTGKDIWYEIEIKPFOQRIYPTLRPATL 112
Db 59 KMWQSEYELIRQPLPIPAKEPNK-LTNPYTNKEIWIYELIVKFTQGVYPSLRPAL 117
Qy 113 VGIDGMSPEPTNPVPGTIVVRFINMATVENSVLHSGSPRAPDGMADVTFFGEYKD 172
Db 118 VGYDGISPGPTIIVPGCTAVVRFINQGDRESSIHLSGSPRAPDGMADDMIMKEYKD 177
Qy 173 YEPNYSARLWYHDHAKMTAENAYFGQAGAYIINDAEALGLPSGYGEFDPILIT 232
Db 178 YTPPNQAARFLMYHDHAKMTAENAYFGQAGAYLITDPAEDALGLPSGYGYDIPVLVS 237
Qy 233 AKYNNADGTLRSTEGEDDQDLMGDVHVNQOPWPFNLVQPRKYRFRFLNAVASRAMLLYLV 292
Db 238 SKYYNADGTLKTSVGEDKSVMGDIIHVNQOPWPFNLVBERKTRRLFLNAVASRNFALYFV 297
Qy 293 RTSSPNVRILPFOVIASDAGLLQAPVQTSNLYLAVEREYIIIDFTNFACQTLDLRNAVET 352
Db 298 KQDNATATRLPFOVIASDAGLLTHPVQTSMDYVAAERYEIVDFAPYAGQOTDLRNFAPA 357
Qy 353 NDVGDEDEARLLEVMRFVSSGTVEDNSQVSTLRDVFPPRHKESPRADKHKFEKRSNH 412
Db 358 NGIGTDDDTAANDKVMRFVSSQTVVANSVPEQLSQIQFPAQKT-DIDHNRFRHRTNGE 416
Qy 413 YLINDVGFADVNERVYLAKPDELCTVEVMELENSSGMSHSHVHILVDKFLIKRTGGRGQ-- 470
Db 417 WRINGGFADVNERVYLAKPRTVELMELENSSGMSHSHIHVLVDFRVAVYAGDGSTRG 476
Qy 471 VMPYESAGLKDVYVWLGSGTLLTEAHYQPTWGTAYMWHCHNLHEDNDMAVENVVTAMEEK 530
Db 477 VMPYESAGLKDVYVWLGSRHETVLEAHYAPWDGVYMFHCHNLHEDODMAAFDVTKLQNF 536
Qy 531 GYLQ--EDFEDPMNPKRAVPYRNDFHARAGNFSAESITARVOELAEQEPYNRDLDELID 589
Db 537 GYNETTDHFDPEDPMNSAPRTAGDLTARSGLFSEESIRARVNELALQEPYSELAQVYAS 596
Qy 590 L 590
```

Db 597 L 597

```
RESULT 6
US-10-080-210-7
; Sequence 7, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080, 210
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 627
; TYPE: prt
; ORGANISM: Curvularia pallescens
US-10-080-210-7
```

```
Query Match          60.5%; Score 1929.5; DB 12; Length 627;
Best Local Similarity 60.5%; Pred. No. 5,5e-152;
Matches 364; Conservative 81; Mismatches 134; Indels 23; Gaps 9;
```

```
OY 2 LKSNQLAASGLSGVLGIPMDTGSHPLEAVDPVEKTEVFADSLAAGD----- 53
DB 6 LPSALQLAS---LAKGIYVAL--SERPAKYIDETPDEEKA--LAAIVEDDPADVFRLL 58
OY 54 -TWESPPVLLRNALPTPPVQKPMIITNPTGDIWYELEIKPFQORITPTLRPATL 112
DB 59 KMWSDPEPILREALPPEPAKEPK-MTNPTNKEIWEYELVKEFNQOVSPSLPATL 117
OY 113 VGYDCKSPPTFNVRGCTEVRFINNATVENSVLHGSPPRAPDGMADVTFFGEYKD 172
DB 118 VGYDGSPEPTITVRGTAFAVRVFNQGDRESSIHLHGSPPRAPDGMADVLIMGQFMD 177
OY 173 YTFPNYQARLLMYHDHAFMKTAEENAYFGQAGAYIINDEADALGPSYGEFDIPLILT 232
DB 178 YTFPNQOARFLMYHDHAFMKTAEENAYFGQAGAYIITDPAEDALGPSYGYKDIPIVLVS 237
OY 233 AKYYNADGTLRSTEGEDDILMGDVIHVNGQPMPEFLNVQPRKTRFRRLNAVSRAMLLXY 292
DB 238 SKFYNSDGTLLQTSVGEDNSLMGDVLIHVNGQPMPEFVNERKTRKRLFLNAVSRNFALYEV 297
OY 293 RTSSPVRIRPFQVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNAVET 352
DB 298 KQQAATRIPLPFQVIASDAGILTHPQVTSIYAAARFYELIVDFAPYACQITDLRNFANA 357
OY 353 NDVGDEDEYARLLEVYRFFVSSGTVEDNSQVPTLRDVPFPKKEGPADKHKFEERSNGH 412
DB 358 NGVGTDDVYATNDKVMRFVSSQAAYVNSVPAQLSQIQPADKTS-IDHHRFHRHTNSE 416
OY 413 YLINDVGFADVNERVLAKELGTVEYWELENSGSGSHVHILVDKILKRTGSG---RG 469
DB 417 WRINGGFADVQNRILAKVPRGTVELLENSGSGMHPRIHNLVDVFRVARQDDESTG 476
OY 470 QWMPYSAGIKDVYMLGREGTELLTEAHYQPTGAYMMHCHNLIHEDDMMAAVENVTAMEEK 529
DB 477 -WMPYESAGIKDVYMLGREGTEYLVENAHYAPMDGVYMFHCHNLIHEDDMMAAFDVTKLON 535
OY 530 KGYLQ-EDFEDPMNPKRAVPYRNDFHARAGNFSAESITARVOELAEQEPYNRRLDELE 588
DB 536 FGYNETTDHPDPSRMSARPFADULTARSGIFSEASTIRARVNELALQPYSELAQVTA 595
OY 589 DL 590
DB 596 SL 597
```

```
RESULT 7
US-09-942-185-4
; Sequence 4, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Convents, Daniel
; APPLICANT: Doornink, Monique
; APPLICANT: van Gastel, Frans
; APPLICANT: Rodrigues, Ana
; APPLICANT: Topozada, Amr
; APPLICANT: De Vries, Cornelis Hendrikus
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1el Phenol
; FILE REFERENCE: C7567
; CURRENT APPLICATION NUMBER: US/09/942,185
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 572
; TYPE: prt
; ORGANISM: Myrothecium verucaria
US-09-942-185-4
```

```
Query Match          54.1%; Score 1724.5; DB 9; Length 572;
Best Local Similarity 60.3%; Pred. No. 4,7e-135;
Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;
```

```
OY 57 SPVYLLYRNALPPIPVKQPKMIITNPTGKDIWYELEIKPFQORITPTLRPATLVGYD 116
DB 43 SPQYP-MFTVPLPIPPVQKPMIITNPTGKDIWYELEIKPFQORITPTLRPATLVGYD 101
OY 117 GMSRGPPTFNVRGCTEVRFINNATVENSVLHGSPPRAPDGMADVTFFGEYKDYP 176
DB 102 GMSRGPPTFNVRGCTEVRFINNATVENSVLHGSPPRAPDGMADVTFFGEYKDYP 161
OY 177 NQOSARLLMYHDHAFMKTAEENAYFGQAGAYIINDEADALGPSYGEFDIPLILTANY 236
DB 162 NQOSARLLMYHDHAFMKTAEENAYFGQAGAYIINDEADALGPSYGEFDIPLILTANY 221
OY 237 NADGTLRSTEGEDDILMGDVIHVNGQPMPEFLNVQPRKTRFRRLNAVSRAMLLYVRS 296
DB 222 TANGNLYTTNCELNSFGWDVIHVNGQPMPEFKVNERKTRFRRLDAVSRSEGLYFADTDA 281
OY 297 PAVRIPLPFQVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNV-AETNDV 355
DB 282 IDTRLPFKVIASDGLLEHPADTSLIYISMAERYEVFPDSYAGTIELRLNLGSGISGI 341
OY 356 GDEDEYARLLEVYRFFVSSGTVEDNSQVPTLRDVPFP-PKKEGPADKHKFEERSNGH 413
DB 342 GDTDTVDNTDKVMRFVSSQAAYVNSVPAQLSQIQPADKTS-IDHHRFHRHTNSE 399
OY 414 LINDVGFADVNERVLAKELGTVEYWELENSGSGSHVHILVDKILKRTGSG--OY 471
DB 400 TINGVAFAADVQNRILANVPVGTVERBELINAGNGWTHPIHILVDVFKYISRTSGNARTV 459
OY 472 MPYESAGIKDVYMLGREGTELLTEAHYQPTGAYMMHCHNLIHEDDMMAAVENVTAMEEK 531
DB 460 MPYES-GLKDVYMLGREGTEYLVENAHYAPMDGVYMFHCHNLIHEDDMMAAFAVTLPLDG 518
OY 532 YLQEDFEDPMNPKRAVPYRNDFHARAGNFSAESITARVOELAEQEPYNRRLDE 585
DB 519 YNATYFVDMELMQRPELGEFQAQSGQSFVQAVTERIQTMATERYRYAADA 572
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RESULT 8
US-09-942-185-2
; Sequence 2, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:
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; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4553
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4553

Query Match          15.7%; Score 500; DB 9; Length 511;
Best Local Similarity 30.8%; Pred. No. 1,2e-33;
Matches 153; Conservative 67; Mismatches 232; Indels 44; Gaps 14;

OY 39 TEVFDSLLAAGD--DWESPYNILYRNALPIPPVKOPKMIINPYGKDIWYEIRI 96
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 19 TVVGAQVAVACSSDDVRGCGEP-----RTLPPIPPAD-----LGTREGSSV-HEALEA 65

OY 97 KPPQORIYPTLRPATLVGYDGMSPGPTENVPRGTEVAFINNAATVENSVLHGSPSRAP 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 66 QGGEQILPDVYTKTW--GNGTHLGP TLVYKKGDVHVIVNNLDEMPTVHMGKLPAT 124

OY 157 PDGMAEDYTFPEBYKDYFEPNQASRLMYHDHAFKKTAEKAYFGQAGYIINDAEADAL 216
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 125 AGGGRHSPIGPQOTWSPMTVANDATLMYHPTHTGLHAYRGLAGMIYEDDATKTL 184

OY 217 GLPSGYEEDIPILITAKYKNADGTLRSTEGEDQDLMGDVHVGOPWPFVLNVPKRYF 276
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 165 DLPRGYVDIDPLVMDHRTLEDGSLDEEDLDLGLDGTPTANGLITNAHFPATTRRYVF 244

OY 277 RFLNAVSRAMLVYVTRSSPVNRIPEOVIASDAGLLQAPVOTSNLYLAVEREYIIDE 336
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 245 RVLNSNMRFYMLAFSDRT-----FGVIASDSGLDEPQDRTFLAIGGRWEIVEL 298

OY 337 TTFACQITDLRVAVETINVG--DEDEYARTL---EVMRFVSSGYEDNSQVASTLRDVF 392
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 299 E--PEDVTLVESGFEDNGVDPDEFVDPFGMSDFOLLITTFGSPDDAAQA--LPG 352

OY 393 PRHKEGPADKHKFFERSNGHYLINVGFAVNV---ERVLAKEPELTVEWELENSGGMS 449
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 353 VLVKSTEPVADATERT---FIMNTFSINDLOMDQKRDVYVLDHQPEVYITVNDNSDP 409

OY 450 HPHVHLVDFKTLKRTGGRGQVMPYESAGLKDVMLGRGETLLTIE--AHYOPWTGAYVM 506
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 410 HNFHVDAFAFKYKKEGIDVELF---NDGMRKDTVGLPFCATATLAVEFGHYDPDPQWYVX 466

OY 507 HCHNLIHEDNDMAVYF 522
   ||| | | | | | | |
DB 467 HCHMLYHEDQMGQF 482

RESULT 11
US-10-080-210-9
; Sequence 9, Application US/10080210
; Patent No. US2002014243A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080, 210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220, 871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338, 723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Ametriosporium alium
```

```
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(114)
; OTHER INFORMATION: Xaa = space of unknown number of aa
US-10-080-210-9

Query Match          11.2%; Score 357.5; DB 12; Length 114;
Best Local Similarity 32.2%; Pred. No. 8.9e-23;
Matches 85; Conservative 13; Mismatches 15; Indels 151; Gaps 4;

OY 194 TAENAYFGQAGYIINDAEADALGLPSGYGEPDIPILITAKYKNADGTLRSTEGEDQLM 253
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1  TAENAYFGQAGFYILHDPEDALGLPS--GKYDVLALSLKAYNSDGLPDPKDDTDSL 58

OY 254 GDVHVGOPWPFVLNVPKRYRFRFLNAVSRAMLVYVTRSSPVNRIPEOVIASDAGLL 313
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 59 GDVHVGOPWYLVVEPRKRYRLRLNALISRA-----

OY 314 QAPVOTSNLYLAVEREYIIDEFTNFAQOTLDLRNVAETNDVGDEDEYARTLEVRFVVS 373
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 92 -----

OY 374 SGTVEDNSQVPTLNDVPRPHKEGPADKHKFFERSNGHYLINVGFAVNVNRLAKPEL 433
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 92 -----FK-----

OY 434 GTEVWELEN--SSGGMSPHPIHL 456
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 94 ---XVWELENTSSGGMSYPVHITHL 114

RESULT 12
US-09-869-877-9
; Sequence 9, Application US/09869877
; Publication No. US20020192792A1
; GENERAL INFORMATION:
; APPLICANT: Schneider, Palle
; APPLICANT: Danielsen, Steffen
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Laccase Mutants
; FILE REFERENCE: 10179, 204-US
; CURRENT APPLICATION NUMBER: US/09/869, 877
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Scytalidium thermophilum
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (218)..(218)
; OTHER INFORMATION: Xaa is Gln
; NAME/KEY: MISC_FEATURE
; LOCATION: (234)..(234)
; OTHER INFORMATION: Xaa is Ala
; NAME/KEY: MISC_FEATURE
; LOCATION: (557)..(557)
; OTHER INFORMATION: Xaa is Trp
US-09-869-877-9

Query Match          6.3%; Score 202; DB 9; Length 616;
Best Local Similarity 23.0%; Pred. No. 7.7e-09;
Matches 146; Conservative 76; Mismatches 239; Indels 174; Gaps 34;

OY 8  LAASGLL-SCVLGIPMDTGSPIEAVDPEVKTEVFADSLAAGDDMESPPYLLRYN 66
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9  LILLAGLLNSGALAAP---STHP--RSNPDILERDHDHSLSTRSG--SCHSPSNRACWS 61

OY 67 ALPIPVKOPKMIINPYTGKDIWYEIEIKPFOORIVP--TLRPATLVGYDGMSPGPTF 124
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 62 GFDINTVYETK---TPNTGV-VRRITFDITEVNDNRPGPDGVYKELMLINDKLL-GPTV 115
```


;; TYPE: PRT
;; ORGANISM: Rhizoctonia solani
US-09-869-877-5

Query Match 6.2%; Score 198.5; DB 9; Length 529;
Best Local Similarity 21.4%; Pred. No. 1.2e-08;
Matches 116; Conservative 78; Mismatches 222; Indels 127; Gaps 25;

```
QY 92 YEIEIKPFOQRIYPTLRPATLVGYDGMSPGFENVRPGETVVRFINNAAYEN-----SV 146
   | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 YKFDIK--NVNVAAPGFGFSIVSGVLPGTLITANKGDTLRINTNOLDPSMRRAFTI 82
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 147 HLHG--SPSRAPFDG-----WAEVTFPEGEYKDYFPNQSARLLMYHDHAKMTAE 196
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 83 HHMGLEQATTADEBDGPAFTQCPRIQNLISY-----TYEIPRLGQGTMYVHAH----LAS 133
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 197 NAYFGQAGAYIIND-----EAEDALGSPGCEFDIPL-ILTAKYYNADGLTRSTE 246
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 134 QYVDGIRGELVLYDPNDPHKSRDYDDASTVVMLEDWYHTPAVLEKQMFSTNTALLSP 193
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 247 GEDDILMGDIYHVNQO-----PWPFLNV-QPRKYRFRFLNAASRWMLLYVTRSS 296
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 194 VPDSDL-----INGGRYVGGPAVRSYINVRKGRKRYRLRVINMSAIGSFIFSIEGHS- 246
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 297 PNVRIPEOVIASDAGLLQAPVQTSNLYLAVEREYELIDFTNAGOTDLRLV----- 349
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 247 -----LTVIYEA-D-GILHQLAVDSFOIYAGORYSYIVE-----ANQTANYIRAPMTVA 295
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 350 -AETNDVGDEDEYARTLEVMRFVSSGTVEDNSQVPSLTDV-----PFPHKREGPAD 401
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 296 GAGTANANLDPTNVFAVLHVEGAPNNAEPTTEGSAIGTALVEENLHALINPGAPGGSAPAD 355
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 402 -----KHKFERNSNGHYLI-----NDYGFADYNERVLAKPEL 433
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 356 VSLNLAIGRSTVDGILRFTFNNIKYEAPSLPTLLKILANNASNDADFP-NEHTIVLPNN 414
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 434 GYVEVWELENSGGMSHPVHILVDFKILKRTGGQVMPYESAGLKDYVWL-GRGETLT 492
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 415 KYIEL-----NITGGADHPHLHGHHVEDIVKSLGGTPN--YVNPRRDVRVKGCGTVVLR 467
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 493 IEAHYOPWTGAYMMHCNHLIHEDNDMAAVFNVTAMEKGYLOEDFEDPNN-----PKWR 546
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 468 FKTDN---PGPMFVHCHIDHMLHLEAGLALVFAEAPSQIRGQVS--VQPNMANNOLOCPKTA 522
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 547 AVP 549
   | : |
Db 523 ALP 525
```

RESULT 15
US-09-732-350-5
; Sequence 5, Application US/09732350
; Patent No. US20010031490A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490A1tr
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,350
; FILING DATE:

;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/032,315
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rozek, Carol
;; REGISTRATION NUMBER: 36,993
;; REFERENCE/DOCKET NUMBER: 5200,200-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-9655
;; TELEFAX: 212-867-0123
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 529 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-732-350-5

Query Match 6.2%; Score 198.5; DB 10; Length 529;
Best Local Similarity 21.4%; Pred. No. 1.2e-08;
Matches 116; Conservative 78; Mismatches 222; Indels 127; Gaps 25;

```
QY 92 YEIEIKPFOQRIYPTLRPATLVGYDGMSPGFENVRPGETVVRFINNAAYEN-----SV 146
   | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 YKFDIK--NVNVAAPGFGFSIVSGVLPGTLITANKGDTLRINTNOLDPSMRRAFTI 82
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 147 HLHG--SPSRAPFDG-----WAEVTFPEGEYKDYFPNQSARLLMYHDHAKMTAE 196
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 83 HHMGLEQATTADEBDGPAFTQCPRIQNLISY-----TYEIPRLGQGTMYVHAH----LAS 133
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 197 NAYFGQAGAYIIND-----EAEDALGSPGCEFDIPL-ILTAKYYNADGLTRSTE 246
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 134 QYVDGIRGELVLYDPNDPHKSRDYDDASTVVMLEDWYHTPAVLEKQMFSTNTALLSP 193
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 247 GEDDILMGDIYHVNQO-----PWPFLNV-QPRKYRFRFLNAASRWMLLYVTRSS 296
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 194 VPDSDL-----INGGRYVGGPAVRSYINVRKGRKRYRLRVINMSAIGSFIFSIEGHS- 246
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 297 PNVRIPEOVIASDAGLLQAPVQTSNLYLAVEREYELIDFTNAGOTDLRLV----- 349
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 247 -----LTVIYEA-D-GILHQLAVDSFOIYAGORYSYIVE-----ANQTANYIRAPMTVA 295
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 350 -AETNDVGDEDEYARTLEVMRFVSSGTVEDNSQVPSLTDV-----PFPHKREGPAD 401
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 296 GAGTANANLDPTNVFAVLHVEGAPNNAEPTTEGSAIGTALVEENLHALINPGAPGGSAPAD 355
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 402 -----KHKFERNSNGHYLI-----NDYGFADYNERVLAKPEL 433
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 356 VSLNLAIGRSTVDGILRFTFNNIKYEAPSLPTLLKILANNASNDADFP-NEHTIVLPNN 414
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 434 GYVEVWELENSGGMSHPVHILVDFKILKRTGGQVMPYESAGLKDYVWL-GRGETLT 492
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 415 KYIEL-----NITGGADHPHLHGHHVEDIVKSLGGTPN--YVNPRRDVRVKGCGTVVLR 467
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 493 IEAHYOPWTGAYMMHCNHLIHEDNDMAAVFNVTAMEKGYLOEDFEDPNN-----PKWR 546
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 468 FKTDN---PGPMFVHCHIDHMLHLEAGLALVFAEAPSQIRGQVS--VQPNMANNOLOCPKTA 522
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 547 AVP 549
   | : |
Db 523 ALP 525
```

Search completed: February 13, 2003, 06:35:08
Job time : 47 secs

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OM protein - protein search, using sw model

Run on: February 13, 2003, 03:10:27 ; Search time 38 Seconds
(without alignments)
1502.733 Million cell updates/sec

Title: US-09-218-702-2

Perfect score: 3189

Sequence: 1 MLFKSQWLAASGLSLGVLG.....AEQEPYNRLELDLIGIEE 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1724.5	54.1	572	2	B48521 bilirubin oxidase
2	713	22.4	513	2	B56904 spore coat protein
3	480	15.1	568	2	B86364 hypothetical prote
4	450	14.1	591	2	G96734 spore coat protein
5	439.5	13.8	527	2	C70397 periplasmic cell d
6	405.5	12.7	533	2	AC0414 probable exported
7	402	12.6	494	2	AC3582 probable blue-copp
8	391	12.3	536	2	AF0523 probable multicopp
9	388.5	12.2	516	2	C64735 probable copper-bi
10	385.5	12.1	516	2	G90644 hypothetical prote
11	385.5	12.1	516	2	G85495 hypothetical prote
12	340.5	10.7	470	2	G65068 hypothetical prote
13	335.5	10.5	470	2	B81116 suppressor of ftsi
14	335.5	10.5	470	2	E85961 suppressor of ftsi
15	323.5	10.1	470	2	AD0888 SufI protein (limp
16	315.5	9.9	513	2	G81298 probable periplasm
17	303	9.5	474	2	AD0083 probable cell divi
18	284	8.9	1662	2	T18540 moA protein precu
19	241	7.6	311	2	H64157 sulf protein homol
20	231.5	7.3	370	2	H87368 copper-binding pro
21	223	7.0	460	2	B83910 hypothetical prote
22	216.5	6.8	503	2	G83175 probable metallo-o
23	215.5	6.8	611	2	G82845 copper resistance
24	214	6.7	721	2	H82528 L-ascorbate oxidas
25	195.5	6.1	632	2	E83387 copper resistance
26	192	6.0	609	1	KSPSCR copper resistance
27	190.5	6.0	529	2	G58120 laccase (EC 1.10.3
28	189.5	5.9	635	2	A36868 copA homolog - Xan
29	188.5	5.9	520	2	S59533 laccase (EC 1.10.3

30	188.5	5.9	520	2	JC5356 laccase (EC 1.10.3
31	187.5	5.9	504	2	F70813 hypothetical prote
32	185	5.8	527	2	JC5357 laccase (EC 1.10.3
33	184.5	5.8	573	2	T02743 laccase (EC 1.10.3
34	183	5.7	619	1	KSNCLD laccase (EC 1.10.3
35	180	5.6	533	2	S62371 laccase (EC 1.10.3
36	180	5.6	621	2	S72493 laccase (EC 1.10.3
37	179.5	5.6	605	2	S52253 copper resistance
38	179	5.6	548	2	S18746 laccase (EC 1.10.3
39	176	5.5	551	2	T02752 probable laccase (
40	176	5.5	619	1	KSNCLT laccase (EC 1.10.3
41	172.5	5.4	520	2	A35883 laccase (EC 1.10.3
42	172.5	5.4	520	2	B35883 ligninolytic pheno
43	171.5	5.4	552	2	A51027 L-ascorbate oxidas
44	169.5	5.3	579	2	S11027 L-ascorbate oxidas
45	167	5.2	512	2	JC5355 laccase (EC 1.10.3

ALIGNMENTS

RESULT 1

B48521 bilirubin oxidase (EC 1.3.3.5) - fungus (Myrothecium verrucaria)

C:Species: Myrothecium verrucaria

C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C:Accession: B48521; A48521

R:Koike, S.; Ando, K.; Kajii, H.; Inoue, T.; Murao, S.; Takeuchi, K.; Samejima, T.

J. Biol. Chem. 268, 18801-18809, 1993

A:Title: Molecular cloning of the gene for bilirubin oxidase from Myrothecium verruca

A:Reference number: A48521; MUID:93366794; PMID:8360171

A:Accession: B48521

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-572 <KO11>

A:Cross-references: GB:D14081; NID:G436236; PIDN:BA03166.1; PID:G456710

A>Note: sequence extracted from NCBI backbone (NCBIN:136730, NCBIPI:136732)

A:Accession: A48521

A>Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-572 <KO12>

A:Cross-references: GB:D14081; NID:G436236; PIDN:BA03166.1; PID:G456710

A>Note: sequence extracted from NCBI backbone (NCBIN:136728, NCBIPI:136729)

C:Keywords: oxidoreductase

Query Match 54.1%; Score 1724.5; DB 2; Length 572;
Best Local Similarity 60.3%; Pred. No. 1.4e-123;
Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;

QY	57	SPPYNLVYRNALPIPPVQPKMTITNPYTGKDIWYVEIFKFPQORITPTLRPAFLVGD	116
DB	43	SFOYP-MFTVPLPIPPVQPKMTITNPYTGKDIWYVEIFKFPQORITPTLRPAFLVGD	101
QY	117	GSPGPTFNVPRTGTEVVAFFINNATVENSVHLGSPSRAPFGMAEDYTFPEYDYRPP	176
DB	102	GASPGPTFQVPRTGTEVVAFFINNATVENSVHLGSPSRAPFGMAEDYTFPEYDYRPP	161
QY	177	NYQASARLLMYHDAHFAKMAENAYFGQAGAYIINDEADALGLPSYGEFDIPLITLTKARY	236
DB	162	NQASARTLWYHDAHFAKMAENAYFGQAGAYIINDEADALGLPSYGEFDIPLITLTKARY	221
QY	237	NADGTLRSTREGEDQDLKGDVYHVNQCPMPFLNVQPRKTRFRFLNAVAASRAVLLYLVRTSS	296
DB	102	TANGMLVYTTNGELNSFGVDYHVNQCPMPFLNVQPRKTRFRFLNAVAASRAVLLYLVRTSS	281
QY	297	PVVRIPFOVIASDAGLQAPVQTSNLYLAVAEYETIIDFTNFAQOTLDLRNV-AETNDV	355
DB	282	IDTRIPFKVIASDAGLQAPVQTSNLYLAVAEYETIIDFTNFAQOTLDLRNV-AETNDV	341
QY	356	GDEDFYARTLEVMRFVSSAGVIE-DNSQVPSYTLRDVPEP-PKKEGPAADKHFERSNGHY	413
DB	342	GNDTVDYNTDKVMRFVSSAGVIE-DNSQVPSYTLRDVPEP-PKKEGPAADKHFERSNGHY	399

[illegible]

Oy 160 MAE-----DVFPPG---KQYFENNYSARLWHDHAFKMTAENAFGQAGAYIINDE 211
 Db 118 YPEAFMSKDEPDGTGPERYREYHYHPNOQGAALWHDHMAALTRLNAYAGLVGAAYIHDR 177
 Oy 212 AEDALGRLSGGGEPIPLITAKYUNAGDTL---RSTEGEODL-----MGDVTHV 259
 Db 178 KEKRLKLP--DEYVPLILITDRITNEDGSLFYPARPENPSRLPNPSIVAFGCEITLV 235
 Oy 260 NGQMPPELVNORPKRYRFRFLNAASRAWLILYVTRTSSPNVRIPFQVIASDAGLLQAPVOT 319
 Db 236 NGKWVPYLEVPERPKRYFRFVIVNASNTRFYNLSDNCGD-----FQIGSDGGLLPKRVKL 289
 Oy 320 SNLYLVAVEREIIIDFNPAAGOTLDRNVAET--NDVDEDEGATLEVMFVVSSGIVE 378
 Db 230 NSFSLAPEREDIIIDTFAYEGESITLANSAGCGDVPETD---ANIMOFRTKPLAQ 345
 Oy 379 -DNSQVPSTLTDVPEPRPKRGKGPADKHFKEFSNGHY-----LINDVGFADVNERLAKPE 432
 Db 346 KDESKRPYKLASYPVQHERIGNITLTLAQODYGRVLLLNKKRHH---PYTERPK 402
 Oy 433 LGTYEWELENSGGGWSHPVHILHDFKILKR-----TGGRGQVMPYES 476
 Db 403 VGTWEIWSIINPTRG--TSPHILHLVSFRVLDRPRFDIARYOESGELSTYGAVPVPPSEK 461
 Oy 477 AGLKQVWLGRGETLTIEAHYQWPVGAMVHCHNLIHEDNMMAVFNT 525
 Db 462 -GKMDTIAHAGEVIRIATGEPYSGRYVMCHILIEDYDMRPMIDT 509

RESULT 3
 B86364
 hypothetical protein F19G10.5 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C:Accession: B86364
 R:Theologian: A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chlin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Iurios, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B86364
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-568 <SNO>
 A:Cross-references: GB:AE005172; NID:92462832; PIDN:AAB72167.1; GSPDB:GN00141
 C:Genetics:
 ;Map position: 1

Query Match 15.1%; Score 480; DB 2; Length 568;
 Best Local Similarity 28.0%; Pred. No. 1.4e-28;
 Matches 146; Conservative 78; Mismatches 167; Indels 130; Gaps 20;

Oy 109 PATLVGYDGM-----PGPTFNVPRGTETVVRFIN-----AT-----V 142
 Db 71 PATPFAVGTGRSKATVPAGPTIEYVGVDTVVTNRNHLPKSHILPMDPTISPAIRPKHGCI 130
 Oy 143 ENSVHLHSGSPRAPDGAEDVTTPGEKKD-----YFPNYSQARLLMYHDHAFMK 193
 Db 131 PTVVHLHGGIHEPTSDGNA-DAMFTAGRFRENGPRKWTKTTLTYENKKOQPGNMVYHDHAGML 189
 Oy 194 TAEANVYFGQACAYIINDBA-EDALGLPSGYGEFDPLITAKYUNAGDTL-RSTEGEDQD 251
 Db 190 TRVNLGLAGVAYIIRHNAVESPPQLPTG-DEFDRPLIIFDRSFRKDSIYMAATGNMPS 248
 Oy 252 L-----MGDVTHVNGQMPPELVNORPKRYRFRFLNAASRAWLILYVTRTSSPNVRIPF 303


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OY 137 INNAITVENS-----HLHGSPR--APPDGAEDVTPGGEKDYFPFYQASRLIM 185
Db 92 SNRLKENXSMYVAGLQVBGPIMLGSGPARMMSPNADAP-----VLPIRONAATLM 140
OY 186 YHDAHFMTAENAYGCGAGAYIINDEADALGIPSGYEPDILITAKYNAOSTLST 245
Db 141 YHANTPNTAQOYVINGLAGMWLVEDEYKSLPIPHNYGVDDPVLIIQDRILNFTPEYN 200
OY 246 EGEDDOLMGDVIHVNGOPWPELNVOPRKRYRFRFLNAAVSRAWLILYVBTSPPNVIPIFOV 305
Db 201 EPGSGGFVGDTLVNVGVSPEYVSGWVRLRLNLAANSRRQOLM-----NDRPLHY 254
OY 306 IASDAGLQAPQVTSNLYLAVEREYIIIDFTNFPAGOTLDIRNAETNDVGD-----DE 360
Db 235 ISGDGFLPAPYSVKQLSLAPERREIILVDMN-----GDEVSITGE 297
OY 361 YARTEVVRFEVYSSGTEVDNSQVSTL-----RDVPRPHKEGPAD 401
Db 298 NASTYDRIR-----GFEPSSILVSTLVTLTRPTGLRLVYDSLRMRLLPTEIMAGSPI- 351
OY 402 KHFKEERSNGHYLINDVFA-----DVNERVLAKPELGTVIEWELENSSGSMHPYHILY 457
Db 352 -----RSRDISLGDGDPGINGQLMDVN--RIDVTAAQGWERTKTVNADE---PQAHIGEV 401
OY 458 DFKILKRTGGRQWAPY-ESAGLKVWVL-GRGEPL 491
Db 402 MFOIRNVNG---AMPFEDRGMRKDTVWVDGQVELL 433

```

RESULT 13
E91116
suppressor of tsx1 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
R:Accession: E91116
C:Haseguchi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasarara, N.; Yasunaga, T.; Kunihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E91116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <HAY>
A:Cross-references: GB:BA000007; PIDN:BAB37324.1; PID:913363373; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
C:Gene: ECs3901

Query Match	10.5%	Score 335.5;	DB 2;	Length 470;
Best Local Similarity	26.7%	Pred. No. 1.1e-17;		
Matches 138;	Conservative 63;	Mismatches 176;	Indels 139;	Gaps 20

QY	20	GIPMDTSGHLEAVDPREKTEVFADSLAAGDDMESPPYNLLRYNMLPIPRVYQKPAMI	79
Dd	13	GIALCAGAVPLKA-----SAAGQ-----QQPLVPALLESR--	43
QY	80	ITNPVTGDIWYEIEIKPFOORIYPTLRP---ATLVGDMSPGPPPNVRCGTETVRF	136
Dd	44	-----RCQPFLFM-----TVQRAHMSEFTPGTRASVMGINRIYLGPITRWAKGGDVKLILY	91
QY	137	INNATVENSV-----HLHGSPSR--APPDGAELVNTTPGETKYDYFFNYQSARLIM	185
Dd	92	SNRLLENVSMTVAGLOVPGPLMGGARMSPNADAP-----VLPIROMAAALWM	140
QY	186	YHDHAFFMTAEANAFGQAGAYIINDEADEDALGPSGEFIDILPLITAKYNNADOTLST	245
Dd	141	YHANPNTTAQOQVNLGLAMWLVEDEVSKSLPIRPHHYGVDDPEVIIOQRKDINDGTPEYN	200
QY	246	ECEDDDLMDGVIVHNQGCPWPLNAVOPRRKYRFRFLNAVASRAMULLYLVRTSSPVNRIFQV	305
Dd	201	EPFGSGGFVGIDLNLNGVQSPVVEYSRGVWRRLRLNANSRSRYOLOM-----SDGRPLHV	254

```

QY 306 IASDAGLLQAPVQISNLYLAVAERYEIIIDFTNAGOTLDRNVAEFTNDYGD-----DE 360
    |||
    |||
    |||
Db 255 ISGDGFLPAPVSVKQLSLAGEERREILLMSN-----GDEVSITCGE 297
    |||
    |||
    |||
QY 361 YARLEWVRFWSSGTVSDNDSQVSTL-----RDVPFPFKBEPAD 401
    |||
    |||
    |||
Db 298 AASIVDRIR-----GFEFPSSILVSTLVTLRLPGLLPLVTDLSPLMLLPTETMAGSP- 351
    |||
    |||
    |||
QY 402 KHFKEERNGHYLLNDYGEA-----DVNERVLAKPELGTVVEWMELENSGGSHPHVHTLV 457
    |||
    |||
    |||
Db 352 -----RSRDISLGDDEPINGQLMDVNR-IDVTAQOGCTWERTWYRADE---PQAFHIEGV 401
    |||
    |||
    |||
QY 458 DFKILKRTGGRGVMPY-ESAGLKDYVWL-GRGETL 491
    |||
    |||
    |||
Db 402 MEQIRNVG-----AMPFEPEDGMDTVAWVGQVILL 433
    |||
    |||
    |||

```

RESULT 14
E85961
suppressor of ftsI (imported) - Escherichia coli (strain O157:H7, substrain EDL933)
C.Species: Escherichia coli
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C.Accession: E85961
R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallantha, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A.Reference number: A85480; MUID:21074935; PMID:11206551

A:Residues: 1-170 N3RO
 A:Cross-references: GB:EE005174; NID:g12517586; PIDN:AAG58153.1; GSPDB:GN00145; UWGP:
 A:Experimental source: strain O157:H7, substrate EDL933
 C:Genetics:

Query Match	10.58	Score 335.5	DB 2	Length 470
Best Local Similarity	26.78	Pred. NO. 1.1e-17		
Matches 138: Conservative	63	Mismatches 176	Indels 139	Gaps 20

[illegible]

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OM protein - protein search, using sw model

Run on: February 13, 2003, 01:08:17 ; Search time 20 seconds

(without alignments)
1231.847 Million cell updates/sec

Title: US-09-218-702-2

Perfect score: 3189

Sequence: 1 MLFRSMQLAASGLSGVLG.....AEQEPYNRDLIEDLGIEE 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1724.5	54.1	572	1	BLRO_MYRVE
2	713	22.4	513	1	COTR_BACSU
3	519	16.3	642	1	PMSA_STRAT
4	405.5	12.7	533	1	CUEO_YERPE
5	391	12.3	536	1	CUEO_SALRT
6	390	12.2	536	1	CUEO_SALRT
7	388.5	12.2	516	1	CUEO_ECOCI
8	385.5	12.1	516	1	CUEO_ECOCI
9	340.5	10.7	470	1	SUFI_ECOCI
10	323.5	10.1	470	1	SUFI_ECOCI
11	241	7.6	311	1	SUFI_HAETN
12	192.5	6.0	520	1	LAC1_TRAVI
13	192	6.0	520	1	LAC1_TRAVI
14	190	6.0	527	1	COPA_PRESM
15	188.5	5.9	520	1	LAC4_TRAVE
16	188.5	5.9	520	1	LAC4_TRAVE
17	185	5.8	527	1	LAC5_TRAVI
18	180	5.6	533	1	LAC2_PLEOS
19	180	5.6	621	1	LAC2_PODN
20	179.5	5.6	605	1	PCOA_ECOCI
21	179	5.6	548	1	LAC1_PHLRA
22	177.5	5.6	520	1	LAC2_AGABI
23	177	5.6	619	1	LAC1_NEUCR
24	176.5	5.5	519	1	LAC2_TRAVI
25	176.5	5.5	520	1	LAC1_AGABI
26	176	5.5	619	1	LAC2_NEUCR
27	174	5.5	591	1	LAC1_CRYPA
28	172.5	5.4	520	1	LAC1_CORNI
29	171.5	5.4	552	1	ASO_CUCPM
30	169.5	5.3	519	1	LAC2_TRAVE
31	169.5	5.3	579	1	ASO_CUCMA
32	166.5	5.2	622	1	FET5_YEAST
33	163.5	5.1	624	1	FET3_CANAL

34	161.5	5.1	531	1	LAC4_THACU
35	160.5	5.0	529	1	LAC1_PLEOS
36	155.5	4.9	608	1	YD56_YEAST
37	155.5	4.9	622	1	YAK8_SCHPO
38	154	4.8	587	1	ASO_CUCSA
39	151.5	4.8	486	1	LAC1_BOTCI
40	139.5	4.4	473	1	LAC3_TRAVI
41	135.5	4.2	636	1	FET3_YEAST
42	126.5	4.0	572	1	LAC3_THACU
43	121	3.8	576	1	LAC1_THACU
44	114	3.6	725	1	NCA2_MOUSE
45	114	3.6	1115	1	NCA1_MOUSE

ALIGNMENTS

RESULT 1	ID	BLRO_MYRVE	STANDARD:	PRT:	572 AA.
AC	012737:				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	Bilirubin oxidase precursor (EC 1.3.3.5).				
OS	Myrothecium verrucaria.				
OC	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.				
OX	NCBI_TaxID=5532;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=MT-1;				
RX	MEDLINE=9336794; PubMed=8360171;				
RA	Koheda S., Ando K., Kaji H., Inoue T., Murao S., Takeuchi K., Samejima T.;				
RT	"Molecular cloning of the gene for bilirubin oxidase from Myrothecium verrucaria and its expression in yeast."				
RL	J. Biol. Chem. 268:18801-18809(1993).				
CC	- FUNCTION: OXIDATION OF BILIRUBIN AND OTHER TETRAPYRROLES.				
CC	- CATALYTIC ACTIVITY: Bilirubin + O(2) -> biliverdin + H(2)O.				
CC	- CORFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR. CONTAINS 2 BLUE COPPER ATOMS PER MOLECULE.				
CC	- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.				
CC	- SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS.				
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CC	EMBL: D14081; BAA03166.1; -				
DR	EMBL: D12579; BAA02123.1; -				
DR	HSSP: P36649; 1kv7.				
DR	InterPro: IPR001117; Cu-oxidase.				
DR	Pfam: PF00394; Cu-oxidase; 1.				
KW	Signal; Copper; Metal-binding; Oxidoreductase; Glycoprotein; Repeat.				
FT	SIGNAL	1	19		PROBABLE.
FT	PROPEP	20	38		
FT	CHAIN	39	572		BILIRUBIN OXIDASE.
FT	DOMAIN	98	194		PLASTOCYANIN-LIKE 1.
FT	DOMAIN	404	526		PLASTOCYANIN-LIKE 2.
FT	METAL	132	132		COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL	134	134		COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL	172	172		COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL	174	174		COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL	436	436		COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL	439	439		COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL	441	441		COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL	494	494		COPPER (TYPE 3) (BY SIMILARITY).


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FT METAL 495 495 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 496 496 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 500 500 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 503 503 COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 510 510 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 572 AA; 63947 MW; 5842D641303E5EFP CRC64;

Query Match 54.1%; Score 1724.5; DB 1; Length 572;
Best Local Similarity 60.3%; Pred. No. 8.6e-119;
Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;

OY 57 SPFYMLLRNALPPIPVKOPKMTITNPYTKGDIWYEIFEIKFPQRIYPTLRPALVCGD 116
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 43 SPQYR-METVPLPIPVKOPKMTITNPYTKGDIWYEIFEIKFPQRIYPTLRPALVCGD 101

OY 117 GMSPGPTFVPRGTEVYVRFINNATVENSVLHGSPSRAPFGMAEDVTFPEGYDYRPP 176
    ||||||| ||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| |||||||
DB 102 GMSPGPTFVPRGTEVYVRFINNATVENSVLHGSPSRAPFGMAEDVTFPEGYDYRPP 161

OY 177 NYQSARLLMYHDAFMKTAENAFSGAGAYIINDEADALGSPGGERDIPILITAKY 236
    ||||| ||||||| ||||||| ||||| ||||| ||||| ||||||| ||||||| |||||||
DB 162 NYQSARLLMYHDAFMKTAENAFSGAGAYIINDEADALGSPGGERDIPILITAKY 221

OY 237 NADGTLRSTEGEDQDKGDVHVNGQPMFPLVNOPRKYRFRFLNAAVSRAMLLYVRS 296
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 222 TANGNLVYTINGLINSFPGVIVHNGQPMFPRKMYRFRFLDAVSRFGLYADTD 281

OY 297 PAVRIPEQVIASDAGLAPVOTSNLYLAVARVEIIFTFNAGOTLRLNV-LETNV 355
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 282 ITRILPFIKIASDGLIEPAPATSLITYSMAREYVFPFSDYAGTTILRLNGSGIGI 341

OY 356 GDEDEYARTLEVMREYVSSGIVE-DNSQVPSYLRDVPF-PKREGADKHFEERSNGHY 413
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 342 GDTDYDNDTKVMREYVADDTQPTSYVPAHLRDVPFSPPTTNP--RQFREGRTGPTW 399

OY 414 LINDGFALVNRVIALKPELGTEVWELENSSGSMRPHIHLYDPKILKRTGGRG--QY 471
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 400 TINGVAFADVQKRLLANVGVTEVERELINAGNMHPRIHLVDEKVISRTSGNARTV 459

OY 472 MPYESAGLKDVMVLGSGFTLTFAHQPWTGAVMMHCHNLIEDNDMMAMVAVNTAAEKG 531
    ||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 460 MPYES-GLKDVYMLGRREYVVEAHAPRPYGMFCHNLIEDNDMMAMAFNATVLPDG 518

OY 532 YLQEDFEDPMKRAVPYRNRFHARAGNFSAESITARVQELAEQEPYNRUDE 585
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 519 YNATVVDMEELMQRPYELGEGFQSGQSVQAVTERIQFWAEYRPAADE 572

RESULT 2
COTA_BACSU
ID COTA_BACSU STANDARD: PRT: 513 AA.
AC P07788; 024818;
DT 01-AUG-1988 (rel. 08. Created)
DT 30-MAY-2000 (rel. 39. Last sequence update)
DT 16-OCT-2001 (rel. 40. Last annotation update)
DE Spore coat protein A.
GN COTA OR PIG.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1423;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97124186; PubMed=8969499;
RA Borris R., Portmollik S., Schroeter R.;
RT "The 52 degrees-55 degrees segment of the Bacillus subtilis
chromosome: a region devoted to purine uptake and metabolism, and
containing the genes cota, gabp and guaA and the pur gene cluster
within a 34960 bp nucleotide sequence.";
RT Microbiology 142:3027-3031(1996).
RL [2]
RP SEQUENCE FROM N.A.
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RC STRAIN=168 / Marburg;
RX MEDLINE=98116660; PubMed=9455482;
RA Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadaie Y.;
RT "Sequence analysis of the groESL-cota region of the Bacillus subtilis
genome, containing the restriction/modification system genes.";
RL DNA Res. 4:335-339(1997).
RN [3]
RP SEQUENCE OF 1-37 FROM N.A.
RX MEDLINE=88011308; PubMed=2821284;
RA Donovan W., Zheng L., Sandman K., Losick R.;
RT "Genes encoding spore coat polypeptides from Bacillus subtilis.";
RL J. Mol. Biol. 196:1-10(1987).
RN [4]
RP SEQUENCE OF 1-34 FROM N.A.
RX MEDLINE=88286730; PubMed=3135411;
RA Sandman K., Kroos L., Cutting S.M., Youngman P., Losick R.;
RT "Identification of the promoter for a spore coat protein gene in
Bacillus subtilis and studies on the regulation of its induction at a
late stage of sporulation.";
RL J. Mol. Biol. 200:461-473(1988).
RN [5]
RP SEQUENCE OF 1-10 FROM N.A.
RX STRAIN=168;
RA Wray L.V., Ferson A.E., Fisher S.H.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: INVOLVED IN BROWN PIGMENTATION DURING SPOROGENESIS.
CC -I- SIMILARITY: TO S.ANTIBIOTICUS PHENOXAZINONE SYNTHASE (PHSA).
CC -----
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CC -----
DR EMBL: U51115; AAB62305.1; -.
DR EMBL: AB007638; BAA22774.1; ALT_INIT.
DR EMBL: 299107; CAB12449.1; -.
DR EMBL: X05678; CAA29165.1; ALT_INIT.
DR EMBL: X07512; CAA30392.1; -.
DR EMBL: U31756; AAC44642.1; -.
DR PIR: A27393; A27393.
DR HSP: P36649; 1KV7.
DR Subtilist; BG10490; cota.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 1.
KW Sporulation; Complete proteome.
FT CONFLICT 347 367 DESRKYLYASPSYQHERIQ -> TKASRSTSPHLRYS
FT FT MKDT (IN REF. 1).
FT CONFLICT 414 420 PIRGTHP -> RHAHIL (IN REF. 1).
FT CONFLICT 451 458 GRAVPPP -> VRCPAA (IN REF. 1).
SQ SEQUENCE 513 AA; 58499 MW; 836B83B458D75F87 CRC64;

Query Match 22.4%; Score 713; DB 1; Length 513;
Best Local Similarity 34.6%; Pred. No. 9e-45;
Matches 183; Conservative 75; Mismatches 175; Indels 96; Gaps 18;

OY 66 NALPIP----PYKOPMITNPYTKGDIWYEIFEIKFPQRIYPTLRPALVCGDMSG 121
    ||||| |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 8 DALPIPDTLKIPYQ-----SKEKTYEVTMECHQHLRDLPRRLMGVYNGLFPG 57

OY 122 PTFNVPRTETVVRFTNNA-----TVENS-----VLHGSPSRAPFG 159
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 58 PTFNVPRTETVVRFTNNA-----TVENS-----VLHGSPSRAPFG 117

OY 160 MAE-----DVTPGGEY----KDYFFPYQASARLLMYHDAFMKTAENAYGQAYTINDE 211
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 118 YPAMWFSKPEFGTGPYFKREYVHYPRQOGALITWYHDAFMALRLNVAAGLVGAYTINDP 177

OY 212 AEDALGPSGGEFDIPLITAKYVNAAGTL--RSTEGEDDL-----WGQVHIY 259
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 178 KEKRLKLPF--DEYDVPILITDRTINDEGSLFPSPAPENPSPSLPSPSLVPAFCGFTILY 235
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OY 260 NGPMPFLNVPKRYRFRFLNAVSRAMLVLTSTSSPNVRIPFOVIASDAGLLQAPVOT 319
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 236 NGKVMYLEVEREKRYFRIRINASNRTYMLSLDNGD-----FIDGSDGGLPPRSVKL 289
OY 320 SNLYLAVEREIIIDFTNFAGOTLDLRNAVET-NDVGEDEVARTLEVMRFVSSGTV 378
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 290 NFSLSLAPARERIIIDFTVAYEGESILANSAGCGGVNPETD---ANIMQFVTRKPLAQ 345
OY 379 -DNSOVPSLTLDVPPPHKEGPAKHEFKERSNGH-----LINDGFADVNERVLAKPE 432
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 346 KQBSRKPKLASTPSVQHRIONIRTKLAGTODEYGRVLLLNKRMD--PVETPK 402
OY 433 LGTEVWELENSGSGMSPVHILHDFKILKR-----TGRCGVMPYRES 476
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 403 VGTTEIWSIINPTRG-THRIHLVSRVLDLRPRPDIAVQESGELSTYCPANVPPRSEK 461
OY 477 AGIKDVWMLGREGTLEIENHYQPTGAYVMHCHNLIEDNDMAVENVT 525
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 462 -GWKDTIQAHAGEVLRIATFGPSGRVYVHCHIEHEDYDMRPMIDT 509

RESULT 3
PNSA_STRAT STANDARD: PRT; 642 AA.
AC 053692;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Phenoxazinone synthase (EC 1.-.-) (Pfs).
GN PNSA.
OS Streptomycetes antibioticus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=1850;
RN 11
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
RC STRAIN=IMRU 3720;
RX MEDLINE=96011355; PubMed=7592317;
RA Hsieh C.-J., Jones G. H.;
RT "Nucleotide sequence, transcriptional analysis, and glucose
RT regulation of the phenoxazinone synthase gene (pnsa) from
RT Streptomycetes antibioticus."
RL J. Bacteriol. 177:5740-5747(1995).
RN 12
RN SUBUNITING.
RP MEDLINE=82066838; PubMed=7305384;
RA Choy H.A., Jones G.H.;
RT "Phenoxazinone synthase from Streptomycetes antibiotics: purification
RT of the large and small enzyme forms."
RL Arch. Biochem. Biophys. 211:55-65(1981).
CC -1- FUNCTION: CATALYZES THE LAST BUT TWO STEPS IN THE PUTATIVE
CC BIOSYNTHETIC PATHWAY OF ACTINOMYCIN.
CC -1- CATALYTIC ACTIVITY: 4 4-methyl-3-hydroxyanthraniloyl pentapeptide
CC + 3 O(2) -> 2 actinomycin acid + 6 H(2)O.
CC -1- COFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH
CC CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE
CC 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (SMALL FORM) OR HOMOHXAMER (LARGE FORM).
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U04283; AA86668.1; ALT_INIT.
DR HSSP: P36649; IKV7.
DR InterPro: IPR001117; Cu-oxidase.
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DR InterPro: IPR002355; MulticCu-oxidase2.
DR Pfam: PF00394; Cu-oxidase 1.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Repeat; Metal-binding; Copper;
KW Antibiotic biosynthesis.
FT INIT_MER 0 0
FT DOMAIN 86 223 PLASTOCYANIN-LIKE 1.
FT DOMAIN 493 620 PLASTOCYANIN-LIKE 2.
FT METAL 161 161 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 163 163 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 201 201 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 203 203 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 524 524 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 527 527 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 529 529 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 602 602 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 603 603 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 604 604 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 608 608 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 613 613 COPPER (TYPE 1) (BY SIMILARITY).
SQ SEQUENCE 642 AA; 70113 MW; E0B39C0BA364E48 CRC64;

Query Match 16.3%; Score 519; DB 1; Length 642;
Best Local Similarity 27.2%; Pred. No. 2e-30;
Matches 175; Conservative 71; Mismatches 223; Indels 174; Gaps 19;

OY 30 IEADVPEKTEVPFADSLAAGDDMESPPYLLRYNALP--IPYKQKMITNPVYTK 87
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 11 IPIDDLVLADGLVDVLAKEKE---QAPAPGLTFPAFLNVPVLRP---ASDEVTR 64
OY 88 DIWYVEIEIKPPQQRIRYPLRLRATLVGYDGMSPGFENPRTGETVYRRINN----- 139
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 T---EIALRPTVRLHPLPLPLMWGYDGVPGPIERKQQRVRIATNTIPKGEYR 120
OY 140 -ATVE-----NSVHLGSPSRAPFDMAEDVTF 166
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VTSVEPLGPRPGPRAPNTEPRGGVPEPKNDVALPAMSTYHLHGQDTGGNGMDNANG 180
OY 167 PGKYDYFPNTQASARLWYHDAEFKTAENAYFGGAGAYITINDEADALGLPSGYGEFD 226
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 FQDAQLESEYRPNHQAYQWYHDAKANNITRMNVMAGLYGTLYVRDDEEDALGLPS--GDRE 238
OY 227 IPLLILAKYNNADGTLRSRSGEDQDLMGDVII-----VN 260
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 239 IPLLILADRLDLD-----EDGRNLRLKRYIVVOGSNPETGKPVSIPEPGYTTVN 290
OY 261 GQMPFLNVPKRYRFRFLNAVSRAMLVLTSTSSPNVRIPFOVIASDAGLLQAPVOTS 320
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 291 GRIMPYADVDDGMYRLRLYNASNAKRYNLVLDEDDRPVPGVYHQDSGGLLPREVYVD 350
OY 321 -----NLVLAVEREIIIDFTNFAGOTLDLRNAVETNDVGEDEV--ARTLEVMRFV 372
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 351 FDDTLPLVLSAAAEERDLVDLFRALGRRRLVLDKGPAPAGTPDLGVRVEWMEFRV 410
OY 373 SSGTYEDNSQVNSTL-----RVVPF-----PRPKKEP 399
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 411 RETCEDSFALPELVSGSFRMSHDIPIGHRLIYLTPPTKSGSGHPETIEMAEVEDPAD 470
OY 400 -----ADKHEFKERSNGHYLINDGFADVNERVLAKPELGTEVWELENSSG 446
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 471 VQVPAEGVLTQVAGDGRKTYRTATATFMDGLGTF-IGF-----GHNEQMTLNLNS- 520
OY 447 GMSHPVNHILHDFKILKR-----GRCGV-----MPESAGLKDQVWL 485
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 521 PLIHNHNLHDLAFQVLTGRVAYDASGFDLALGSTRPVRLDPTPVPLAPNELGHRDVFQV 580
OY 486 GSGETLTTEAHYQPTGAYVMHCHNLIEDNDMAVENVTANE 528
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 581 PEPQGLRVYMGKFDGAYGRMYHCHLEHEDMGMRPFVMPPE 623

RESULT 4
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CUEO_YERPE STANDARD: PRT; 533 AA.
ID CUEO_YERPE
AC Q82BK0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Blue copper oxidase cueo precursor (copper efflux oxidase).
GN CUEO OR YP03409.
OS Versinia pests.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Versinia.
NCBI_TaxID=632;
OX NCB1
RN [1]
RM SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Tlthall R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Barker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Versinia pests, the causative agent of plague";
RL Nature 413:523-527(2001).
CC -i FUNCTION: Probably involved in periplasmic detoxification of
CC copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake
CC into the cytoplasm. Possesses phenoloxidase and ferroxidase
CC activities and might be involved in the production of polyphenolic
CC compounds and the prevention of oxidative damage in the periplasm
CC (By similarity).
CC -i COFACTOR: This protein belongs to the multicopper oxidases which
CC contain three distinct Cu centers known as type 1 or blue, type 2
CC or normal, and type 3 or coupled binuclear (By similarity).
CC -i SUBUNIT: Monomer (Probable).
CC -i SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat
CC pathway (By similarity).
CC -i INDUCTION: By cueR, at increased levels of cytoplasmic cuprous
CC ions (Probable).
CC -i DOMAIN: The methionine-rich domain could provide binding sites for
CC exogenous copper ions. This methionine-rich region is probably
CC important for copper tolerance in bacteria.
CC -i SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -i SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC
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CC
CC -----
CC EMBL: AJ14157; CAC92639.1; -
CC InterPro: IPR001117; Cu-oxidase.
CC InterPro: IPR002355; MultiCu_oxidase2.
CC Pfam: PF00394; Cu-oxidase; 1.
CC PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
CC Oxioreductase: Copper; Metal-binding; Periplasmic; Signal; Repeat;
KW Complete proteome.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 533 BLUE COPPER OXIDASE CUEO.
FT DOMAIN 68 164 PLASTOCYANIN-LIKE 1.
FT DOMAIN 165 425 PLASTOCYANIN-LIKE 2.
FT DOMAIN 426 533 PLASTOCYANIN-LIKE 3.
FT DOMAIN 356 415 MET-RICH
FT METAL 102 102 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 104 104 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 142 142 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 144 144 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 458 458 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 461 461 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 463 463 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 514 514 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 515 515 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 516 516 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 520 520 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 525 525 COPPER (TYPE 1) (BY SIMILARITY).
SQ SEQUENCE 533 AA; 58328 MW; ED1570CE9B93135 CRC64;
Query Match 12.7%; Score 405.5; DB 1; Length 533;
Best Local Similarity 27.1%; Pred. No. 3.2e-22;
Matches 146; Conservative 57; Mismatches 217; Indels 119; Gaps 18;
QY 68 LPIPVKQPK---MITNPVTKGDIWYEIEIKRQQRITPLRPATLV---GYDGMSPG 121
DB 34 LPIPLLPDANGKTNLNIQTGSVWL-----PSTITQWGNGLLG 76
QY 122 PTFNPRGTEVFVRFINNAVENSYHLGSPSRAPFDGMADVTPGGEYKDYPPNYSOA 181
DB 77 PAIRLRGRKATVIDITNLNPREATVHMHGELRPGVDGPPALQPGAKROVFAVEQPA 136
QY 182 RLWYHDAEMKTAENAVFGAGAVIINDEADALGDPGSGEFDIPLITAKYINADGT 241
DB 137 ATCWHPHTHSKTHQVAMGLGLVLIDSDSETLPLRKMCGVDPIYLDDKLLDKHGQ 196
QY 242 LRSTGEEDQD-----MGDVIHVGQRPWFNLVQPRKY-RPRFLNAAVSRAWLLYL 291
DB 197 V-----DYLDVMTAAVWGVEFDRMLTNGVTPR-QQITPRGVRRLRLNGCARSLNAL 249
QY 292 VRTSSPNVRIPROVIASDAGLLQAPVQTSNLYLAVEREIIIDFTNAGOTLDRNVAE 351
DB 250 -----SGGRPMYVIAISDGLAEFVVYRELPLMGEREVLVTRD--GGSLDLVTLPV 301
QY 352 TNDVDEDEVIARTLEVNRFPVSSGIVEDNSQV-PSTLRDVPRPPKKEGRADKHF----- 404
DB 302 TDMGTWLPAPFDQPLRYLRQPS--LAIGSYVLPESLVVIRLADVTVGVQERWFLMDP 358
QY 405 KEERSNGHYLI-----NDYGFAD----- 422
DB 359 KIDMLGMQALVARYGKAMAGMNMHNGDVGANDHGRNPRMSGKKKMGDHGTMCNAPAFN 418
QY 423 -----VNERVLAKEP-----LGTVEWLELSSGSHPNHILVDFKILRTGGRGQ 470
DB 419 FSHNRINKAFSPMEPAADAKQKEYEKVTISGEGDMLHPRHVGTQFRILTEG---- 474
QY 471 VMPYE-SAGLKQVWL--GRGETLITEAHYQPTGAYMHCHNLIEDNDMAVNVTA 526
DB 475 KPAPAEHRGRKDIVREGARSELIVRFNYLAPASTPYMAHCHLEHEDGMGLGFTVA 533
RESULT 5
CUEO_SALTI STANDARD: PRT; 536 AA.
ID CUEO_SALTI
AC Q829EL;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Blue copper oxidase cueo precursor (copper efflux oxidase).
GN CUEO OR SY0190.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
NCBI_TaxID=601;
OX NCB1
RN [1]
RM SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Barker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant *Salmonella* enterica serovar Typhimurium".
RL Nature 413:848-852(2001).
CC -1- FUNCTION: Probably involved in periplasmic detoxification of copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake into the cytoplasm. Possesses phenoloxidase and ferroxidase activities and might be involved in the production of polyphenolic compounds and the prevention of oxidative damage in the periplasm (By similarity).
CC -1- COFACTOR: This protein belongs to the multicopper oxidases which contain three distinct Cu centers known as type 1 or blue, type 2 or normal, and type 3 or coupled binuclear (By similarity).
CC -1- SUBUNIT: Monomer (Probable).
CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat pathway (By similarity).
CC -1- INDUCTION: By copper, at increased levels of cytoplasmic cuprous ions (Probable).
CC -1- DOMAIN: The methionine-rich domain could provide binding sites for exogenous copper ions. This methionine-rich region is probably important for copper tolerance in bacteria.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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DR EMBL: AL627265; CAD01326.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; MultiCu_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat; Complete proteome.
KW SIGNAL.
FT CHAIN 1 28 BY SIMILARITY.
FT DOMAIN 29 536 BLUE COPPER OXIDASE CUEO.
FT DOMAIN 164 430 PLASTOCYANIN-LIKE 1.
FT DOMAIN 431 536 PLASTOCYANIN-LIKE 2.
FT DOMAIN 355 420 PLASTOCYANIN-LIKE 3.
FT METAL 101 101 MET-RICH.
FT METAL 103 103 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 141 141 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 143 143 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 463 463 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 466 466 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 468 468 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 519 519 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 520 520 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 521 521 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 525 525 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 530 530 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 530 530 COPPER (TYPE 1) (BY SIMILARITY).
SQ SEQUENCE 536 AA; 58624 MW; 2410581D287C3E80 CRC64;
Query Match 12.3%; Score 391; DB 1; Length 536;
Best Local Similarity 25.8%; Pred. No. 3,7e-21;
Matches 140; Conservative 68; Mismatches 215; Indels 120; Gaps 18;
OY 65 RAALIPKPKKMTITNVTKDQIWIYIEIKFPQQRITPLRLPRLTGLVGYGMSGPRFF 124
DB 31 RAALIPD-----LTLTADASNR---MQLIVKAGOSTF--AGKNATMTWYNGNLTGPAY 78
OY 125 NVPRGTEIVAREINNATVENSYHLGSPSRAPDGAEDVTFPGGEKKOYFPNYSARLL 184
DB 79 QAHKRSYTVVDHNLQAEFTLHMHGLEIRPGIVDGGPOSIIRAGGRITVTFPQQRALIC 138
OY 165 WYHDAIFKTAENAVFGQAGAYIINDEADALGLPSGYGEFDIPLLTAKYNNADGTLRS 244
DB 139 WHPHKGKGTGQVAMGLAVLIEDDEIRKLRLPKMGIDIDVPIIQKRSADQI-- 196

245 TSEGDQD-----MGDVIVHNGQPPPLNVQPRKRYRFRPLNAVASRAWLLYVRS 295
DB 197 ----DQLDMITPAANGWEDDTLTNGAITPOHSAPKGMRLRLKNCNARS-----LNTIA 248
OY 296 SPNVRIPIFOVIASDGLDAPVQTSNMLYLAVERYEIIIDTFNAGQOTDLRNVAETNDV 355
DB 249 SDN--RPLVIASDGLDAPVKVTEPLRLMGERFEVLIDIS--GKAPDLVTL-PIVSGM 303
OY 356 G-----DEDEKARTLEVMRFVVSSTVEDNSOVPTSLRDVPPRPKESGRADKHFE--- 406
DB 304 GMAIAFDPKRPVHMRIQPLR-ITASGT-----LPDTLTMPALPSLEGLTVRNKLISMD 356
OY 407 -----ERSNGHYLINDVGNAD----- 422
DB 357 PRLDMKGMOLMKKKGQAQMSGMDHSMANHOGGMNGHDHGMDSHNNHGAMGM 416
OY 423 -----VNERV--LAKP-----ELGTVVEWLENSSGWSHPVHILVDFKILK 463
DB 417 NNGKRFDPHNANFINQVDEDMKPMFAQGRHRRVIVSGVDMMHPRHIGTORILS 476
OY 464 RTGGRGQVMPYESAGLKDVLVWL--GRGETLTTEAHYQPTGAYMMHCHNLIEDNDMAV 521
DB 477 E--NKGAPAAHRTGKDYRVREGISEVLVRFHDPAKREHAYMAHCHLLEHEDTGMIG 533
OY 522 FNV 524
DB 534 FTV 536
RESULT 6
CUEO_SALTY
ID CUEO_SALTY STANDARD; PRT; 536 AA.
AC Q8ZRS2; Q938E6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Blue copper oxidase cueo precursor (copper efflux oxidase).
GN CUEO OR CUID OR STM0168.
OS *Salmonella typhimurium*.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC *Salmonella*.
OX NCBI_TaxId=602;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee I.S., Lim S.Y., Choi S.-Y.;
RT "cuid", a gene encoding a multicopper oxidase from *S. typhimurium*:
RL cloning and characterization.";
RN Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan K.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
LT2.";
RT Nature 413:852-856(2001).
CC -1- FUNCTION: Probably involved in periplasmic detoxification of copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake into the cytoplasm. Possesses phenoloxidase and ferroxidase activities and might be involved in the production of polyphenolic compounds and the prevention of oxidative damage in the periplasm (By similarity).
CC -1- COFACTOR: This protein belongs to the multicopper oxidases which contain three distinct Cu centers known as type 1 or blue, type 2 or normal, and type 3 or coupled binuclear (By similarity).
CC -1- SUBUNIT: Monomer (Probable).
CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat pathway (By similarity).
CC

```
CC -1- INDUCTION: By cueR, at increased levels of cytoplasmic cuprous
CC ions (Probable).
CC -1- DOMAIN: The methionine-rich domain could provide binding sites for
CC exogenous copper ions. This methionine-rich region is probably
CC important for copper tolerance in bacteria.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AY053392; AAL15149.1; -.
CC EMBL: AE008702; AAL19132.1; -.
CC STYGENE: SG72727?; cueO.
CC InterPro: IPR001117; Cu-oxidase.
CC InterPro: IPR002355; Multicu_oxidse2.
CC Pfam: PF00394; Cu-oxidase; 1.
CC PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
CC Oxidoreductase: Copper; Metal-binding; Periplasmic; Signal; Repeat;
CC Complete proteome.
CC SIGNAL 1 28 BY SIMILARITY.
CC CHAIN 29 536 BLUE COPPER OXIDASE CUEO.
CC DOMAIN 67 163 PLASTOCYANIN-LIKE 1.
CC DOMAIN 164 430 PLASTOCYANIN-LIKE 2.
CC DOMAIN 431 536 PLASTOCYANIN-LIKE 3.
CC MET-1 355 420 MET-RICH.
CC COPPER (TYPE 2) (BY SIMILARITY).
CC METAL 101 101 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 103 103 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 141 141 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 143 143 COPPER (TYPE 1) (BY SIMILARITY).
CC METAL 463 463 COPPER (TYPE 1) (BY SIMILARITY).
CC METAL 466 466 COPPER (TYPE 2) (BY SIMILARITY).
CC METAL 468 468 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 519 519 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 520 520 COPPER (TYPE 1) (BY SIMILARITY).
CC METAL 521 521 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 525 525 COPPER (TYPE 1) (BY SIMILARITY).
CC METAL 530 530 COPPER (TYPE 1) (BY SIMILARITY).
CC CONFLICT 322 323 LR -> AA (IN REF. 1).
CC CONFLICT 334 334 L -> F (IN REF. 1).
CC SEQUENCE 536 AA; 58625 MM; E4C04555AF621DF CRC64;
Query Match 12.2% Score 390; DB 1; Length 536;
Best Local Similarity 25.8%; Pred. No. 4.4e-21;
Matches 140; Conservative 68; Mismatches 215; Indels 120; Gaps 18;
OY 65 RNALRIPVYKQPMITITNPGKIMWYEIEIKPQORITPTLRPATLVGDGMSGPTF 124
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
DB 31 RPLALIPD-----LLTADASNR-----MQLIVKAGSGTF--AGKNATGTGYNGLGPAV 78
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
OY 125 NVPRGFEYVFRINNATVENSVHLGSPRARPDGMAEYVTPGEEKDYFFNYQSARLL 184
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
DB 79 QLHKGASVTVDIHNOLAEPTJLHMHGLIPGIVDGGPQGIIPAGGRTVTTFPEQAAATC 138
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
OY 185 WYHDAFMKTAENAYFGQAGAYIINDEADALGPSYGEFPIPLITLAKYVNAODGLRS 244
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
DB 139 WHPHKGHTGQVAMGLAGLVIEDDETRKRLRKQKQIDVVPVLIQKRSSADQIT-- 196
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
OY 245 TEGEDODL-----MGDIVHVGQWPPLNVQPRKRFREFLNAASRAMLLYLVRTS 295
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
DB 197 ----DYGLDIMAAGWGFDDTLTNGALIRPQHSAPKGMRLRLNLNCNARS-----LNTIA 248
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
OY 296 SPNVRIRPFQVYASDGLQAPVQTSNLYLAVERITIIIDTFNFAQGLTDLRNAVETNDV 355
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
DB 249 SON--RPLVVIASDGLLAEPVKVTELPRLMGERFEVLVDSI--GKARDVTL--PVSQM 303
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
*OY 356 G-----DEDEVARTLEVARFVSSGTVEDNSOVPTSLDVPFPPIKREPRAKKHFF-- 406
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
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DB 304 GMAIAPEDKPHVMIQPLR-ITASGT-----LPDTLTMPALPDSLGIVRNKLKMSD 356
OY 407 -----ERSNGHYLINDVGFAD----- 422
DB 357 PRLDMGQMILMKKXYGAQAMSGMDHDSMNAHMGGMGHGMDHSGNNHGMNGM 416
OY 423 -----VNERV--LAKP-----ELGTVEYWELENSGGSHPVHHLVDKFLTK 463
DB 417 NHGKFEFDHNAFINGQVFDINKPMPFAQKGRHNRWVISGVDMMLHPPHILHGTQFRLS 476
OY 464 RTGGRGVMPYESAGLKDVVWL--GRGETLTTEAHYOPMTGAYMMHCHNLJHEDNDMAV 521
| | | | | : : : : : : : : : : : : : : : : : : : : : : :
DB 477 E--NGKAPAAHRTGQKPTVRVEGGISELYKFHDAPKEAHYMAHCHLEHEDTGMMLG 533
OY 522 FNV 524
| |
DB 534 FTV 536
RESULT 7
CUEO_ECOLI STANDARD: PRT: 516 AA.
ID CUEO_ECOLI
AC P36649; P75655;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Blue copper oxidase cueO precursor (copper efflux oxidase).
GN CUEO OR B0123.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=94261430; PubMed=8202364;
RA Fujita N., Mori H., Yura T., Ishihama A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
RL the 2.4-4.1 min (110,917-193,643 bp) region.";
RN Nucleic Acids Res. 22:1637-1639(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[3]
RN SEQUENCE OF 29-40.
RP STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RL in the genome of Escherichia coli K-12.";
RN ElectroPhoresis 18:1259-1313(1997).
[4]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10493123;
RA Pountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RL hydroxyapatite chromatography.";
RN ElectroPhoresis 20:2181-2195(1999).
[5]
RP POSSIBLE FUNCTION IN COPPER HOMEOSTASIS.
RX MEDLINE=21123583; PubMed=11222619;
RA Grass G., Rensing C.;
RT "Genes involved in copper homeostasis in Escherichia coli.";
RL J. Bacteriol. 183:2145-2147(2001).
[6]
RP POSSIBLE FUNCTION IN COPPER HOMEOSTASIS.
```

CC STRAIN-K12; PubMed=11399769;
 RX Outten F.W., Huffman D.L., Hale J.A., O'Halloran T.V.;
 RT "The independent cue and cus systems confer copper tolerance during
 RT aerobic and anaerobic growth in *Escherichia coli*.";
 RL J. Biol. Chem. 276:30670-30677(2001).
 RN [7]
 RP CHARACTERIZATION.
 RC STRAIN-K12 / DH5-alpha;
 RX MEDLINE=20469457; PubMed=10915804;
 RA Outten F.W., Outten C.E., Hale J.A., O'Halloran T.V.;
 RT "Transcriptional activation of an *Escherichia coli* copper efflux
 RT regulon by the chromosomal *mer* homologue, *cueR*.";
 RL J. Biol. Chem. 275:31024-31029(2000).
 RN [8]
 RP CHARACTERIZATION.
 RC STRAIN-K12 / C600;
 RX MEDLINE=21359329; PubMed=11466290;
 RA Kim C., Lorenz W.W., Hoopes J.T., Dean J.F.D.;
 RT "Oxidation of phenolate siderophores by the multicopper oxidase
 RT encoded by the *Escherichia coli* *yacK* gene.";
 RL J. Bacteriol. 183:4866-4875(2001).
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-500 AND HIS-501.
 RC STRAIN-K12 / W3110;
 RX MEDLINE=21418784; PubMed=11527384;
 RA Grass G., Rensing C.;
 RT "CueO is a multicopper oxidase that confers copper tolerance in
 RT *Escherichia coli*.";
 RL Biochem. Biophys. Res. Commun. 286:902-908(2001).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
 RC STRAIN-K12 / W3110;
 RX MEDLINE=21874132; PubMed=11867755;
 RA Roberts S.A., Weichsel A., Grass G., Thakali K., Hazzard J.T.,
 RT Tolin G., Rensing C., Montfort W.R.;
 RT "Crystal structure and electron transfer kinetics of CueO, a
 RT multicopper oxidase required for copper homeostasis in *Escherichia*
 RT *coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:2766-2771(2002).
 CC -1- FUNCTION: Probably involved in periplasmic detoxification of
 CC copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake
 CC into the cytoplasm. Possesses phenoloxidase and ferrioxalase
 CC activities and might be involved in the production of polyphenolic
 CC compounds and the prevention of oxidative damage in the periplasm.
 CC -1- COFACTOR: This protein belongs to the multicopper oxidases which
 CC contain three distinct Cu centers known as type 1 or blue, type 2
 CC or normal, and type 3 or coupled binuclear.
 CC -1- SUBUNIT: Monomer (Probable).
 CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat
 CC pathway.
 CC -1- INDUCTION: By *cueR*, at increased levels of cytoplasmic cuprous
 CC ions.
 CC -1- DOMAIN: The methionine-rich domain could provide binding sites for
 CC exogenous copper ions. This methionine-rich region is probably
 CC important for copper tolerance in bacteria.
 CC -1- MISCELLANEOUS: This protein is sensitive to oxygen deprivation. It
 CC probably plays a significant role in copper efflux under aerobic
 CC conditions.
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
 CC FRAMESHIFT IN POSITION 464.
 CC
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 CC EMBL; D26562; BAA05579.1; ALT_FRAME.

DR EMBL; AE000121; AAC73234.1; .
 DR PIR; S45200; S45200.
 DR PDB; 1KV7: 06-FEB-02.
 DR Ecogene; EG12318; *cueO*.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR002355; MultiCu_oxidase2.
 DR Pfam; PF00394; Cu-oxidase; 1.
 DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
 DR Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;
 KM 3D-structure; Complete proteome.
 FT SIGNAL 1 28
 FT CHAIN 29 516 BLUE COPPER OXIDASE CUEO.
 FT DOMAIN 67 163 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 164 410 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 411 516 PLASTOCYANIN-LIKE 3.
 FT DOMAIN 355 400 MET-RICH.
 FT METAL 101 101 COPPER (TYPE 2).
 FT METAL 103 103 COPPER (TYPE 3).
 FT METAL 141 141 COPPER (TYPE 3).
 FT METAL 143 143 COPPER (TYPE 3).
 FT METAL 443 443 COPPER (TYPE 1).
 FT METAL 446 446 COPPER (TYPE 2).
 FT METAL 448 448 COPPER (TYPE 3).
 FT METAL 499 499 COPPER (TYPE 3).
 FT METAL 500 500 COPPER (TYPE 1).
 FT METAL 501 501 COPPER (TYPE 3).
 FT METAL 505 505 COPPER (TYPE 1).
 FT METAL 510 510 COPPER (TYPE 1).
 FT METAL 510 510 CH-SR: RESIDUAL ACTIVITY AND LOSS OF
 FT MUTAGEN 500 501 RESISTANCE TO COPPER.
 SQ SEQUENCE 516 AA; 56556 MW; 37D96B1C331CF30B CnC64;

Query Match 12.2%; Score 368.5; DB 1; Length 516;
 Best Local Similarity 26.1%; Pred. No. 5.3e-21;
 Matches 142; Conservative 65; Mismatches 208; Indels 129; Gaps 19;
 66 NALPI-----PPYQOPKMITNPVTGKDIWYEIEIKRFOORTYPTL----- 107
 17 SALPLMSRAVFAERPTLPIDLLTTDA-----RNRLQTLTGAGQSTFG 60
 108 -RPATLVGYDGMSPPTENVPRGTETVAFINNAIVENSVLHGSPSRAPFDGMAEDVTF 166
 61 GKTATWTGNGNGLDPAYVQLGRKAVTVQIDVNLQLEETLTHMHGLEGVEVDGPGQGIIP 120
 167 PEETDYFRPNQSRRLMYHNDHAFKTRAEKAYFEOAGAVYINDAEADALGIPSTGEPED 226
 121 PGKRSVTLNVDPATCFHPRHOGKTGRQYAMGLAVIEDEILKMLPKOMGIDD 180
 227 IPIILTAKYNNADGTLRSTEGEDDL-----WGDIYHNGQRPWPLVNPARKY-RF 276
 181 VPIYVDKKFSADGQI-----DYQLDVNTAAVGFQDILLTNGAIYR-QHAPRGMLRL 233
 277 RFLNAVSRAMLVLTVRTSSPNVRIIPFOVIASDAGILQAPVQTSMLYLAVEREYIIDEF 336
 234 RLNCGNMRSL--LNFAITSDN--RPLVYIASDGLLEPRVYSLPVLMDGRFEVLVEV 287
 337 TN---FAGQTLDRVNAETENDVGDDEYARTLEWRFPVYVSSGTVEDNSQVSTLDDVPP 393
 288 NDKRPFDLVTLFVSOMGMA--IAPEDKRPVARIPIAISA-----SGALPDTLSSLPAL 340
 394 PKKEPRA-----DKH----- 403
 341 PSEGLTVARKQLQSLMDPMLDMKGMQLMEKVGDDQAMAGDSOMMGHNGHMNNHNGC 400
 404 -FKPERSNGHYLINDVGFADVNERVLAKPELTGVTEWELENSGGSHPRHILVDVFKIL 462
 401 KDFEHNAN--KINGQAF-DNKKRPFYAAK-GQYERWVISCQGMILRPNHIHGQFRIIL 455
 463 KRTGGRGQMPRESAGLDVYWL--GRGETLTLEHYQRPWGTAGYVWAGHNLIHEDNDKMA 520
 456 SE--NGKRPRAHRAQGMWDYKVEGNSVEVLVKEFNHDAIPKEHAYVAHCHLLEHEDTGML 512
 521 VENV 524

DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein sufi precursor.
 CN SUFI OR B3017.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE OF 1-89 FROM N.A.
 RX MEDLINE=92212294; PubMed=1557036;
 RA Coleman J.;
 RT "Characterization of the Escherichia coli gene for
 RT 1-acyl-sn-glycerol-3-phosphate acyltransferase (pisc).";
 RL Mol. Genet. 232:295-303(1992).
 RN [3]
 RP SEQUENCE OF 28-39.
 RC STRAIN-K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 RT in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 CC -1- FUNCTION: INVOLVED IN CELL DIVISION. SUPPRESSES A FIRST MUTATION.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
 CC -----
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 CC -----
 CC
 DR EMBL: U28377; AAA69185.1;
 DR EMBL: AE000384; AAC76053.1;
 DR EMBL: M63491; AAA24398.1;
 DR PIR: S20461; S20461.
 DR HSSP: P36649; 1KV7.
 DR Ecogene; EG11376; SUFI.
 DR InterPro; IPR001117; Cu-oxidase.
 DR Pfam; PF00394; Cu-oxidase; 1.
 KW Periplasmic; Signal; Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 470 PROTEIN SUFI.
 FT DOMAIN 68 164 PLASTOCYANIN-LIKE.
 SO SEQUENCE 470 AA; 51858 MW; C643A5ACB146688 CRC64;

Query Match 10.7%; Score 340.5; DB 1; Length 470;
 Best Local Similarity 26.9%; Pred. No. 1.5e-17;
 Matches 139; Conservative 62; Mismatches 176; Indels 139; Gaps 20;

QY 20 GIPMDTGHPLEAVDEPKTEVPADSLAAGDDDESPYNLLRYNALPTIPVKPKPMI 79
 DB 13 GIALCAGVPLKA-----SAAGQ-----QQLPVPPLLESR-- 43
 QY 80 ITNPVTGMDIVYEIEIKPFOQRIYPLR--ATLVGDDMSBPGRNVNRCGTETVVR 136
 DB 44 -----RGQPLM-----TYORAHWSFTPTGRASVWINGRYLGPTLVWKGDDVKKLY 91
 QY 137 INNAIVENS-----HLGSPSR--APFDGAEDVTFPGEXKYDYFFNYQSARLLM 185

DB 92 SNRLTENVSMFVAGLQVPGPLMGSPARMSPNADWAP-----VLPIRMQAATLM 140
 QY 186 YHDAFMKTAENAIYFGQAGATIIINDEADALGPGCYGEPDIPLLTPKKYINADGTLAST 245
 DB 141 YHAMPNRTAQOVVYNGLAGMVLVEDEVSKSLPIPNHYGVDPVPIIDKRLDNFGTPEYN 200
 QY 246 ECEDDDLWGDVHYVNGQWMPFLNVQPRKYRPFRLAAVSRAMLVLTVTSSPNVRIPOV 305
 DB 201 EFGSGEFGVDTLVNGVOSPIYEVSRGWVRLRLNANSRRKQLOM-----NDGRPLHV 254
 QY 306 IASDAGLLQAPVQTSNLYLAVAREYIIIDFTNFAQOTLDLRNNAETNDVDE-----DE 360
 DB 255 ISDQGFIPAPYSVQSLAPCEBREILVDSN-----GDEVSITGCE 297
 QY 361 YARTLEWRFVYSSGTVEDNSOVFTL-----RQVPPRPKEGAD 401
 DB 298 AASIVDRIR-----GFPEPSITVSTLVLTLPKPTGLPLVYDLSLPMRLPTEIMAGSP- 351
 QY 402 KHFKFERSNGHYLINDVFA-----DVNERVLAKPELGTVEYWELENSSGMSHPVHILV 457
 DB 352 -----RSRDISLGDPPGINGQLMDVN-RIDVTAAQGTWERTVRADE---PQAFHICV 401
 QY 458 DEKILKRTGRCQVMPY-ESAGLKDVMWL-GRGETL 491
 DB 402 MGIIRNVG----AMPPEDRGMKDTVMVQGVYELL 433

RESULT 10
 SUFI_SALTY STANDARD: PRT: 470 AA.
 ID SUFI_SALTY
 AC P40799;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein sufi precursor.
 GN SUFI OR STM3172 OR STY3349.
 OS Salmonella typhimurium, and
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NCBI_TaxID=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2;
 RA Cong J., Schmidt M.B.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Aili J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahinla M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltham T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jorgels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).

CC -1- FUNCTION: INVOLVED IN CELL DIVISION, SUPPRESSES A FTSI MUTATION
(BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in position 413.
CC -----
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CC -----
DR EMBL; U09309; AAA56679.1; ALT_FRAME.
DR EMBL; AE008845; AAL22046.1; -.
DR EMBL; AL672777; CAD03004.1; -.
DR HSSP; P36649; 1KV7.
DR StyGene; SG10522; sufl.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 1.
KW Periplasmic; signal; Complete proteome.
FT SIGNAL 1 27 BY SIMILARITY.
FT CHAIN 28 470 PROTEIN SUFI.
FT DOMAIN 68 164 PLASTOCYANIN-LIKE.
SQ SEQUENCE 470 AA; 51858 MW; 61E84D4D2B025FB CRC64;

Query Match 10.1%; Score 323.5; DB 1; Length 470;
Best Local Similarity 25.8%; Pred. No. 2.7e-16;
Matches 142; Conservative 58; Mismatches 190; Indels 161; Gaps 21;
QY 1 MLFQSMQAAASGLSGVLPMDTGSHPTEAVDPEVTEVFADSLAAGDDWESPYPY 60
DB 1 MSFSRQFLQAS-----GALCGAIPLR-----NAAG----- 30
QY 61 NLLYNALPIPPYKPKMTITNPYTKDIWYEIEIKPQQRITPTLR-----PA 110
DB 31 ----OQPLVPPLELSRR-----GQPLEMTLDRAHWSFTQGTGRA 65
QY 111 TLVGYDGSPPGTFFVPPGTETVVRFINNAVENS-----HLHGSPSR--APFDG 159
DB 66 PVMGVNGRYLGTIRVWKGDDVKLIYSNRRLAENVSMTVAGLLPGLMGCPARMMSPNAND 125
QY 160 WAEDVTPGEYKDYFFPNYQASRLIWDHAFMKTAEANAYFGQAGAYIINDEAEDALGP 219
DB 126 WAP-----VLPTROSAATLMYHANTPNRTAQOQVYNGIAGMWLVEDDISKTLPIP 174
QY 220 SGYGFEDIPILITAKYVYAADGFLRSTEGEDQDLMDGVTHVNGQPPPLNVQPRKRYRREL 279
DB 175 NHYGVDDPEVITIOQRKLNFGTPEXSEPGSGGVGDITLLVNGAOSPVEVSRGWVRLRL 234
QY 280 NAAVSRAWMLLVYRTSSPNVRIPEFOVIVASDAGLLQAPVQTSNLYLAVEREIIIDFTNF 339
DB 235 NASNSRRRQLOMSDRA-----LHVISGDGFLPAPVSVKOLSLAPGERRIILVDMTN- 287
QY 340 AGQTLDLRNVAETNDVGE-----DEVARTLEVMRFVYVSSGTVEDNSOVPSTL----- 387
DB 288 -----GDEVSTICEAASIYDRIR-----GFEBSISILVSTLVTLRLRPT 326
QY 368 -----RDVPFPKHKEGPADKHFKFRSNGHYLLINDVGA-----DYNENYLAKEP 431
DB 327 GLPLVLTNPLRMLLPTETMSGAPV-----RSRDISLGDDPGINGOLMDVN-RIDITTA 378
QY 432 ELGTVEVELEMSGSGWSPVHIHLVDFKILKRTGCGRGQVMPY-RSAGLKDVVMIGRGRT 490
DB 379 QOGTERTKTVR---ADMQSFHIEGVSFLIRNVNG-----AMPFEDRGKKTIVWD-GCV 430
QY 491 LITEAHYOP-W 500
DB 431 ELVYVYGQPSW 441

RESULT 11
SUFI_HAEIN
ID SUFI_HAEIN STANDARD: PRT; 311 AA.
AC P44847;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein sufi homolog precursor.
GN SUFI OR H10733.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC Haemophilus
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudke D.M., Brandon R.C.,
RA Fine L.D., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC -1- SIMILARITY: STRONG, TO E.COLI AND S.TYRHIMORIUM SUFI.
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL; U32756; AAC22390.1; -.
DR HSSP; P36649; 1KV7.
DR TIGR; H10733;
KW Periplasmic; signal; Complete proteome.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 311 PROTEIN SUFI HOMOLOG.
FT DOMAIN 68 164 PLASTOCYANIN-LIKE.
SQ SEQUENCE 311 AA; 34496 MW; 436173F59F1E1772 CRC64;
Query Match 7.6%; Score 241; DB 1; Length 311;
Best Local Similarity 28.6%; Pred. No. 1.6e-10;
Matches 78; Conservative 39; Mismatches 134; Indels 22; Gaps 5;
QY 65 RNALPIPPYKPKMTITNPYTKDIWYEIEIKPQQRITPTLR-----LRPATVIGYDGSNGP 122
DB 31 REKLIVPPLEIEVR-----RGRPI-----VLMOENINYPIDGSHNVTVGWFENNYLGP 77
QY 123 TFNVPPGTETVVRFINNAVENSIVHLHGSPSRAPDGAEDVTPGEYKDYFFPNYQASR 182
DB 78 TIKISGSAFALNINNNLPQSVALSIOGLQASGELFGCAARLKKGSEMAPVPIEQRAA 137
QY 183 LLWYDHAFMKTAENAYFGQAGAYIINDEAEDALGLPSGGEFDPILITLAKYVYAADGTL 242
DB 138 SCWYSASATLANSAYOTYVGLAGMWLIEDQSLKANLPMKYGVDDIPILIDMEFNNDC-L 196
QY 243 RSTEGEDDLMDGVTHVNGQPPPLNVQPRKRYRFFFLAANASRAWMLLVYRTSSPNVRIIP 302
DB 197 QLFKONQPHFVGNRLVNGIEAPYLDVARGWIRLRLNLAASLARAYDLRLDNDQ----- 250
QY 303 FOYIVASDAGLLQAPVQTSNLYLAVEREIIID 335
DB 251 MLIIADUGFLPKAKSVKSVLSVSPGERAEITLVN 283

FT	CARBOHYD	75	75	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	229	229	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	238	238	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	354	354	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	361	361	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	457	457	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
SO	SEQUENCE	520 AA;	55545 MM;	046AB6D/4737C60E	CRC64;	
Query Match						
Best Local Similarity		21.5%	Pred. No. 1,2e-06;			
Matches 111;		Conservative % 65;	Mismatches 209;	Indels 131;	Caps	
QY	108	RPAITVGDGMSPPCTFVPRGCTETVVRFTINNAI-----VENSYHILGSSSRAPFDQNAE	162	108	108	108
DB	43	KQAVVY--NGSTPGLITGNKGRFQLVLDVINDLNIHTWVKSTSHMGFPQKG--TNWAD	98	43	43	43
QY	163	DVTF-----PGEKDDYFPFNYSARLLWHDHAFKTAEMNAFYGOAGAYII--NDEA	212	163	163	163
DB	99	GRAFINQCRPISSGSHFLDQVPPQAGFGFWHSHLSIQYCD-----GLRGFFVYDPRDPA	154	99	99	99
QY	213	EDALGPSGYGFDPILPLITAKYYNADGTLKSTEGEDODLMGDIYHNGO-----P	263	213	213	213
DB	155	ADLYDVND-----DDYITLVDMYHVAKL-----GAPRLGADATLILNGGRSPSTTAD	205	155	155	155
QY	264	WPLNVQD-RKVRFRFLNAASRAMLLYLVRTSSPNVRIPPO-----VIASDAGLLQAPV	317	264	264	264
DB	206	LSVISTVPGKRYFRRLVSL-----SCDPNTFFSIDGHNMIIETDS--INTAPL	252	206	206	206
QY	318	QTSNLYAVARREIILIDFTNFAQOTLD-----LRVAETHNDGDE-----DEYART	364	318	318	318
DB	253	VVDSIQIAADRYSEFLE---AAQAVDNTWIRANPNFNGVNGFGGINSAILRYDGAAY	308	253	253	253
QY	365	LEVAFVYSSGTVSDNSQVPTSLRDVFPFPHKEG---PADKHEKFEKSNHYLLINDGFA	421	365	365	365
DB	309	EPTTQTTSTARPLMEVNLHLPLVTTAVGSPYAGVDLAINMAFNENGTN--FPLNGSTFT	366	309	309	309
QY	422	DVNERVL-----AKPELGTVEWLELSSG-----GMSHPVHILVDK	460	422	422	422
DB	367	PPTVPLLQIISGQANODLLPSSGYSVLPSPNADIEISPATAAPAPAPPHPLHGHAFA	426	367	367	367
QY	461	ILKRTGGGQGVMPRESAGIKRQVYVLG---RGETLITLTAHQ---PWGALAMMHCHNLHE	514	461	461	461
DB	427	VVRSGG--STYNTNDNPIFRVYVSTGPAPAGDNTITFRITDNGPQW---FLCHIDFHL	480	427	427	427
QY	515	DNDMAVFNTYAMEKGYLQDEFPD-----PMNPKW	545	515	515	515
DB	481	EAQFAVVF-----AEDITDVASANDVPQAW	505	481	481	481
RESULT 13						
COPA_PSESM						
AC	PI237A;	STANDARD;	PRT;	609	AA.	
DT	01-OCT-1989	(Rel. 12, Created)				
DT	01-OCT-1989	(Rel. 12, Last sequence update)				
DT	16-OCT-2001	(Rel. 40, last annotation update)				
DE	Copper resistance protein A precursor.					
GN	COPA.					
OS	Pseudomonas syringae (pv. tomato).					
OC	Plasmid pPT2D.					
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;					
OC	Pseudomonas.					
OX	NCBI_TaxID=323;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=88227880; PubMed=3372485;					
RT	Mellano M.A., Cooksey D.A.,					
RT	"Nucleotide sequence and organization of copper resistance genes from					
RL	Pseudomonas syringae pv. tomato."					
RL	J. Bacteriol. 170:2879-2883(1988).					
RP	[2]					
RP	CHARACTERIZATION, AND SEQUENCE OF 33-37.					
RC	STRAIN=PT23.2;					

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RX MEDLINE=92020961; PubMed=1924351;
RA Cha J.-S., Cooksey D.A.;
RT "Copper resistance in Pseudomonas syringae mediated by periplasmic and
RT outer membrane proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8915-8919(1991).
CC -!- FUNCTION: MEDIATES COPPER RESISTANCE BY SEQUESTRATION OF COPPER IN
CC THE PERIPLASM ALONG WITH THE COPPER-BINDING PROTEIN COPC. MAY HAVE
CC OXIDASE ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- INDUCTION: BY COPPER.
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES. COPA
CC SUBFAMILY.
-----
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CC or send an email to license@sib-sib.ch).
-----
CC EMBL, M19930; AAA25806.1; -.
CC PIR, A32018; KSPSCY.
CC HSSP: P36649; 1KV7.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicopper oxidase2.
DR Pfam: PF00394; Cu-oxidase; 2.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Copper; Repeat; Signal; Plasmid; Metal-binding;
KW Periplasmic.
FT SIGNAL 1 32
FT CHAIN 33 609 COPPER RESISTANCE PROTEIN A.
FT DOMAIN 367 434 5 X 8 AA TANDEM REPEATS OF D-H-X-X-M-X-
FT 1.
FT REPEAT 367 374 1.
FT REPEAT 375 382 2.
FT REPEAT 408 415 3.
FT REPEAT 419 426 4.
FT REPEAT 427 434 5.
FT METAL 100 100 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 102 102 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 142 142 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 144 144 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 542 542 COPPER (TYPE 1) (POTENTIAL).
FT METAL 545 545 COPPER (TYPE 2) (POTENTIAL).
FT METAL 547 547 COPPER (TYPE 3) (POTENTIAL).
FT METAL 590 590 COPPER (TYPE 3) (POTENTIAL).
FT METAL 591 591 COPPER (TYPE 1) (POTENTIAL).
FT METAL 592 592 COPPER (TYPE 3) (POTENTIAL).
FT METAL 596 596 COPPER (TYPE 1) (POTENTIAL).
FT METAL 601 601 COPPER (TYPE 1) (POTENTIAL).
SQ SEQUENCE 609 AA; 67354 MW; 9C086528E8135252 CRC64;
Query Match 6.0%; Score 192; DB 1; Length 609;
Best Local Similarity 20.5%; Pred. No. 1.7e-06;
Matches 138; Conservative 80; Mismatches 214; Indels 242; Gaps 35;

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QY 249 -----DODLWG-----DVIVNGQMPF-LNVQP-----RKYRFP 278
DB 214 ADKGWATVADRMKMAEMKMPDLDVDSGATYTLNGQAPNMWTFGRPEKRLRF 273
QY 279 LNAASRAULLLVKRTSSNVRIP----FOYIASDGLDAPQVTSLYLVAVERIILI- 334
DB 274 INSGA---MTYF-----DIRIPGLKTVASD-GQVNPVEVDRLVAVETFDVIVE 322
QY 335 -----DFTNFGQT-----LDLRNVAETNDVG----- 356
DB 323 PRAEATVFAQSDMRKGYARGTLAVREGLVAYPPLDPRPLVTMDMGAGMDHSGMDM 382
QY 357 -----DEDEYARTLEVRFVSSGVEDNSQV-----P 384
DB 383 SGMDSGADDGMQMSMG--GDSMPAMDHSKMSMGMDHGMAGMDGMVMSHP 440
QY 385 SLYRDVFP-----PPHK-EGP-----AKHKEFEKSNH----- 412
DB 441 ASBNDPLVDQAMSPYAKLNDPGLGLRNNRKRYLADLKTFEEDPDREPSRTIELHL 500
QY 413 -----YLINDVGFADYNERVYLAKEPGLTVEWELSSGMSHPVHILV----- 457
DB 501 TGMMEKFAVSFDIKRADQPLLKXGE--RVRIYLVNDTM--MTRPHILHGMSDLDE 556
QY 458 --DEKILKRTGRCGYVPYESAGLKDVLGRCETLPTBAHYOPWTGAYVMHCHNIHED 515
DB 557 DGNFRVRKHTID---MP---PGSK-----RSYRVTADA---LGRWAYHCHLLYHME 598
QY 516 NDKMAVFNTYAMEE 529
DB 599 --GMFREVREE 609
RESULT 14
LACS_TRAVE STANDARD: PRT: 527 AA.
ID LACS_TRAVE
AC Q12717;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Laccase 5 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Irishiol oxidase) (diphenol oxidase) (Laccase IV).
GN LC5 OR LC5IV.
OS Trimetres versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphellobasiales; Trimetres.
OX NCBI_TaxID=5325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=52J;
RX MEDLINE=97464057; PubMed=9322748;
RA Ong E., Pollock W.B., Smith M.;
RT "Cloning and sequence analysis of two laccase complementary DNAs from
RT the ligninolytic basidiomycete Trimetres versicolor."
RL Gene 196:113-119(1997).
CC -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenesemiquinone + 2
CC H(2)O.
CC -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
-----
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CC EMBL: U04431; AAC49829.1; -.
DR HSSP: P37064; IAOZ.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicu_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW Lignin degradation; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 527
FT DOMAIN 25 150
FT DOMAIN 162 306
FT DOMAIN 373 488
FT METAL 87 87
FT METAL 89 89
FT METAL 132 132
FT METAL 134 134
FT METAL 425 425
FT METAL 428 428
FT METAL 430 430
FT METAL 480 480
FT METAL 481 481
FT METAL 482 482
FT METAL 486 486
FT METAL ? ?
FT CARBOHYD 74 74
FT CARBOHYD 77 77
FT CARBOHYD 156 156
FT CARBOHYD 209 209
FT CARBOHYD 233 233
FT CARBOHYD 242 242
FT CARBOHYD 276 276
FT CARBOHYD 317 317
FT CARBOHYD 358 358
FT CARBOHYD 366 366
FT CARBOHYD 393 393
FT CARBOHYD 402 402
FT CARBOHYD 464 464
FT SEQUENCE 527 AA; 56094 MW; D5957491F1F79825 CRC64;

Query Match 6.0%; Score 190; DB 1; Length 527;
Best Local Similarity 21.7%; Pred. No. 1.9e-06;
Matches 107; Conservative 61; Mismatches 206; Indels 118; Gaps 25;

QY 108 RPAATVGYGMSBPTENVPRGTETVVRFINNATVE-----NSVHLGSPSRAPFDGMAE 162
DB 45 RAAVLNAG--GVFPPGPLITGNKGFQINVIDNLNETMLKSTIIMHGIFQAG--TNMAD 100
QY 163 DVTF-----PGEYKDYFFPNQASRLMYHDAFMKRAENKYPQOAGAYIINDAEDEA 215
DB 101 GAAFVNOCIATNGSFLLYDFVTPDQAGTWFYHSHLSTOYCD---GLRGPVLYVD--PDA 155
QY 216 LGLPSGVG--EPDIPLLITAKYNNADGLTST--EGEDODLMGDVIVHVNOCMPFLNV--- 269
DB 156 NA--SLYDVDDDTVTYTLADWYHTAKLPAPAPAGDSVLINLGRFSODGGATMLTYI 213
QY 270 ---QPKKVFRLNAVSAAMLYLVRTSSPNVRIFP---QVIASDAGILLOAPVOTSMU 322
DB 214 TVTQGRYFRFLVSI-----SCDPNTEFSIDGNHNMIIIVGVGVNHALDVDSI 261
QY 323 YLAVEREYIIDFTNFAAGTLD-----LRNAETNDVGDDEDEYARTELVAMF-----VY 372
DB 262 QIFAGGRYSFILN---AAQSIDNWIRAIPTNGTDTTGGVNS-----ALIKYTAEEI 312
QY 373 SSGTVEDNSOVSTLRDVPFPHKEGSPADKH-----FKFRSRNGHYLINDVGA 421
DB 313 EPTTNTATSVILTERDVLPLDNPAPAGDPQVGVGLVSLDSFNGSN--FFINNETEV 370
QY 422 D-----VNERVLAKPELGTVEV--MELENSSC-----GMSHPVHIH 455

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DB 371 PPTVPLVLIQLISGAODASALLPNSGVYTLPSNSTIEISPIITTDGALNAPGAPHPFH 430
QY 456 LVDFKILKRTGRGQVMPYESAGLKDVYMLGR--GELLTIEAHNQPT-----GAYMHCHN 510
DB 431 GHTFSVVRSG--STFNTANPVRRDTVSTGNSGDVYTR-----FTTDPGFWFLHCH 483
QY 511 LIHEDNDMAV 522
DB 484 DFLIDAGFAIVE 495

RESULT 15
LAC4_TRAVE
ID LAC4_TRAVE STANDARD; PRT; 520 AA.
AC 012719;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Laccase 4 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN LC4 OR LC41.
OS Trameetes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trameetes.
OX NCBI_TaxID=5325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRL 572;
RA MEDLINE=95399443; PubMed=7669813;
RA Joensson L.J., Sjoestrom K., Haeggstrom I., Nyman P.O.;
RT "Characterization of a laccase gene from the white-rot fungus
RT Trameetes versicolor and structural features of basidiomycete
RT laccases."
RL Biochim. Biophys. Acta 1251:210-215(1995).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenesemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC
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CC or send an email to license@slb.ch).
CC
CC EMBL: X84683; CAA59161.1; -.
DR HSSP: P37064; IAOZ.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicu_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW Lignin degradation; Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 520
FT DOMAIN 24 149
FT DOMAIN 161 303
FT DOMAIN 370 491
FT DISULFID 107 509
FT DISULFID 139 227
FT METAL 86 86
FT METAL 88 88
FT METAL 131 131
FT METAL 133 133

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 05:12:13 ; Search time 74 Seconds
(without alignments)
1653.946 Million cell upd

Title: US-09-218-702-2
 Perfect score: 3189
 Sequence: 1 MLFKSWQAAASGLLSGVLG.....AEQEPYNRLDEILDGIEE 594

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

```

1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mhc.*
8: sp.organella.*
9: sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.vertebrate.*
14: sp.unclassified.*
15: sp.virus.*
16: sp.bacteriap.*
17: sp.archaeap.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			Length	DB	ID	Description
	Score	Match					
1	1705	53.5	602	3	Q9P8C3	Q9P8C3	acremionium
2	612.5	19.2	475	2	Q93M03	Q93M03	streptomyce
3	513	16.1	431	2	Q8RMC6	Q8RMC6	streptomyce
4	497.5	15.6	582	10	Q9AWU4	Q9AWU4	oryza sativ
5	480	15.1	568	10	O23J23	O23J23	arabidopsis
6	485	14.6	581	10	Q949X9	Q949X9	arabidopsis
7	484	14.6	637	10	Q9FTS3	Q9FTS3	oryza sativ
8	459	14.4	581	10	O8W4N2	O8W4N2	arabidopsis
9	450	14.1	591	10	Q9C9A4	Q9C9A4	arabidopsis
10	439.5	13.8	527	16	O67206	O67206	aquifex ae
11	432	13.5	614	10	Q9FTS5	Q9FTS5	oryza sativ
12	430.5	13.5	588	10	Q9FTS6	Q9FTS6	oryza sativ
13	423.5	13.3	502	16	Q98FW8	Q98FW8	rhizobium l
14	402	12.6	494	16	O8YCF0	O8YCF0	bruceella m
15	375.5	11.8	515	16	Q9CJQ6	Q9CJQ6	pasteurella
16	375	11.8	477	17	O8ZWA8	O8ZWA8	pyrobaculum

```
Db 124 GISPGPTFQEGKRESVVRFNKATVSESIHLHGSFSRAPWDGWAEDVTNPGEYKDYYP 183
Qy 177 NYOSARLLWYHDHAPMKTAENAYFGQAGAYIINDAEADALGPSYGEFIDPLILITAKY 236
Db 184 NAQAGRFWYHDHAPMKTAENAYNGOAGGYIITHPAEDSLGPSYGEYDIPLIITSKOY 243
Qy 237 NADGTLRSPEGEDQDLGWDIVHVGQPPFLNVQPRKYRFRFLNAAVSRWLLYLVRTSS 296
Db 244 NSDGLFLSTKGETSLMGVDIOVNGVPWPYFDVPRKYRFRLLDAAVSRFSFLYFVDIAD 303
Qy 297 PNVRIPFOVIASDAGLLOAPVOTSNLYLAVAEYRVEIITDFTNFAQOTLDLRNVAETNDVG 356
Db 304 EDTRIPFQVIASDSGLLEPVTTSKLVLSIABRYEIIIDFSDFEGKTIELRNEPAPVGLG 363
Qy 357 DEDEVARTLEVNRVYVSSGTV--DNSQVPSLTRDVPPPHKEGPAADKHKFERSNGHYL 414
Db 364 IEVNDYDDTKVMRFNVAEGPLSPDTSVVPSTRDVPPSPSTSTTIDHSFRFARTAGQWS 423
Qy 415 INDVGFADYVNRVLAKPELGTVEVWELENSGGWGHSHPHVHILVDFKILKRTGG-----R 468
Db 424 INGVTFSDVENRLLANVPLGTVOLQLNAAQGWTHPIHILVDFKILSRGTAATGATTR 483
Qy 469 GQVMYESAGLKDVVWLGRGETLTIEAHYQPTWGTAYMMHCHNLIEDNDMMAVFNVTAME 528
Db 484 G-VEPYESAGLKDVVYLGKGETVWVVEAHYAPWPVGMVFHCHNLIEDNDMMAAFNVTVLP 542
Qy 529 EKGYLQEDFEDPMNPKWRAPVYNNRDNFARAGNFSAESITARVOELAEQEPYNRLD 584
Db 543 DYGYNSTALADPMQDEFRAPKPYVDNDVEVRENAFSTDEIEAQVQLMASYLPYDNFD 598

RESULT 2
Q93M03
ID Q93M03 PRELIMINARY; PRT: 475 AA.
AC Q93M03;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE Oxidoreductase-like protein.
GN AUR2f.
OS Streptomyces aureofaciens.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCM3239;
RA Kormanec J., Bistakova J., Novakova R., Homerova D., Rezuchova B.;
RT "Cloning and characterization of a new polyketide gene cluster in
RT Streptomyces aureofaciens CCM3239.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY033994; AAK61713.1; -.
SQ SEQUENCE 475 AA; 52602 MW; A2ED9A4CG38DD0C9 CRC64;
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Query Match 19.2%; Score 612.5; DB 2; Length 475;
Best Local Similarity 34.9%; Pred. No. 1.1e-38;
Matches 168; Conservative 62; Mismatches 188; Indels 64; Gaps 19;

Qy 64 YRNALDIPVVKPMIITNPVTKDIWYVEIEIKPQRIYTLRPAITLVGYDGMSPGPT 123
Db 39 FAHAMPPLKPLK----TSFTATSDL--YEIRMQEAQVEIVKGLM-SKVRTYDGTFFPGPT 91

Qy 124 FNVPRGTETVVRFINNATVENSVHLHGSPRAPFDGWAEDVTFPEYKDYYPNPQSARL 183
Db 92 IRATOGREVVYQINELQVNTAVHLGHAVLSEHGLPMDTIVPGGERTYRYPNQPAAS 151

Qy 184 LMYHDAFMKTAENAYFGQAGAYIINDEADALGPSYGEFIDPLILITAKYNNADGTLR 243
Db 152 LMYHDAHLEAENVFMGLHGLYLLTDHNERTLPLPS--GPYDVLPIVIRDAVEADGILL 209

Qy 244 STEGEDQDLWGVDVIH--VNGQPWFLNVQPRKYRFRFLNAAVSRWLLYLVRTSSPNVRI 301
Db 210 YTRP-----SDCPHMLVNGKERPYFQVAARKYRFRVYNACANRYVKLRFAD-----GI 257
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Qy 302 PFOVIASDAGLLOAPVOTSNLYLAVAEYRVEIITDFTNFAQOTLDLRNVAETNDVGD---- 357
Db 258 EFTQITDGGFLETVPQOSELLMGLGERADIVVDFSR-----KVGDSSVVL 303
Qy 358 EDEVARTL---EVMRFVYSSGTVEDNSQVPSLTRDVPPPHKEGPAADKHKFERSNGHYL 414
Db 304 ENPGAQSIERPVEVMREDIVR-TAPDYSEVPGR--TTYPQOPTPTVERDFEI-RTEPAMT 359
Qy 415 INDVGFADYVNRVLAKPELGTVEVWELEN-----SSGG-----WSHPVHIHLVDFKILKR 464
Db 360 INQOQY-DPN-RVDITAKLTGTEVTVTRNVEAPAPGKPDFHLW-HSFHTLTYFVRLER 416
Qy 465 TGGRGVMPYESAGLKDVVWLGRGETLTIEAHYQPTWGTAYMMHCHNLIEDNDMMAVFN 524
Db 417 ---NGRPAGTRDLGLKDVITLPGDGTVKIAMTGWGTGTYLHCHOLGHSSGGQGRIDI 473
Qy 525 TA 526
Db 474 VA 475

RESULT 3
Q8RMC6
ID Q8RMC6 PRELIMINARY; PRT: 431 AA.
AC Q8RMC6;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DE Jadz (Fragment).
GN JADZ.
OS Streptomyces venezuelae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=54571;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISP5230;
RX MEDLINE=21930291; PubMed=11932454;
RA Wang L., White R.L., Vining L.C.;
RT "Biosynthesis of the dideoxysugar component of jadomycin B: genes in
RT the jad cluster of Streptomyces venezuelae ISP5230 for L-digitoxose
RT assembly and transfer to the angucycline aglycone.";
RL Microbiology 148:1091-1103(2002).
DR EMBL: AY026363; AAL82808.1; -.
FT NON_TER 431 431
SQ SEQUENCE 431 AA; 47033 MW; 867152A032DIA300 CRC64;

Query Match 16.1%; Score 513; DB 2; Length 431;
Best Local Similarity 33.8%; Pred. No. 4.2e-31;
Matches 155; Conservative 53; Mismatches 195; Indels 56; Gaps 16;

Qy 11 ASGLLSGVLGIPMDTGSHPDIEAVDPEVTEVFADSLAAAGDDDDWESSPPYNLLYNALDI 70
Db 21 ASGLLISRTSL-SDTRAGGPAGASPFAPVAAQAL-----APIVPTFTAMPI 68

Qy 71 PPVKOPKMIITNPVTKDIWYVEIEIKPQRIYTLRPAITLVGYDGMSPGPTFNVPRCT 130
Db 69 PPVAPVSVTSTDT-----YSIPVTOATAEIIIPGVRTPLVT-YGGSPGPGTIKARSGR 121

Qy 131 ETVVRFINNATVENSVHLHGSPRAPFDGWAEDVTFPEYKDYYPNPQSARLLWYHDHA 190
Db 122 RVVVKQPNRIITGTSMLHGAVVDPANDGGPMDLITPGGORTYTYPNPOVAATLWYHDHA 181

Qy 191 FMKTAENAYFGQAGAYIINDEADALGPSYGEFIDPLILITAKYNNADGTL-----RSTE 246
Db 182 HMEAEHVRVYSGSYGLISDDNEDALPLPR--GTVDVPIVVRDGLNPDGTLFFDHNFTP 239

Qy 247 GEDQDLWGVDVIHVGQPPWFLNVQPRKYRFRFLNAAVSRWLLYLVRTSSPNVRIPFQVI 306
Db 240 GRRS--WS-----TKPQPYFQVAARKYRRLILNGSNQRP---FEFRJSDGG---EFTQI 286

Qy 307 ASDAGLLOAPVOTSNLYLAVAEYRVEIITDFTNFAQOTLDLRNV--AETNDVGDEDEYAR 363
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Qy	7	QLAAAGLLSGVLGIPMDTGSHPIEADVETKTEVFADSLAAGD-----DDWESPP--	59
Db	6	ELAVLLLVGVGVA-----AGTRPSAPP-----VTEDTLQKVAGSLEMYVDLQPMPKI	55
Qy	60	YLLRYNALPIPPVKQPKMIITNPVTGDKDIWYIEIEIKPFQORIYPTLRPATLVGDGMS	119
Db	56	YGFSMRHHGHPSP-----TLTIGMYQKK-WKAFHRDL-----PASTVFVFGTS	96
Qy	120	-----PGPTFNVPGRTETVVVRIN-----NATVENSVVHLHGSPS	153
Db	97	AATATFPGPTIEAAGVPLSVTQWNYLPARHILPMDPTVPTAIPRRGGVPTVVHLHGGAH	156
Qy	154	RAPPDQ-----WAEDVTFPCEYKD-----YYPFYQSARLLWYHDHAEKMTAENAYF	200
Db	157	PPOSDCSAFAW-----FTAGFGETGANSTPYITYPNAQSPGVLYWYHDHALGLTANLLA	211
Qy	201	GQAGAYIINDEAEDA-LGLPSGVGEFDPLILITAKYIYNADGTLRST-----EGEDQ	250
Db	212	GLLGAVYIRNPVAPLPGVPCG--DEPDRVILMIADRSFYADGSTIYWNVTGIIINIPHOPOW	270

Query Match	15.1%	Score 480;	DB 10;	Length 568;
Best Local Similarity	28.0%;	Pred. No. 2.2e-28;		
Matches 146;	Conservative	78;	Mismatches 167;	
			Indels 130;	Gaps 20;


```

Query Match      13.5%; Score 432; DB 10; Length 614;
Best Local Similarity 28.6%; Pred. No. 1.2e-24;
Matches 165; Conservative 67; Mismatches 172; Indels 172; Gaps 30;

QY 69 PIPPVKQPKMIITNPVTG--KDIWYIYEIKPFQRIY-PTLRPATLVCYDGMSPGPT-- 123
DB 79 PVP-----TNLTIGWKNYKTFHDMPTTPVFVIGOSLQTATF-----PGPTIV 122

QY 124 --FNVP-----RGTEVVRFEI--NNATVENSVHLHGSRSRAPDGNW---- 161
DB 123 ARYNVPLVYVWENHLPDAHILPMDPTVPTAIPKNGGVPTVHLHGAAPDSGDHFAFW 182

QY 162 -EDVTFEGE--YKDYFPNQ-SARLLWYHDHAFKMTAENAYFCQAGAYIIN-DEADA 215
DB 183 TRDFAENGSTWQKTYTYPNQPAAGNIYHDHGLGLRASLGLLAAYIIVWPELEMP 242

QY 216 LCLPSGYGEFDIPLILITAKIYNADGTL-RSTEGE-----DQDLWDGVIHVNGQPWF 266
DB 243 FNLPS--GEFDLHVIADRKFNVDGTIFMDTVGAVPSVHPQWQPFYFGEVITVNGKAWPF 300

QY 267 LNVQPKRYRFRFLNAASRAMLLYLVR7SSPNVR-----IPFQVIASDAGLLQAPVQTSNL 322
DB 301 QAVQRRYRLRLNASNAR----YL-----NIRFNGSLPFTVVIASDATYLSRPVTVSNL 350

QY 323 YLAVEREIIIDFT-----NFAGQTLDLR-----NVAETNDV 355
DB 351 LLSPAEIEFDVIVDFSLVNPANATDIELLSAPYPPPTGTPANATLDGKVMFNVSAKQV 410

QY 356 GDEDEVARTLEVMRVVSSGTVDNSQVSPSTLRDVPF-----PPHKEGPADKHKFEERS 409
DB 411 GDD-----MPQEPENSTVVPET--GVFFAKVTALPPTMTKTRYILVLYENMTS 455

QY 410 NG-----HYLINDVGADVNERVLAKPELGTVEVWELENSGGWSHPVHILHVDK-- 460
DB 456 NDPNTAKTMNLVINGLRLDPPPTET--PISGTTLHWHVNLITPD-NHPLHLHLAEFQAV 511

QY 461 -----ILKRTG-----GRGVMPYESAGLDKVVWLGRTETLTIEA 495
DB 512 QMLQLVDPDTFKSCMKINDTFACLDQHAVGALQVPVEEKTWNKVVYKIPPAYVTSVV 571

QY 496 HYQ-----PW-----TGA--YMHCHNLIHEDNDNM 519
DB 572 AFLRVHNNWPPFDATAAGVYVYHCHILHEDNAMI 607

RESULT 12
Q9FTS6
ID Q9FTS6 PRELIMINARY; PRT; 588 AA.
AC Q9FTS6:
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Putative spore coat protein-like protein.
GN P0409B08.11 OR P0404F08.29.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
clone:P0409B08."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
clone:P0404F08."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AP002860; BAB18284.1; -.
DR EMBL; AP002909; BAB21194.1; -.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1.
SQ SEQUENCE 588 AA; 64290 MW; 6C6CB995060C4A82 CRC64;

Query Match      13.5%; Score 430.5; DB 10; Length 588;
Best Local Similarity 27.0%; Pred. No. 1.5e-24;
Matches 142; Conservative 70; Mismatches 180; Indels 133; Gaps 20;

QY 109 PATLVGYDMS-----PGPTENVPRGTEVTVVRFIN-----NATV 142
DB 90 PATPVFVYQCPSDTSATFGPTIMARHDVPLFVRWENHLPASHILPMDPTVPTAIPKNGV 149

QY 143 ENSVHLHGSRSRAPDGNW-----WAEDVTTFPGCEYKDYYPNPQSAARLLWY 186
DB 150 PTVVHLHGSAPHPQSDGSFAFWTAGFAEKGPAMTQ-----ATYRYPNVQPGNLMY 201

QY 187 HDHAFMKTAENAYFCQAGAYII-NDEAEDALGPSYGEFDIPLILITAKIYNADGTL-RS 244
DB 202 HDHALGLTRANLLAGLLGAYVIEKPEVDTMDLPC--DDDDLHLVIADRSFNVDSGLYWN 259

QY 245 TEGEDQDL-----WGDVIHVNGQWPFNLVQPKRYRFRFLNAASRAMLLYLVR7SS 296
DB 260 SFGVAPNIHPHWAPEYFGEAITVNGKAMPFLVHRRYRLRLILNASNARYENVSL----- 314

QY 297 PNVRIPFQVIASDAGLLQAPVQTSNLYLAVEREIIIDFTNFAGQTLDLRNVAE7NDVG 356
DB 315 -SNGPLPIHVSGDSYLSAPVTVSNLLSPAEIFDVVDVSQSPATAEIELLSAPYPPPT 373

QY 357 DEDEVARTLEVMRVVVS-SGTVE--DNSQVSPSTLRDVPF-----PPHKEGPADKHKFE 407
DB 374 GAAPGLNGKVMKFLVQNPGLDPPDNDSTVDP--HEVPIASVTALPPTMTKTRYIVWIEYL 431

QY 408 RNSG---HYLINDVGADVNERVLAKPELGTVEVWELENSGGWSHPVHILHVDKILKR 464
DB 432 TPTGQSTHLYINGLLED--PVTETPKSGTTLQAVINLTGD-NHPLHLHLMGFAQVAKM 487

QY 465 TGGRCQVMPYES-----AGLDKVVWL-----GRGETLTIEAHYQVWTG----- 502
DB 488 Q-----QLVNLQAFTDCMTAVNDVAVRCNVDOHAVGVVPPVDPDEKTMKNVIKVPVPGFVTSV 543

QY 503 -----AYMHCHNLIHEDNDMMAVENVTA 526
DB 544 VIAFKLVDTNQTYPDPTTAEPGYVYHCHILHEDNAMIPLKLLA 588

RESULT 13
Q98FW8
ID Q98FW8 PRELIMINARY; PRT; 502 AA.
AC Q98FW8:
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE Putative periplasmic oxidoreductase.
GN MLL3586.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

```

RT	Mesorhizobium loti.;	DR	InterPro: IPR001117; Cu-oxidase.
RL	DNA Res. 7:331-338(2000).	DR	InterPro: IPR002355; MultiCu_oxidase2.
DR	EMBL; AF003002; BAB50448.1; --	DR	Pfam: PF00394; Cu-oxidase; 1.
DR	InterPro: IPR001117; Cu-oxidase.	DR	PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
DR	InterPro: IPR002355; MultiCu_oxidase2.	KW	Complete proteome.
DR	Pfam: PF00394; Cu-oxidase; 3.	SQ	SEQUENCE 494 AA; 53849 MW; BE3627202A3B8287 CRC64;
DR	PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.		
KW	Complete proteome.		
SQ	SEQUENCE 502 AA; 53995 MW; AE96D894241B36CE CRC64;		
Query Match 13.3%; Score 423.5; DB 16; Length 502;			
Best Local Similarity 31.4%; Pred. No. 4.1e-24;			
Matches 139; Conservative 53; Mismatches 189; Indels 61; Gaps 19;			
QY	112 LVGVGMSQPTENVPRGTETVVRFINN-ATVENSVHLHGSPSRAPFDGWAEDVTFPGEY 170		
DB	95 ILAYNGSPGLLEAVEGDRVEITFANRIANEASTIHWGMPVPADODGNMPDPVATGTD 154		
QY	171 KDYYF--PNYQSARLLWYHDHAFMKTAENAYFGQAGAYIINDAEADALGPSYGGEFDIP 228		
DB	155 RTYSFDLPE-ASAGSYWYHPHPHGKTAEOVYRGLAGAFVVKRADP---IPAAYG--DTV 208		
QY	229 LILTAKYNNADGTLRSTEGED--QDLGWDVIHVGQWPFELNQ-PRKYRFRFLNAAVSR 285		
DB	209 LVFTDLRLAADGTLPDNTMTDLNMGVRGDHVLVNGQKNPTLTVPFGAKRFRFYNA---- 264		
QY	286 AWLLYLVRTSSPNVRIPFQ-----VIASDAGLLQAPVOTSNLYLAVAEYEEIIDFTN-- 338		
DB	265 -----TNARFLRISFDGASMTIIGTDGGLLEAPVAAGDILLSPAERLELVVSFKPG 316		
QY	339 -FAGQTLDL----RNVAETNDVGDDEYARTLEVNRFRVSSGTVEDNSQVPSTLRDVPFP 393		
DB	317 AALTTLDYDRGMWGPCRPADAG-----LTLTLTVNSQTEADPVPPLPDLRPI--- 365		
QY	394 PHKEGPA-DKHFKFRSNG-----HYLLINDVGFADVNERVLAKPELGTVEVWELENS 444		
DB	366 AOLGAPAVRSRFRVFTETNAMNAGMGMGFLNGAADFQMRIDVVAK--AGQVELWEIVNE 423		
QY	445 SGGWSHPVHILVDFKILKRTGGQGVMPYESAGLKDVVWLGRGETLITIEAHYQFWTGGAY 504		
DB	424 A-DMDHFPVHGTOFQVVEHERG-GNTSKPAYRAWKOTVNVARGEAVALLLR-QDRPGPR 480		
QY	505 MWHCHNLHEDNDMMAVFNVT 526		
DB	481 MYCHHLEHEQLGMGVVVDQA 502		
RESULT 14			
Q8YCF0	PRELIMINARY; PRT; 494 AA.		
AC	O8YCF0;		
DT	01-MAR-2002 (TrEMBLrel. 20, Created)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Probable blue-copper protein YACK precursor.		
GN	BMEI0580.		
OS	Brucella melitensis.		
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;		
OC	Brucellaceae; Brucella.		
OX	NCBI_TaxID=29459;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=16M / ATCC 23456 / BIOTYPE 1;		
RX	MEDLINE=20020109; PubMed=11756688;		
RA	Delvecchio V.G., Kaparatl V., Redkar R.J., Patra G., Mujar C., Los T.,		
RA	Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,		
RA	Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,		
RA	Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,		
RA	Hasselkorn R., Kyrides N., Overbeek R.;		
RT	"The genome sequence of the facultative intracellular pathogen		
RT	Brucella melitensis.";		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).		
DR	EMBL; AE009694; AAL53822.1; --		
Query Match 12.6%; Score 402; DB 16; Length 494;			
Best Local Similarity 26.4%; Pred. No. 1.8e-22;			
Matches 142; Conservative 65; Mismatches 208; Indels 122; Gaps 17;			
QY	56 ESPYNLLYRNALPIPPVKOPKMIITNPVTGKDIWYIEIKFPQQR-IYPTLRPAFLVG 114		
DB	7 KAPP-----LPLPLVEP-----DASG-----IVRLKVQKGRHSAKSTASAG 46		
QY	115 YDGMSQPTENVPRGTETVVRFINNATVENSVHLHGSPSRAPFDGWAEDVTFPGEYKDY 174		
DB	47 INGAYLGLPRLVMSGESVTLSENAMDEETLHHWGLFVPSHLDDGGPHNVIAPGAKWEK 106		
QY	175 FPNYQSARLLWYHDHAFMKTAENAYFGQAGAYIINDAEADALGPSYGGEFDIPLITAK 234		
DB	107 VAVNQPAFNFHPLHGHGHTARQAHHGIAGLMIVRDGKDAERGLPETYGVDDLPVLQDR 166		
QY	235 YYNADGTLRSTEGED-----QDL-----WGDVIHVGOPWPFELNVQPKYRFRFLNAAVS 284		
DB	167 -----RVIEGDVAVPADIMDLIHGRGDLVINGAIAPAEARVPAAWVRLLLNGANA 218		
QY	285 RAWLLYLVRTSSPNVRT-----PFOVIASDAGLLQAPVOTSNLYLAVAEYEEIIDFTNFA 340		
DB	219 RNF-----HIRPADGRPLLVIASDGGFISQPVSIETQITISPGERYEVLVDFSN-- 266		
QY	341 GOTLDLRNVAETNDVGDDEYARTLEVNRFRVSSGTVEDNSQVPSTLRDVPFPHPKEGPA 400		
DB	267 GEAVDLVTYGD-NGSGD-----GLHLMRFTVDPALBGRVAKPPVSLDGPAPDEKLSVQ 319		
QY	401 DKHFKFER-----SNHYLLINDVGFADVN----- 424		
DB	320 RRSFFDERMAENKMLMRQSPSNPHASGDDNDHMEKSMAGMDHMHGSRSAADAGPAL 379		
QY	425 -----ERVLAKEPLGTVEVWELENSGGWSHPVHILVDFKILKRTG 466		
DB	380 DALTSQVQMAIADKPFDMERIDVEAKLGSWEIWEI--TSREMAHPFHIGHASFRILSMNG 437		
QY	467 GRGQVMPYESAGLKDVVWL-CRGETLTIEAHYQFWTGGAYMWHCHNLHEDNDMMAVE 522		
DB	438 K---PPAHOQTGWKDTALIDGKAEILVHFDREAAKSHPFMFHCHLLEHEDVGMMMAQF 491		
RESULT 15			
Q9CJQ6	PRELIMINARY; PRT; 515 AA.		
AC	Q9CJQ6;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Hypothetical protein PM1938.		
GN	PM1938.		
OS	Pasteurella multocida.		
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;		
OC	Pasteurella.		
OX	NCBI_TaxID=747;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=PM70;		
RX	MEDLINE=21145866; PubMed=11248100;		
RA	May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;		
RT	"Complete genomic sequence of Pasteurella multocida Pn70.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).		
DR	EMBL; AE006230; AAK04022.1; --		
DR	InterPro: IPR001117; Cu-oxidase.		
DR	InterPro: IPR002355; MultiCu_oxidase2.		
DR	Pfam: PF00394; Cu-oxidase; 1.		
DR	PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.		

Search completed: February 13, 2003, 06:33:35
Job time : 78 secs

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 17:10:31 ; Search time 9250.33 Seconds
(without alignments)
11568.344 Million cell updates/sec

Title: US-09-218-702-3
Perfect score: 3677
Sequence: 1 ctggtgacctcacttgta.....gataactgacctgggtcaat 3677

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_or.*
- 21: em_ov.*
- 22: em_pat.*
- 23: em_ph.*
- 24: em_pl.*
- 25: em_ro.*
- 26: em_sts.*
- 27: em_sy.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3676.6	100.0	3677	6	AR211554	AR211554 Sequence
2	1474	40.1	1791	6	AR211556	AR211556 Sequence
3	1462.6	39.8	7259	6	AX384798	AX384798 Sequence
4	507.6	13.8	2126	8	AM0271104	AJ271104 Acremoniu
5	460.8	12.5	2905	6	AR211555	AR211555 Sequence
6	455.6	12.4	2063	6	AR211557	AR211557 Sequence
7	382.6	10.4	1942	8	MVRBOR	D12579 M. verrucar
8	382.6	10.4	1959	6	E05283	E05283 Bilirubin o
9	300.4	8.2	1958	6	AR122996	AR122996 Sequence
10	300.4	8.2	1958	6	AX101096	AX101096 Sequence
11	300.4	8.2	1958	6	AX108672	AX108672 Sequence
12	300.4	8.2	1958	6	AX456852	AX456852 Sequence
13	300.4	8.2	2095	6	AR122997	AR122997 Sequence
14	300.4	8.2	2095	6	AX101098	AX101098 Sequence
15	300.4	8.2	2095	6	AX108674	AX108674 Sequence
16	300.4	8.2	2095	6	AX456854	AX456854 Sequence
17	150	4.1	858	6	AR211558	AR211558 Sequence
18	138.2	3.8	3241	8	MVRBOR	D14081 M. verrucar
19	63.8	1.7	9531	1	AY033994	AY033994 Streptomy
20	60.8	1.7	134673	8	AP002860	AP002860 Oryza sat
21	60.2	1.6	14731	1	AE000724	AE000724 Aquifex a
22	60	1.6	1533	6	AX121137	AX121137 Sequence
23	60	1.6	1614	6	AX065821	AX065821 Corynebac
24	60	1.6	333150	1	AP005277	AP005277 Corynebac
25	60	1.6	349980	6	AX127146	AX127146 Sequence
26	58	1.6	7218	6	I66494	I66494 Sequence 14
27	54.6	1.5	3446	6	AX204969	AX204969 Sequence
28	53.8	1.5	125020	9	AF429315	AF429315 Homo sapi
29	53.4	1.5	12543	1	AY026363	AY026363 Streptomy
30	53.2	1.4	134673	8	AP002860	AP002860 Oryza sat
31	53.2	1.4	141528	8	AP002909	AP002909 Oryza sat
32	51.6	1.4	137879	8	AP003233	AP003233 Oryza sat
33	50	1.4	15897	1	BS051115	U51115 Bacillus su
34	50	1.4	16585	1	AB007638	AB007638 Bacillus
35	50	1.4	21066	2	AC092489	AC092489 Oryza sat
36	50	1.4	213190	1	BS080004	Z99107 Bacillus su
37	49.6	1.3	5585	1	D86821	D86821 Streptomyce
38	49.6	1.3	27887	1	SC050	AL163672 Streptomy
39	49.6	1.3	125020	9	AF429315	AF429315 Homo sapi
40	49.4	1.3	141528	8	AP002909	AP002909 Oryza sat
41	47	1.3	10186	1	AE004583	AE004583 Pseudomon
42	46.6	1.3	34893	1	SGI7	AL096743 Streptomy
43	46.4	1.3	14461	6	AX256438	AX256438 Sequence
44	46	1.3	157362	2	CNS08CAU	AL844497 Oryza sat
45	45.8	1.2	2302	1	SAPHSA	U04283 Streptomyce

ALIGNMENTS

RESULT 1	AR211554	AR211554	Sequence 1 from patent US 6399329.	3677 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AR211554	Sequence 1 from patent US 6399329.					
DEFINITION	AR211554	Sequence 1 from patent US 6399329.					
ACCESSION	AR211554	Sequence 1 from patent US 6399329.					
VERSION	AR211554.1	GI:21514906					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 3677)						
AUTHORS	Wang, H. and Bodie, E.A.						
TITLE	Phenol oxidizing enzymes						
JOURNAL	Patent: US 6399329-A 1 04-JUN-2002;						
FEATURES	Location/Qualifiers						

source	1. .3677					
BASE COUNT	822 a	1057 c	849 g	948 t	1 others	
ORIGIN						
Query Match	100.0%;	Score 3676.6;	DB 6;	Length 3677;		
Best Local Similarity	100.0%;	Pred. No. 0;				
Matches 3677;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1	CTGGCTAGCCTCACTTGGTGTAGACAGCCCTGACAGCCTCACTGGCTGGGGTTCGAAAGGCC	60			
Db	1	CTGGCTAGCCTCACTTGGTGTAGACAGCCCTGACAGCCTCACTGGCTGGGGTTCGAAAGGCC	60			
Qy	61	AGTCAATATCTTGGTCACTGCTTAATAGTTCTTCTGTACGCCCAAAAAGCTCCTTGCCGAA	120			
Db	61	AGTCAATATCTTGGTCACTGCTTAATAGTTCTTCTGTACGCCCAAAAAGCTCCTTGCCGAA	120			
Qy	121	GGGCGACAGACTATCAAGTGAGACATATAGGATGCATGCTCTTTTCATAGCCACAGTTAGGG	180			
Db	121	GGGCGACAGACTATCAAGTGAGACATATAGGATGCATGCTCTTTTCATAGCCACAGTTAGGG	180			
Qy	181	TGGTGACCTACTCGAAGAGGCCCGGACTTGCATGACATACGACATGCTCGCTTCCATGCAAC	240			
Db	181	TGGTGACCTACTCGAAGAGGCCCGGACTTGCATGACATACGACATGCTCGCTTCCATGCAAC	240			
Qy	241	ATGTATGGCACATCGCGGATCAGGCACCCCTCTGCATCGAGAATAGAACCCCTTGGTTT	300			
Db	241	ATGTATGGCACATCGCGGATCAGGCACCCCTCTGCATCGAGAATAGAACCCCTTGGTTT	300			
Qy	301	CGTTTGTGTTCTTTTCCCTTCTCAACGACGGTGAGCGTGGTTAACTTGAAGCAAGCCGA	360			
Db	301	CGTTTGTGTTCTTTTCCCTTCTCAACGACGGTGAGCGTGGTTAACTTGAAGCAAGCCGA	360			
Qy	361	GTGTCGTGTTTCACGAGGTTACCATCGAACTCTCTCTTTTCCCAATCATGACCTGCCGCC	420			
Db	361	GTGTCGTGTTTCACGAGGTTACCATCGAACTCTCTCTTTTCCCAATCATGACCTGCCGCC	420			
Qy	421	GAGTTTAGCCCCATCAGGGCTGTGAATCCACTTTCGATAATCCTAGCCTAGTGCTACTC	480			
Db	421	GAGTTTAGCCCCATCAGGGCTGTGAATCCACTTTCGATAATCCTAGCCTAGTGCTACTC	480			
Qy	481	TTCAATAGTTGCTCTGATGGGCACTTTGGTCACATTTGGCTTGGTTTCTCCTACTCGT	540			
Db	481	TTCAATAGTTGCTCTGATGGGCACTTTGGTCACATTTGGCTTGGTTTCTCCTACTCGT	540			
Qy	541	TCCTCTCCGCATCAAGCCTCTATGCCGAGCAACACCTCATTTGGCCGGGACCACTTTG	600			
Db	541	TCCTCTCCGCATCAAGCCTCTATGCCGAGCAACACCTCATTTGGCCGGGACCACTTTG	600			
Qy	601	AGCGGCGACGACCTTCGCGCGGAAGGAGTTGATAAACACCCCTTACCCCTTGCCCAATGAT	660			
Db	601	AGCGGCGACGACCTTCGCGCGGAAGGAGTTGATAAACACCCCTTACCCCTTGCCCAATGAT	660			
Qy	661	GGAGTTTGGTCTATTTGTTCATGATCACTTCACTACATGATACAGGATCCTGGAAGA	720			
Db	661	GGAGTTTGGTCTATTTGTTCATGATCACTTCACTACATGATACAGGATCCTGGAAGA	720			
Qy	721	GGGTGTGAAGCCAGACAGCTTGTCCCTGTCTTTCGACACTCAGGTCACTTACGGG	780			
Db	721	GGGTGTGAAGCCAGACAGCTTGTCCCTGTCTTTCGACACTCAGGTCACTTACGGG	780			
Qy	781	CTATCAGCTCAGGATTTATCAAGTCCCGTAAAGTCCAGACCCCTTTTCATTTGATGATGC	840			
Db	781	CTATCAGCTCAGGATTTATCAAGTCCCGTAAAGTCCAGACCCCTTTTCATTTGATGATGC	840			
Qy	841	TGCTTAATTTGGCTATCTCTATGCGGTAGCAGCGGCTTGGCTACAACTGGCTGCCATG	900			
Db	841	TGCTTAATTTGGCTATCTCTATGCGGTAGCAGCGGCTTGGCTACAACTGGCTGCCATG	900			
Qy	901	GCTGAAGCATCGTGAATCTATAAAGGCTCTCCGAATCCCTCGGTGAAGTCAGAAATCGTCTC	960			
db	901	GCTGAAGCATCGTGAATCTATAAAGGCTCTCCGAATCCCTCGGTGAAGTCAGAAATCGTCTC	960			

Qy	961	TCCACACCAGTCAACAACAAGCTTTCTTCTCTTACAGCTTAGCCTGAGCACATTCACAGA	1020
Db	961	TCCACACCAGTCAACAACAAGCTTTCTTCTCTTACAGCTTAGCCTGAGCACATTCACAGA	1020
Qy	1021	ACTCTTCCCTTTCTTCTGCTCAATATGCTTGAAGTATGCAACTGCGCAGCAGCCTCCG	1080
Db	1021	ACTCTTCCCTTTCTTCTGCTCAATATGCTTGAAGTATGCAACTGCGCAGCAGCCTCCG	1080
Qy	1081	GGCTCCTGTCTGGAGTCCCTGGCATCCCGATGGACACGGCAGCACCCCATTTAGGCTG	1140
Db	1081	GGCTCCTGTCTGGAGTCCCTGGCATCCCGATGGACACGGCAGCACCCCATTTAGGCTG	1140
Qy	1141	TTGATCCGGAAGTGAAGACTGAGGTCTTCGCTGACTCCTCTTCTGCTCAGCAGCGGATG	1200
Db	1141	TTGATCCGGAAGTGAAGACTGAGGTCTTCGCTGACTCCTCTTCTGCTCAGCAGCGGATG	1200
Qy	1201	ACGACTGGAGTCACTCCATACAACTTGTCTTACAGGTGAGACACCTGTCCCACCTGTT	1260
Db	1201	ACGACTGGAGTCACTCCATACAACTTGTCTTACAGGTGAGACACCTGTCCCACCTGTT	1260
Qy	1261	TTCCCTCGATAAATACTTCTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCA	1320
Db	1261	TTCCCTCGATAAATACTTCTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCA	1320
Qy	1321	AGATGATGTCTTTGATTTTCTACGAAGCAACTCGGCCCGGACTAATGATTTCTAGGATC	1380
Db	1321	AGATGATGTCTTTGATTTTCTACGAAGCAACTCGGCCCGGACTAATGATTTCTAGGATC	1380
Qy	1381	ATTACCAACCTGTCAACGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTT	1440
Db	1381	ATTACCAACCTGTCAACGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTT	1440
Qy	1441	CAGCAAAAGGTTGAGTTGCTCAGAAAACCTTGTGGTAATTAATCATTTGTTACTGACCTTT	1500
Db	1441	CAGCAAAAGGTTGAGTTGCTCAGAAAACCTTGTGGTAATTAATCATTTGTTACTGACCTTT	1500
Qy	1501	CAGATTTACCCACCTTGGGCCCTGCCACTCTCGTGGCTAGCATGGCATGAGCCTGGT	1560
Db	1501	CAGATTTACCCACCTTGGGCCCTGCCACTCTCGTGGCTAGCATGGCATGAGCCTGGT	1560
Qy	1561	CCTACTTTCAATGTTCCAGAGGAACAGAGACTGTAGTTAGTTTCATCAACAATGCCACC	1620
Db	1561	CCTACTTTCAATGTTCCAGAGGAACAGAGACTGTAGTTAGTTTCATCAACAATGCCACC	1620
Qy	1621	GTGGAGAACTCGGTCCATCTGCAACGGCTCCCATCGCGTGGCCCTTTGATGGTTGGGT	1680
Db	1621	GTGGAGAACTCGGTCCATCTGCAACGGCTCCCATCGCGTGGCCCTTTGATGGTTGGGT	1680
Qy	1681	GAAGATGACCTTCCCTGGCGAGTACAGGATTTACTACTTTCCCAACTACCAATCCGCC	1740
Db	1681	GAAGATGACCTTCCCTGGCGAGTACAGGATTTACTACTTTCCCAACTACCAATCCGCC	1740
Qy	1741	CGCCTTCTGTGTAGTACATGACCACGCTTTCATGAAGGTATGCTAGAGGCTTTATCTTTC	1800
Db	1741	CGCCTTCTGTGTAGTACATGACCACGCTTTCATGAAGGTATGCTAGAGGCTTTATCTTTC	1800
Qy	1801	TTGGCTACCTTTGGCTAAACAATCTTCTTCTGCTAGACTGCTGAGAATGCTACTTTGGTC	1860
Db	1801	TTGGCTACCTTTGGCTAAACAATCTTCTTCTGCTAGACTGCTGAGAATGCTACTTTGGTC	1860
Qy	1861	AGGCTTGGCGCTTACATTTATCAACGAGGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCT	1920
Db	1861	AGGCTTGGCGCTTACATTTATCAACGAGGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCT	1920
Qy	1921	ATGGCGAGTTGATATPCCCTCTGACTCTGACGGCCAAAGTACTATACGCCGATGTTACCC	1980
Db	1921	ATGGCGAGTTGATATPCCCTCTGACTCTGACGGCCAAAGTACTATACGCCGATGTTACCC	1980
Qy	1981	TGCGTTTCGACCGAGGTTGAGGACCGAGCCTGTGGGAGATGTCATCCATGTCAACGGAC	2040
Db	1981	TGCGTTTCGACCGAGGTTGAGGACCGAGCCTGTGGGAGATGTCATCCATGTCAACGGAC	2040
Qy	2041	AGCCATGGCCTTTCTTTAAGCTCCAGCCCGCAAGTACCGTTCCGATTCCTCAACGGCTG	2100

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Db 2041 AGCCATGGCCCTTCCCTTACAGTCCAGCCCGCAAGTACCCTTCCGATTCCTCAAGCGTG 2100
QY 2101 CCGTGCTCGTGCTGGCTCCTTACCTCGTCAGGACCAAGCTCTCCCAACGTCAGAAATTC 2160
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Db 2101 CCGTGCTCGTGCTGGCTCCTTACCTCGTCAGGACCAAGCTCTCCCAACGTCAGAAATTC 2160
QY 2161 CTTTCCAAGTCATTTGGCTCTGATGTGGTCTCCTTCAAGCCCGGTTTCAGACCTCTTAACC 2220
Db 2161 CTTTCCAAGTCATTTGGCTCTGATGTGGTCTCCTTCAAGCCCGGTTTCAGACCTCTTAACC 2220
QY 2221 TCTACCTTCTGTGTGCGAGCGTTAGGAGATCATTTAGTATGGTATGCCCTCCCTCTCAAGA 2280
Db 2221 TCTACCTTCTGTGTGCGAGCGTTAGGAGATCATTTAGTATGGTATGCCCTCCCTCTCAAGA 2280
QY 2281 ATGAGTCAAGAACTCTTAAGACTTAACACTTTGTAGACTTTCACCAACTTTGCTGCCAGACTC 2340
Db 2281 ATGAGTCAAGAACTCTTAAGACTTAACACTTTGTAGACTTTCACCAACTTTGCTGCCAGACTC 2340
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QY 2581 ATGAGCGTCTCTGCGCAAGCCGAGCTCGGCACCGTTGAGGCTCGGGAGCTCGAGAACT 2640
Db 2581 ATGAGCGTCTCTGCGCAAGCCGAGCTCGGCACCGTTGAGGCTCGGGAGCTCGAGAACT 2640
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Db 2641 CCTCTGGAGGCTGGAGCCACCCCGTCCACATTCACCTTTGACTTCAAGATCCTCAAGC 2700
QY 2701 GAACGTGGTGGTGGCCAGGTGATGCCCTACGAGTCTGCTGGCTTAAAGGATGCTGCT 2760
Db 2701 GAACGTGGTGGTGGCCAGGTGATGCCCTACGAGTCTGCTGGCTTAAAGGATGCTGCT 2760
QY 2761 GGTGGGAGGGGTGAGACCTTGACCATCGAGGCCCACTACCAACCCCTGGAGTGGAGCTT 2820
Db 2761 GGTGGGAGGGGTGAGACCTTGAGCCCTGAGCCATCGAGGCCCACTACCAACCCCTGGAGTGGAGCTT 2820
QY 2821 ACATGTGGCAGTGTCAACACCTCATTACGAGGATAAAGACATGATGGCTGTATTCAAGC 2880
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QY 2881 TCACGCCCATGAGGAGAGGAGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCA 2940
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Db 3001 CCGAGTCCATCACTGCCCAGTGCAGGAGCTGGCCGAGCAGGAGCCGTACAACCCCTCG 3060
QY 3061 ATGAGATCCTGGAGGATCTTGGAAATCGAGGAGTAACACCCCGGACCAAGCTCTACAATC 3120
Db 3061 ATGAGATCCTGGAGGATCTTGGAAATCGAGGAGTAACACCCCGGACCAAGCTCTACAATC 3120
QY 3121 GTTTTGTAGTCTTAACAGAGGCTCTTTGGTGCGTATTTCTTCTCCCTACGCGGAACTCC 3180
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Db 3121 GTTTTGTAGTCTTAACAGAGGCTCTTTGGTGCGTATTTCTTTCTCCCTACGCGGAACTCC 3180
QY 3181 GCTGTCCACTGCGATGTGAAGGACCATCACAAAGCAACGCTATATATTGGACTCACCACATG 3240
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Db 3181 GCTGTCCACTGCGATGTGAAGGACCATCACAAAGCAACGCTATATATTGGACTCACCACATG 3240
QY 3241 TCATTACCCGCCACTTTGTACCTATTTCGATTCCTTGTTCAAACTTTTCTAGTGCAGAGTGT 3300
Db 3241 TCATTACCCGCCACTTTGTACCTATTTCGATTCCTTGTTCAAACTTTTCTAGTGCAGAGTGT 3300
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QY 3361 COTGGAGTAGATGCTCAATTTGTGATGAGACACAGTAAATACGGTATATCTTTTCCCTAGGAC 3420
Db 3361 COTGGAGTAGATGCTCAATTTGTGATGAGACACAGTAAATACGGTATATCTTTTCCCTAGGAC 3420
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Db 3421 TACAGGATCAGTTTCTCATGAGATTACATCCCTCTAAATTTTGTCCATGAGAGTCTAGCT 3480
QY 3481 AAGGTTGAGATGTCATCAGACGGAATCATTTGATGCTCTCAGCTCGTATTACCGATGTA 3540
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QY 3661 AACTGACCTGGGCTCAAT 3677
Db 3661 AACTGACCTGGGCTCAAT 3677

RESULT 2
AR211556
LOCUS AR211556 1791 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from patent US 6399329.
ACCESSION AR211556
VERSION AR211556.1 GI:21514909
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1791)
AUTHORS Wang, H. and Bodie, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 5 04-JUN-2002;
FEATURES Location/Qualifiers
source 1..1791
BASE COUNT 380 a 551 c 451 g 409 t
ORIGIN

Query Match 40.1%; Score 1474; DB 6; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

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Db 199 -----AGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCCAAGAT----- 239
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Db 261 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCAATTTTCAGCAAG----- 311
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Qy 1878 ATCAACGAGGAGGCTGAGGATGCTCTCGGCTCTCTAGTGGCTATGGGAGTTTCGATATC 1937
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Qy 1998 GAGGACCAAGGACCTGTGGGAGATGTATCCATGTCAAGGACAGCCATGGCCCTTTCCTT 2057
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Qy 2358 GCTGAGACCAACGATGTGCGGACGAGGATGAGTACGTCGCACTCTCGAGGTGATGGC 2417
Db 1054 GCTGAGACCAACGATGTGCGGACGAGGATGAGTACGTCGCACTCTCGAGGTGATGGC 1113
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RESULT 3
AX384798 LOCUS AX384798 7259 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 3 from Patent WO0196543.
ACCESSION AX384798
VERSION AX384798.1 GI:19577933
KEYWORDS .
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1
AUTHORS Hood,E., Howard,J.A., Bailey,M., van Gastel,F.J., Ward,M., Wang,H. and Woodward,S.
TITLE Method of increasing recovery of heterologous active enzymes produced in plants

JOURNAL Patent: WO 0196543-A 3 20-DEC-2001;
Prodigene, Inc. (US) ; Genencor, Inc. (US)
FEATURES Location/Qualifiers
source 1..7259
/organism="unidentified"
/db_xref="taxon:32644"
/note="Stachybotrys sp."
BASE COUNT 1928 a 1745 c 1583 g 1997 t 6 others
ORIGIN

Query Match 39.8%; Score 1462.6; DB 6; Length 7259;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 1806; Conservative 0; Mismatches 24; Indels 269; Gaps 6;
QY 1030 TTCTTTTCGTCATATGCTTTCAAGTCATGCGCACTGGCAGCAGCCTCCGGGCTCCTGT 1089
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DB 5193 TTCCGGCTTGTCAATATGCTTTCAAGTCATGCGCACTGGCAGCAGCCTCCGGGCTCCTGT 5252
QY 1090 CTGGAGTCCTCGGCATCCCGATGGACACCGCGAGCCAGCCACCCATTTGAGGCTGTTGATCCGG 1149
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DB 5253 CTGGAGTCCTCGGCATCCCGATGGACACCGCGAGCCAGCCACCCATTTGAGGCTGTTGATCCGG 5312
QY 1150 AAGTGAAGACTGAGGCTTTCGCTGACTCCCTCTGCTGTCAGCAGCGGATGACGACTGGG 1209
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DB 5313 AAGTGAAGACTGAGGCTTTCGCTGACTCCCTCTGCTGTCAGCAGCGGATGACGACTGGG 5372
QY 1210 AGTCACCTCCATACAACTTTCGCTTTACAGGTGAGACACCTGTCCCACTGTTTTCCTCTCGA 1269
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DB 5373 AGTCACCTCCATACAACTTTCGCTTTAC----- 5398
QY 1270 TAACTAACTCTTATAGGAATGCCCTGCCAAATTCACCTGTGCAAGCAGCCCAAGATGTATG 1329
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DB 5399 -----AGGAATGCCCTGCCAAATTCACCTGTGCAAGCAGCCCAAGAT----- 5439
QY 1330 TCTTTGATTTCTACGAAGCAACTCGGCCCGCACCTAAATGATTTCTAGGATCATTTACCAAC 1389
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DB 5440 -----GATCAITTACCAAC 5452
QY 1390 CTGTACCGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCAATTTTCAGCAAAAG 1449
||| |
DB 5453 CTGTACCGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCAATTTTCAGCAAAAG- 5511
QY 1450 GTGAGTTTCTCAGAAACCTTGTGGTAATTAATCATTTGTTACTGACCCCTTTCAGATTTAC 1509
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DB 5519 CCACCTTTCGCCCTGCCACTCTCGTGGCTAGCATGGCATGAGCCCTGGTCTCTACTTTC 5578
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DB 5579 AATGTTCCAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGAGAAAC 5638
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QY 1690 ACCTTCCCTGGCGAGTACAAGGATTACTACTTTCACCACTACCAATTCGSCCGCCTCTTG 1749
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DB 5820 CGCTTACATTATCAACGAGGCGTGAGGATGCTCTCGGCTCTTCTCTAGTGGCTATGGCGA 5879

QY 1928 GTTCGATATCCCTCTGATCCTGACGCCAAGTACTATAACGCCGATGGTACCTCGCTTC 1987
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DB 5880 GTTCGATATCCCTCTGATCCTGACGCCAAGTACTATAACGCCGATGGTACCTCGCTTC 5939
QY 1988 GACCGAGGTGAGGACCGAGGACTGTGGGGAGATGTCCATCCATGTCAACGGACAGCCATG 2047
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DB 6211 -----GACTTACCACAACTTTGTGGCCAGACCTCTTGACCT 6245
QY 2348 GGGCAACGTTGCTGAGACCAACGATGTGGCGACAGGAGTACGCTCGACACTCTCGA 2407
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DB 6246 GGGCAACGTTGCTGAGACCAACGATGTGGCGACAGGAGTACGCTCGACACTCTCGA 6305
QY 2408 GGTGATGCGCTTCGCTGCTGAGCTCTGGCACTGTGAGGACAAACAGCAGCTCCCTCCAC 2467
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DB 6306 GGTGATGCGCTTCGCTGCTGAGCTCTGGCACTGTGAGGACAAACAGCAGCTCCCTCCAC 6365
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DB 6786 CATGAGGAGAGAGGATATCTTTCAGGAGACTTCGAGGACCCCAAGTGGGG 6845
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Qy	2800	ACCAACCTCGGACTGGAGCTTACATGTGGCACTGTACAACTCTATTCACGAGGATAAG	2859
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Qy	2980	CTCGCGTGGAACTTCTCCGCGAGTCCATCACTGCCCGAGTGCAGGAGCTGGCCGAGC	3039
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RESULT 5			
LOCUS	AR211555	2905 bp	DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 3 from patent US 6399329.		
ACCESSION	AR211555		
VERSION	AR211555.1	GI:21514907	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2905)		
AUTHORS	Wang, H. and Bodie, E.A.		
TITLE	Phenol oxidizing enzymes		
JOURNAL	Patent: US 6399329-A 3 04-JUN-2002;		
FEATURES	Location/Qualifiers		
source	1..2905		
BASE COUNT	714 a	792 c	664 g 734 t 1 others
ORIGIN			
Query Match 12.5%; Score 460.8; DB 6; Length 2905;			
Best Local Similarity 59.3%; Pred. No. 8.8e-104;			
Matches 976; Conservative 0; Mismatches 537; Indels 133; Gaps 6;			
Qy	1491	CTGACCCCTTCAGATTACCCACCTTGGCCCTCGCCACTCTCGCTCGGCTACGATGGCAT	1550

Db	478	CTTCAACCAGAGGTCTATCCAAAGCCTGGCCCTGCTGCTTTAGTAGGCTATCAGCGCAT	537
QY	1551	GAGCCCTGGTCTACTTTCATATGTTCCAGAGAAACAGAGACTGTAGTTAGGTTTCATCAA	1610
Db	538	CTCCCAAGTCTCTAGATCATAGTCCGAGAGAAACAGAAGCTGTGTACGGTTTATAAA	597
QY	1611	CAATGCCACCTGGAGAACTCGGTCTCATCTGACGGCTCCCATCGCGTCCCTTTTCCA	1670
Db	598	CCAGGGTGATCCGAAAGCTCCATCATCTCCAGGCTCCCGCTCCCGTCCCGCTTTTGA	657
QY	1671	TGGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAA-----	1709
Db	658	CGATGGGCTGATGATATGATCATGAAGGGGAATACAAAGGTACGATAGCGTGTGATTC	717
QY	1710	-----GGATTACTACTTTTCCC	1725
Db	718	TACGCATCAGGAAGCCTCTATCATATAACAGGACTTTCTTCTCAGACTACTACTACCCG	777
QY	1726	AACTACCAATCCGCCCGCCTTCTGTGTACCATGACCAGCCTTTCATGAAGGTA--TGCT	1783
Db	778	AAACAACCAAGCTGCCAGATTTTGTGTACACGATCATGCTATGCATGTTTGAAGTCTT	837
QY	1784	ACGAGCCTTATCTTCTTGTGCTACCTTTGGCTAACCAACTTCTTCTAGACTGCTGA	1843
Db	838	TACCACTTTTCATGCTAGTGAACGGAAGGATTAAGCTAACTCTGTCGACACCCGACA	897
QY	1844	GAATCCCTACTTTGGTGAAGCTGGCGCCTACATTAACAACGAGAGGCTGAGGATGCTCT	1903
Db	898	AAATGCCATTTCGGGCAAGCGCGCCTACCTGATACAGACCCGCGTGAAGTCTCT	957
QY	1904	CGGTCTTCTAGTGGCTATGCGGAGTTCGATATCCCTCTGATCTCGACGGCCAAAGTACTA	1963
Db	958	CGGCTTCTCTCAGTTACGGAAATACGACATTCGCTGGTCTCAGTTCCAAGTACTA	1017
QY	1964	TAAACCGATGTACCTGCGTTTCGACCGAGGTGAGGACACGAGCTCTGTGGGAGATCT	2023
Db	1018	CAACCGCATGGAACCTCTTAAGACCAAGTGTGGGAGAGACAAGAGTGTGGGGGACAT	1077
QY	2024	CATCATGTCAACGACAGCCTATGGCCTTCTTAACTCCAGCCCCCGCAAGTACCGTTT	2083
Db	1078	CATCCATGTCAACGCTGAGCCCTGCGCATTTCTTAAATGTTGAGCCTCGAAAGTATCGTCT	1137
QY	2084	CGATTTCTCAACGCTGCGGTGTCTGCTGCTTGGCTCTCTACCTCGTCAAGCAGCTC	2143
Db	1138	TCGATTCTCTCAACGCGGCTGTTTCTAGGAACTTTGCCCTTTACTTCGTCGAAGACAAA	1197
QY	2144	TCCCAAGCTCAGAATTCTTCCAAAGTTCATTCCTCTGATGCTGCTCTCTTCAAGCCCC	2203
Db	1198	CACTGCCACTAGGCTTCTTCCAGGTCAATGCCCTCTGATGAGGCTACTCACACACCC	1257
QY	2204	CGTTCAGACCTCTAACCTCTACTTTGCTGTTGCCGAGCGTTACGAGATCATTTTGGTAT	2263
Db	1258	GGTTCAAACTTCAGATATGTATGTTGCAGCCGCGACAGCCTACGAGT-----	1305
QY	2264	GCCCTCCCTCTCAGGAATGATCAAGAACTTAAGACTTAACACTTGTAGACTTTCACCAA	2323
Db	1306	-----TGTGTTGCGATTTTCGCGCC	1323
QY	2324	CTTGTGTCGCCAGACTCTTGACCTCGCAACGCTGCTGAGACCAACGATGTCCGCGACCA	2383
Db	1324	CTATGCCGCCAAAGCTGGGATCTCGCAACTTCGAAAGGCCAATGGTATCGGTACCCA	1383
QY	2384	GGATGAGTACGCTCGCACTCTCGAGGTGATGCGCTTCGTCGTCAGCTCTGGCACTGTGGA	2443
Db	1384	CGACGACTACGCAAACTGACAAGTCTATGCTTTCCACGTCAGCAGCAACACAGTCTGT	1443
QY	2444	GGACAACAGCAGGTCCCTCCACTCTCGGTGACGTTCCTTTCCCTCTCTCACAAGGAAG	2503
Db	1444	CGATAACTCCGTGGTACCCGAGCAGCTATCTCAGATCCAGTTCCCGCGCGACA---AAAC	1500
QY	2504	CCCCCGGACAGCACTCAAGTTTGAACGCGACGACGACACTACCTGATCAACGATGT	2563
Db	1501	CGACATAGACCATCACTTCCGTTTCCATCGTACCAACGCGAGTGGCGCATCAACGGCAT	1560

QY	2564	TGGCTTTGCCGATGTCAATGAGCGTGTCTCGCCAAAGCCCGAGCTCGGCACCGCTTGAGGT	2623
Db	1561	CGGGTTTTTCAGACGTCGAGAACCGTGTCTTGGCCAAAGGTACCGCGGGTACTGTCGAGCT	1620
QY	2624	CTGGGAGCTCGAGAACTCCTCTTGAGGCTGGAGGCCACCCCGTCCACATTCACCTTGTGTA	2683
Db	1621	TTGGGAACCTTGAGAACAGCTCCGGCGGCTGGTTCACACCCCATCCACGTCACCTAGTAGA	1680
QY	2684	CTTCAAGATCCTCAAGCGAACTGG-----TGGTGTGGCGAGGTTCATGCCCTTACGAGTC	2737
Db	1681	CTTCCGAGTCTGCGACGCTACGGCGACGAAGGCACTCGCGGGCTCATGCCCTATGAGGC	1740
QY	2738	TGCTGGTCTTAAGGATGTCGTGTGGTGGCGAGGGTGAGACCTTGACCATCGAGGCCCA	2797
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QY	2858	CGACATGATGGCTGTATTCAACGTCACCGCCATGGAGGAGAAAGGATATCTTCAGAG--	2915
Db	1861	AGACATGATGGCGCGCTTTCGACGTGACTAAACTCCAGAACTTTGGGTACAACGAGACG	1920
QY	2916	-GACTTCGAGGACCCATGAACCCCAAGTGGCGGCGTTCCTTTACAACCGCAACGACTT	2974
Db	1921	TGATTTCCACGATCTCGAGGATCTTCGCTGGTGTCAAGAAGACTTTTACCGGGGTGATCT	1980
QY	2975	CCATGCTCGCGCTGGAAACTTCTCCGCGAGTCCATCACTGCCGAGTGCGAGGCTGGC	3034
Db	1981	CACGCGCGATCGGGTATCTTTTCAGAGAATCCATCAGGGCTAGAGTAATGATTTGGC	2040
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RESULT 6			
AR211557			
LOCUS	AR211557	2063 bp	DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 6 from patent US 6399329.		
ACCESSION	AR211557		
VERSION	AR211557.1 GI:21514910		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2063)		
AUTHORS	Wang, H. and Bodie, E.A.		
TITLE	Phenol oxidizing enzymes		
JOURNAL	Patent: US 6399329-A 6 04-JUN-2002;		
FEATURES	Location/Qualifiers		
source	1..2063		
BASE COUNT	501 a	604 c	510 g 448 t
ORIGIN			
Query Match 12.4%; Score 455.6; DB 6; Length 2063;			
Best Local Similarity 59.1%; Pred. No. 1.7e-102;			
Matches 971; Conservative 0; Mismatches 544; Indels 129; Gaps 6;			
QY	1501	CAGATTATCCCACTTGGCGCCTGCCACTCTCGTCGGCTAGGATGGCATGAGCCCTGGT	1560
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Db	436	CCTACGATCATCGTCCGAGAGAACAGAGCCGTGTACGATTCTGTAAACACCGGTGAT	495
QY	1621	GTGGAGAACTCGGTCATCTGCACGGCTCCCATCGCTGCCCTTTTCGATGGTGGGCT	1680
Db	496	CGCGAGAGTTTCGATTTCATGTTTCTCCCTCCCGTGGCCCTTTGACGGATGGGCT	555

Qy	1681	GAAGATGTGACCTTCCCTGGCGAGGTACAAGAT-----	1713
Db	556	GAAGATTTGATATGAGAGGCCAATTCARAGGTACACAGACAAATCTTATGCAATCAGG	615
Qy	1714	-----TACTACTTTTCCCACTACCAATCCG	1738
Db	616	TGCGCTCTTTTATAACACGACGCTGTTCTTAGACTACTACTACCCGAACAACAGGCTG	675
Qy	1739	CCGCGCTTCTGTGTACCATGACCAACGCT-TTCATGAAGGTATGTACGAGGCTTTATCT	1797
Db	676	CCAGATTCCTGTGTGTACCAACGATCATGCTATGCTATGTTGAAGTCTTGCAGACTAATCAT	735
Qy	1798	TTCTTTGGCTACCTTTGGCTAACCAACTTCTTTCGTAGACTGCTGAGAACTGCTACTTTG	1857
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Qy	1858	GTCAGGCTGGGCGCTTACATTTATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTTAGTG	1917
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Qy	1918	GCTATGGCGAGTTGATATCCCTCTGATCCTGACGGCCAAAGTACTATTAACGCCGATGGTA	1977
Db	856	GTTACGGAATAATACGACATCCCACTGGTGCCTCAGTTCCAAAGTTCTACAAACAGTATGGA	915
Qy	1978	CCCTCGCTTCGACCGAGGCTGAGGACAGGACCTCTGTGGGAGATGCTATCCATGTCAACG	2037
Db	916	CTCTCAGACCAAGTGTGGGAGAAGACACAGTCTCTGGGCGAGCTATCCATGTCAACG	975
Qy	2038	GACAGCCTAGGCTTTTCCCTTAACGTCACGCGCCGCAAGTACCGTTTCCGATTTCCCTCAAG	2097
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Qy	2158	TTCTTTTCAAGTCAATGCTCTGATGCTGCTCTTCAAGCCCGCTTCAAGCCCGCTTCAAGCTCTA	2217
Db	1096	TTCTTTTCCAGGTCAATGCTCTGATGAGGCTACTCAGCACCCTGCTCCAAACCTCAG	1155
Qy	2218	ACCTCTACCTTTGCTTTGCCGAGCTTACGAGATCATTTATGTTATGCCCTTCCCTCTCA	2277
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Qy	2398	GCACCTCTCAGGTGATGCGCTTCTGCTGAGCTTGGCACTTGGAGGACAAACAGCCAGG	2457
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Qy	2458	TCCCTCTCACTCTCCGTGACGTTTCTTCCCTCTCACHAGGAAGGCCCGCCGACACAAGC	2517
Db	1342	TACCGCGACAGTATCTCAGATCCAGTTTCCCGCGCAGACA---AAACCGGCATTCGACACC	1398
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Qy	2578	TCAATGAGCGTCTCTGGCCAAAGCCGAGCTCGGACCCGTTGAGGTCTGGGAGCTCGAGA	2637
Db	1459	TCCAGAACCGTATCTTGCCAAAGTACCGCGGCGACTGTCGAGCTATGGGAACCTCAGA	1518
Qy	2638	ACTCTCTGGAGGCTGGAGCCACCGCTCCACATTCACCTTTGTTGACTTCAGATTCCTCA	2697
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QY 2698 AGGAACTGGTG-----CTCGTGGCCAGGTCATGCCCTACGAGTCTGCTGCTTAAAGG 2751
Db 1579 CAGCGTACGGTGACGAAACACTCGCGCGGTCATGCCCTACGAGTCCGCGCTCAAGG 1638
QY 2752 ATGCTGCTCTGGTGGCCAGGGTGAGACCTGACCATCGAGGCCCACTACCAACCTCGA 2811
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QY 2929 CCATGAACCCCAAGTGGCGCGGTCCTTTACAAACCGCAACGACTTCCATGCTCGCGTG 2988
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QY 2989 GAACTTCTCCGCGGAGTCCATCACTGCGCGGAGTGCGAGGATGGCCGAGGAGCGCT 3048
Db 1879 GTATCTTCTCAGAAGCATCCATCAGGCTAGAGTGAACGAGTTGGCGCTGGAACAGCCGT 1938
QY 3049 ACAACCGCTCGATGATGATCTGG 3072
Db 1939 ACAGCGAACTGGCACAGGTACCGG 1962

RESULT 7
MYRBOR MYRBOR 1942 bp mRNA linear PLN 01-FEB-2000
LOCUS M. verrucaria mRNA for bilirubin oxidase, complete cds.
DEFINITION D12579
ACCESSION D12579.1 GI:456711
VERSION bilirubin oxidase.
KEYWORDS Myrothecium verrucaria (strain:MT-1) cDNA to mRNA.
SOURCE Myrothecium verrucaria
ORGANISM Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.
REFERENCE 1 (bases 1 to 1942)
AUTHORS Koikeda,S., Ando,K., Kaji,H., Inoue,T., Murao,S., Takeuchi,K. and Samejima,T.
TITLE Molecular cloning of the gene for bilirubin oxidase from Myrothecium verrucaria and its expression in yeast
JOURNAL J. Biol. Chem. 268 (25), 18801-18809 (1993)
MEDLINE 93366794
REFERENCE 2 (bases 1 to 1942)
AUTHORS Ando,K.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1992) Kelichi Ando, Amano Pharmaceutical Co., Ltd., Tsukuba Research Laboratories; 22 Miyukigaoka, Tsukuba, Ibaragi 305, Japan (Tel:0298-56-5026, Fax:0298-56-5012)
COMMENT On Feb 26, 1994 this sequence version replaced gi:436235.
Submitted (07-JUL-1992) to DDBJ by:
Kelichi Ando
Tsukuba Research Laboratories
Amano Pharmaceutical Co., Ltd.
22 Miyukigaoka
Tsukuba
Ibaragi 305
Japan
Phone: 0298-56-5026
Fax: 0298-56-5012.

FEATURES
source
1. .1942
/organism="Myrothecium verrucaria"
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Query Match 10.4%; Score 382.6; DB 8; Length 1942;
Best Local Similarity 57.5%; Pred. No. 2.9e-84;
Matches 907; Conservative 0; Mismatches 539; Indels 131; Gaps 7;
QY 1501 CAGATTTACCCACCTTGGCCCTGCCACTCTCGTCCGCTACGATGGCATGAGCCCTGGT 1560
Db 324 CAGGTTTACCCCTGACCTTGGATCCGCTGATCGTGGGTATGATGAATGTCTCTGGC 383
QY 1561 CCTACTTTCAATGTTCCAGAGAGACAGACTGTAGTTAGTTGTTTCATCAACATGCCACC 1620
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QY 1621 GTGGAGAACTCGGTCCATCTGCACGCTCCCATCCGCTGCCCTTTTCGATGGTTGGGT 1680
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Db 598 -----TCACTGCTGAGACGCTACCGTGGCC 624
QY 1861 AGGCTGGCCCTTACATTAACAAGAGAGGCTGAGGATGCTCTCGGTCTTCTTAGTGGCT 1920
Db 625 AGGCTGGTCTCTACATGCTGCTGACCCAGCGAAGACGCTCTCAACTTTGCCAAGTGGAT 684
QY 1921 ATGGCGAGTTCGATATCCCTCTGATCCTCAGCGCAAGTACTATACGCGGATGGTACCC 1980
Db 685 ATGGCGAGTTCGATATTCCAATGATCCTCACGTCGAAGCAATATACCGCAACGGCAACT 744
QY 1981 TGGCTTCGACCCGAGGCTGAGGACAGGACCTGTGGGAGATGTCATCCATGTCACCGGAC 2040
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QY 2041 AGCCATGGCTTTTCTTTAACGTCCAGCCCGCGAAGTACGTTTCCGATTTCCCAACGCTG 2100
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QY 2101 CCGTGTCTGCTTGGCTCTCTACCTCGTCAGGACAGCTCTCCCAAGGTCAGAAATTC 2160
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Db 925 CTTTCAAGGTTATTGCCCTCCGATTCTGGTCTTCTTGAACACCTCGCGGATACCAAGTTCG 984
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[illegible]

[illegible]

RESULT 9				
LOCUS	AR122996			
DEFINITION	Sequence 1 from patent US 6168936.		1958 bp	DNA
ACCESSION	AR122996			
VERSION	AR122996.1			
KEYWORDS	. GI:14107962			
SOURCE	Unknown.			
ORGANISM	Unknown.			
			linear	PAT 16-MAY-2001

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Db 1163 GTGCTGACGGTCTCGGTTTGAGCTGAGTTGTATGAACACTGACAAAGTATCATGCGATTTCG 1222

Qy 2422 TCGTCAGCTCTGGCAGCTGTTGAG---GACAACAGCCAGGTCCTCCACTCTCCGTGACG 2478

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Qy 2479 TTCCTTTCCCTCTACAAGAAAGCCCGCCGACAAGCAC-----TTCA 2523

Db 1283 TTCCTTTCCCGAGGGCGGAACCTGGGACCCCGCAACCCCACTGATGACGAGACTTTCA 1342

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Qy 2584 AGCGTCTCTGGCCAGCCGAGCTCGCAGCTTGAGGTCGGGAGCTCGAGACTCCT 2643

Db 1403 ACCGTCCTCGCAATGTGCCCGCGACACTGTGTAGATCTGGCGACTTGAGAACAACT 1462

Qy 2644 CTGGAGGCTGGAGCACCCCGTCCACATTCACCTTGTGTGACTTCAAGATCTCAAGCGAA 2703

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Db 1700 CTGCCACAACCTGATCCAGGAGGACACGACATGATGCTGCTTTCAATGTCACTGTTCT 1759

Qy 2891 GGAGGAGAGGATATCTTCAGGAGACTTCAGAGACCCCATGAACCCCAAGTGGCGCC 2950

Db 1760 CGGTGACTATGGCTACAACCTACACCGAGTTCAATTGACCCCATGGAGCCTCTCTGGAGGCC 1819

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RESULT 10

AX101096

LOCUS AX101096 1958 bp DNA linear PAT 10-APR-2001

DEFINITION Sequence 1 from Patent WO0121809.

ACCESSION AX101096

VERSION AX101096.1 GI:13619951

KEYWORDS Stachybotrys chartarum.

SOURCE Stachybotrys chartarum

ORGANISM Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.

REFERENCE 1 (bases 1 to 1958)

AUTHORS Wang,H.

TITLE Stachybotrys phenol oxidizing enzyme

Patent: WO 0121809-A 1 29-MAR-2001;

JOURNAL

GENENCOR INTERNATIONAL, INC. (US)

Location/Qualifiers

1. .1958

/organism="Stachybotrys chartarum"

/db_xref="taxon:74722"

BASE COUNT 394 a 593 c 490 g 481 t

ORIGIN

Query Match 8.2%; Score 300.4; DB 6; Length 1958;

Best Local Similarity 55.2%; Pred. No. 9.6e-64;

Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;

Qy 1491 CTGACCCCTTCAGATTTACCCACCTTCGCGCCCTGCCACTCTCGTCGCTACGATGGCAT 1550

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Qy 1551 GAGCCCTGGTCTCACTTTCAATGTTCCAGAGAAACAGAGACTGTAGTTAGTTCATCAA 1610

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Db 496 CTTTGTATGGTTGGCTGAGGACACTACCCAGCGCTGGCGAGTACAAGGATTACTACTACC 555

Qy 1725 CAACTACCAATCCGCGCCCTTCTGTGTGATCATGACCAACGCTTTTCATGAAGGTATGCTA 1784

Db 556 CAACAGGAGGCTGCCCGCATGCTTTGGTACCATGACCATGTC----- 597

Qy 1785 CGAGCTTTTATCTTTCTTGGCTACCTTTTGGTTAACAACTTTCCTTTGCTAGACTGCTGAG 1844

Db 598 -----CATGCTCCATCACCGCCGAG 616

Qy 1845 AATGCTACTTTGTCAGGCTGGCGCCCTACATTTACAACGAGGAGGCTCAGGATGCTCTC 1904

Db 617 AACGCTACATGGGTGAGGCTGGTGTCTACATGATCCAGGACCCGGCTGAGATGCCCTG 676

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LOCUS AX108672 1958 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1 from Patent WO0121748.
ACCESSION AX108672
VERSION AX108672.1 GI:13923900
KEYWORDS
SOURCE Stachybotrys chartarum.
ORGANISM Stachybotrys chartarum
REFERENCE Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.
AUTHORS 1 (bases 1 to 1958)
TITLES Convents,D.U., Doornink,M.U., de Vries,C.H. and Wang,H.
Detergent compositions comprising phenol oxidizing enzymes
JOURNAL Patent: WO 0121748-A 1 29-MAR-2001;
FEATURES Location/Qualifiers
1..1958
/organism="Stachybotrys chartarum"

BASE COUNT 394 a 593 c 490 g 481 t
ORIGIN
Query Match 8.2%; Score 300.4; DB 6; Length 1958;
Best Local Similarity 55.2%; Pred. No. 9.6e-64;
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RESULT 12
AX456852
LOCUS AX456852 1958 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 1 from Patent WO0220711.
ACCESSION AX456852
VERSION AX456852.1 GI:21715723
KEYWORDS stachybotrys chartarum.
SOURCE Stachybotrys chartarum
ORGANISM Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.
REFERENCE 1
AUTHORS Aehle,W., Convents,D., Doornink,M., van Gastel,F., Rodriguez,A.M., Topozada,A., de Vries,C.H. and Wang,H.
TITLE Detergent compositions comprising phenol oxidizing enzymes
JOURNAL Patent: WO 0220711-A 1 14-MAR-2002;
UNILEVER PLC (GB); LEVER HINDUSTAN LTD (IN); UNILEVER NV (NL)
FEATURES
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1..1958
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BASE COUNT 394 a 593 c 490 g 481 t

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Query Match 8.2%; Score 300.4; DB 6; Length 1958;
Best Local Similarity 55.2%; Pred. No. 9.6e-64;
Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;
Qy 1491 CTGACCCTTTTTCAGATTTTACCACCACCTTGGCCCTGCCACTCTCTCGTCGGCTACGATGGCAT 1550
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ACCESSION	ARL122997			
VERSION	ARL122997.1			
KEYWORDS	GI:14107963			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 2095)			
TITLE	Phenol oxidizing enzymes			
JOURNAL	Patent: US 6168936-A 3 02-JAN-2001;			
FEATURES	Location/Qualifiers			
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ORIGIN	/organism="unknown"			
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RESULT 14
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LOCUS Sequence 3 from Patent WO0121809.
DEFINITION AX101098
ACCESSION AX101098
VERSION AX101098.1 GI:13619952
KEYWORDS Stachybotrys chartarum.
SOURCE Stachybotrys chartarum
ORGANISM Stachybotrys chartarum
REFERENCE Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.
1 (bases 1 to 2095)
AUTHORS Wang,H.
TITLE Stachybotrys phenol oxidizing enzyme
JOURNAL Patent: WO 0121809-A 3 29-MAR-2001;
GENECOR INTERNATIONAL, INC. (US)
FEATURES Location/Qualifiers
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BASE COUNT 437 a 618 c 510 g 530 t
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Best Local Similarity 55.2%; Pred. No. 9.6e-64;
Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;

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RESULT	15		
AX108674			
LOCUS	AX108674	2095 bp	DNA
DEFINITION	Sequence 3 from Patent WO0121748.		linear
ACCESSION	AX108674		
VERSION	AX108674.1	GI:13923901	
KEYWORDS	Stachybotrys chartarum.		
SOURCE	Stachybotrys chartarum.		
ORGANISM	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys		
REFERENCE	1 (bases 1 to 2095)		
AUTHORS	Convents,D.U., Doornink,M.U., de Vries,C.H. and Wang,H.		
TITLE	Detergent compositions comprising phenol oxidizing enzymes		
JOURNAL	Patent: WO 0121748-A 3 29-MAR-2001;		
FEATURES	Location/Qualifiers		
source	1..2095		
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BASE COUNT	437 a 618 c 510 g 530 t		
ORIGIN			
Query Match	8.2%;	Score 300.4;	DB 6;
Best Local Similarity	55.2%;	Pred.No. 9.6e-64;	Length 2095;
Matches	957;	Conservative 0;	Mismatches 501;
		Indels 276;	Gaps
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Db	440	GTCCCAGGACCTACCATCATCTGTTCCCTGGCCACTGAGAGTGTTGTCCCGCTTCGTGGAA	499
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Db	500	CAGCGGAGAGAACACTCTCCCAACAGCGTCCACTTTGCACAGCTCTTTCTCTCGAGCTCC	559
Qy	1665	TTTCGATGGTTGGCTGAAGATGTGACTTTCCTGGCGAGTACAAGGATTACTACTTTC	1724
Db	560	CTTTGATGGTTGGCTGAGACACTACCCAGCGCTGGCGAGTACAAGGATTACTACTACCC	619
Qy	1725	CAACTACCAATCGCGCGCTCTGTGGTACCATGACCAAGCTTTTCATGAAGGTATGCTA	1784
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Qy	1785	CGAGCCTTATCTTTCTTGCTACCTTTGGCTAACCAACTTCCTTTTCGTAGACTGCTGAG	1844
Db	662	-----CATGTCNATCAGCGCCGAG	680
Qy	1845	AATGCCACTTTTGGTCAGGCTGGCGCTACATTAATCAACGAGGCTGAGAGTCTCTC	1904
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Qy	1905	GGTCTTCCTAGTGGCTATGCGAGTTTCGATATCCCTCTGATCCTCAGCGCCAACTACTAT	1964
Db	741	AACCTCCCCAGCGCTACGCGGAGTTTGATATCCCTTTGGTTCTGACTGCCAAGCATAC	800
Qy	1965	AACCGCATGTCACCTTGCCTTCGACCGAGGGTGAGGACAGGACTCTGGGAGATGTC	2024
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Qy	2062	TCCAGCCCGCAAGTACCGCTTTCGGATTCTCCTCAACGCTCCGCTGTCTCGTCTTGGCTCC	2121
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Qy	2122	TCTACCTCTGCAGGACCAAGCTCTCCCAAGCTCAGAAATTCCTTTTCCAAGTCAATGCCTCTG	2181
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Qy	2182	ATGCTGCTCTCCTTCAAGCCCCGTTCAAGACCTCTAACCTCTACCTTCTGTTGGCCGAGC	2241
Db	1101	ACGTTGCTCTGCTTGAGGGCCCTTGTGACACTGACACTCTGTACATCTCTATGGCCGAGC	1160
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Qy 2584 AGCETGTCTCTGGCCAAAGCCCGAGCTCGGCACCGTTGAGGCTCTGGAGCTCGAGAATCCT 2643
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Db 1704 CCTTTTACCTAACTGGTTTTCACCTCATGCTAACATCTACAAGTGGTGTCTACATGTTGCA 1763
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Qy 2831 CTGTCACAACTCATTCACGAGGATACGACATGATGGCTGTATTCACGTCACCGCCAT 2890
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Db 1944 CACTGACCGCATTCAGGAGATGGCTAGCTTCAACCCCTACGCCCGAGGCTGATGA 1997
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Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	3676.6	100.0	3677	21	AAA50018		Stachybotrys chart
2	3676.6	100.0	3677	21	AAA51313		Stachybotrys chart
3	3676.6	100.0	3677	24	AAU47582		S chartarum phenol
4	3675.8	100.0	3677	20	AAZ27602		Stachybotrys pheno
5	3664.6	99.7	3676	20	AAZ25728		Stachybotrys chart
6	2034	55.9	2067	20	AAZ25735		Stachybotrys chart
7	2034	55.9	2067	20	AAZ27609		Stachybotrys pheno
8	1474.6	40.1	7248	24	AAZ92911		Stachybotrys chart
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Key	Location/Qualifiers
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PD			
XX	20-DEC-1999;	99WO-EPI0287.	
XX			
PR	23-DEC-1998;	98US-0220871.	
PR	23-JUN-1999;	99US-0338723.	
XX			
PA	(UNIL) UNILEVER NV.		
PA	(UNIL) UNILEVER PLC.		
PA	(HIND-) HINDUSTAN LEVER LTD.		
XX			
PI	Bodie EA, Van Der Velden S, De Vries CH, Wang H;		
XX			
DR	WPI; 2000-514528/46.		
DR	P-PSDB; AAY95537.		
XX			
PT	Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria,		
PT	useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition -		
XX			
PS	Claim 1; Fig 1A-B; 45pp; English.		
XX			
CC	The present sequence is that of the Stachybotrys chartarum MUCL 38898 phenol oxidising enzyme gene, including promoter and terminator sequences. The gene was isolated from genomic DNA using primers (see AA50023-24) based on isolated peptides of the enzyme. The gene codes for a 594-amino acid protein (see AAY95537). The invention relates to detergent compositions comprising novel phenol oxidising enzymes that are encoded by nucleic acids capable of hybridizing to the present DNA sequence, provided the enzymes are capable of modifying the colour associated with dyes or coloured compounds, and are produced from a bacterium, yeast or fungus (see AAY95538-40). The phenol oxidising enzymes can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. They may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidising enzyme, methods for producing the phenol oxidising enzyme, and methods for constructing expression hosts are provided.		
XX			
SQ	Sequence 3677 BP; 822 A; 1057 C; 849 G; 948 T; 1 other;		
	Query Match	100.0%; Score 3676.6; DB 21; Length 3677;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 3677; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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Qy	61 AGTCAATATCTTGTCCTACTGCTTAAGTTCCTCTAGCGCAAAAAGCTCCTTGCCCAA	120	
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Qy	121 GGGGCACAGACTATCAAGTGTAGACATATAGGATGCATGCTCTTTCATAGCCACAGTTAGGG	180	
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Db 1861 AGGCTGGCGCTACATATATCAACAGAGGCTGAGGATGCTCTCGGCTTCCTAGTGGCT 1920
Qy 1921 ATGGCGAGTTCCGATATCCCTCTGATCTGACGGCCAACTACTATAACGCCCATGGTACCC 1980
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Qy 3661 AACTGACCTGGGTCAAT 3677
Db 3661 AACTGACCTGGGTCAAT 3677

RESULT 2
AAA51313
ID AAA51313 standard; DNA; 3677 BP.
XX
AC AAA51313;
XX
DT 09-OCT-2000 (first entry)
XX
XX Stachybotrys chartarum phenol oxidizing enzyme genomic DNA.
XX Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
KW pulp; paper bleaching; ds.
XX Stachybotrys chartarum.
OS
XX
XX Key Location/Qualifiers
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FT CDS /*tag= a
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FT exon 2314..3095
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FT /partial
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PN WO200037654-A2.
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XX 29-JUN-2000.
XX
XX 20-DEC-1999; 99WO-US311009.
XX
XX 23-DEC-1998; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.
XX
XX (GENM) GENENCOR INT INC.
XX
XX Wang H, Bodle EA;
XX
XX WPI; 2000-452191/39.
DR

DR P-PSDB; AAY96761.
XX
XX New phenol oxidizing enzyme for modifying colors associated with dyes
PT or colored compounds, is obtained from fungus and is encoded by a
PT nucleic acid comprising a specific nucleotide sequence
XX
XX Claim 10; Fig 1A-B; 45pp; English.
XX
XX This genomic DNA encodes Stachybotrys chartarum phenol oxidizing enzyme.
CC Phenol oxidizing enzymes encoded by nucleic acid sequences which
CC hybridize to this DNA are claimed, as long as the enzyme is capable of
CC modifying the colour associated with dyes or coloured compounds. The
CC enzymes are useful in detergent compositions and for modifying colors
CC associated with dyes or colored compounds which occur in stains in a
CC sample. The enzymes are also useful for pulp and paper bleaching,
CC anti-dye transfer in detergent and other textile applications.
XX
XX Sequence 3677 BP; 822 A; 1057 C; 849 G; 948 T; 1 other;
SQ

Query Match 100.0%; Score 3676.6; DB 21; Length 3677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 AGTCAATATCTTGGTCACTGCTAATAGTTCTTCTGAGCGCAAAAAGCTCTTGGCCGAA 120

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Db 181 TGGTGACCTACTCGAAGAGGCCCGGACTTGCATGCATACGACATGTCGCTTCCATGCAAC 240

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Db 1021 ACTCTTCCCTTTTTCGTCATATGCTTCAAGTCAATGCACTGSCAGCAGCCCTCCG 1080
QY 1081 GGCTCCTGTCTGGAGTCTTCGGCATCCGATGGACACGGGACGCCACCCCATAGGCGTG 1140
Db 1081 GGCTCCTGTCTGGAGTCTTCGGCATCCGATGGACACGGGACGCCACCCCATAGGCGTG 1140
QY 1141 TTGATCCGGAAGTGAAGACTCAGGTCTTCGCTGACTCCCTCTTTCGTCAGCAGCGCATG 1200
Db 1141 TTGATCCGGAAGTGAAGACTCAGGTCTTCGCTGACTCCCTCTTTCGTCAGCAGCGCATG 1200
QY 1201 ACGACTGGAGTCACTCCATACAACTTGCCTTACAGGTGAGACACCTGTCCCACTGTT 1260
Db 1201 ACGACTGGAGTCACTCCATACAACTTGCCTTACAGGTGAGACACCTGTCCCACTGTT 1260
QY 1261 TTCCTCGATAACTTCTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGGCCA 1320
Db 1261 TTCCTCGATAACTTCTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGGCCA 1320
QY 1321 AGATGTATGCTTTTGTATTTCTACGAAGCAACTCGGCCCGGACTTAATGTATTTAGGATC 1380
Db 1321 AGATGTATGCTTTTGTATTTCTACGAAGCAACTCGGCCCGGACTTAATGTATTTAGGATC 1380
QY 1381 ATTACCAACCTGTACCGGCAAGACATTTGGTACTATGAGATCGAGATCAAGCCATTT 1440
Db 1381 ATTACCAACCTGTACCGGCAAGACATTTGGTACTATGAGATCGAGATCAAGCCATTT 1440
QY 1441 CAGCAAGGGTGAGTTGCTCAGAAACCTTGTGGTAAATTAATCATTTACTGACCCCTTT 1500
Db 1441 CAGCAAGGGTGAGTTGCTCAGAAACCTTGTGGTAAATTAATCATTTACTGACCCCTTT 1500
QY 1501 CAGATTTACCCCACTTCGCGCCCTGCCACTCTCTCGGCTACGATGCGATGCGCCCTGGT 1560
Db 1501 CAGATTTACCCCACTTCGCGCCCTGCCACTCTCTCGGCTACGATGCGATGCGCCCTGGT 1560
QY 1561 CCTACTTTCAATGTTCCAGAGGAACAGAGACTAGTTAGTTTTCATCAACAATGCCACC 1620
Db 1561 CCTACTTTCAATGTTCCAGAGGAACAGAGACTAGTTAGTTTTCATCAACAATGCCACC 1620
QY 1621 GTGAGAACTCGGTCATCTGCACGGCTCCCCATCGCGTGCGCCCTTTTCGATGGTGGGCT 1680

Db 1621 GTGAGAACTCGGTCATCTGCACGGCTCCCATCGCGTGCCCTTTTCGATGGTGGGCT 1680
QY 1681 GAAGATGTGACCTTCCCTGGCGAGTACAAGATTACTACTTTTCCCAACTACCAATCCGCC 1740
Db 1681 GAAGATGTGACCTTCCCTGGCGAGTACAAGATTACTACTTTTCCCAACTACCAATCCGCC 1740
QY 1741 CGCCTTCTGTGGTACCATGACCAAGCTTTTCAAGAGTATGCTACGAGCCCTTATCTTTTC 1800
Db 1741 CGCCTTCTGTGGTACCATGACCAAGCTTTTCAAGAGTATGCTACGAGCCCTTATCTTTTC 1800
QY 1801 TTGGCTACCTTTGGCTAACCAACTTCTTTTCTGAGACTGCTGAGAAATGCTTGGTC 1860
Db 1801 TTGGCTACCTTTGGCTAACCAACTTCTTTTCTGAGACTGCTGAGAAATGCTTGGTC 1860
QY 1861 AGGCTGGCGCCTACATTAATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTACTGGCT 1920
Db 1861 AGGCTGGCGCCTACATTAATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTACTGGCT 1920
QY 1921 ATGCGAGTTTCGATATCCCTCTGATCTCTGACGGCAAGTACTATAACGCCGATGGTACCC 1980
Db 1921 ATGCGAGTTTCGATATCCCTCTGATCTCTGACGGCAAGTACTATAACGCCGATGGTACCC 1980
QY 1981 TGCCTTCGACCGAGGTCAGGACGAGGACCTGTGGGAGATGTATCATGATCAAGGAC 2040
Db 1981 TGCCTTCGACCGAGGTCAGGACGAGGACCTGTGGGAGATGTATCATGATCAAGGAC 2040
QY 2041 AGCCATGGCCTTTCTTAACGTCCAGCCCCCAAGTACCGTTTCCGATTTCTTCAACGGTG 2100
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Db 2101 CCGTGTCTCGTGTGGCTCTCTACCTCTGTCAGGACAGCTCTCCCAACGTCAAGATTC 2160
QY 2161 CTTTCCAAAGTCAATTCGCTCTGATGCTGTGCTCTCTTCAAGCCCCCGTTTCCAGACCTTAACC 2220
Db 2161 CTTTCCAAAGTCAATTCGCTCTGATGCTGTGCTCTCTTCAAGCCCCCGTTTCCAGACCTTAACC 2220
QY 2221 TCTACCTTGTCTTGGCGAGGCTTACGAGATCATTTATTTGGTATGCCCCCTCTTCAAGCA 2280
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QY 2281 ATGAGTCAAGAACTCTAAGACTTAACACTTTAGACTTTACCAAACTTTGCTGGCCAGACTC 2340
Db 2281 ATGAGTCAAGAACTCTAAGACTTAACACTTTAGACTTTACCAAACTTTGCTGGCCAGACTC 2340
QY 2341 TTGACCTGCGCAACGTTCTGAGACCAACGATGTGCGGACGAGGATGAGTACGCTCGCA 2400
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QY 2401 CTCTCGAGGTGATGGCTTTCGTCGTCAGCTCTGGCAGCTGTTGAGGACAACAGCCAGGTCC 2460
Db 2401 CTCTCGAGGTGATGGCTTTCGTCGTCAGCTCTGGCAGCTGTTGAGGACAACAGCCAGGTCC 2460
QY 2461 CCTCCACTCTCCGTGAGCTTCTTCCCTCTCAAGAAAGGCCCGCCGACAGCACT 2520
Db 2461 CCTCCACTCTCCGTGAGCTTCTTCCCTCTCAAGAAAGGCCCGCCGACAGCACT 2520
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Db 2521 TCAAGTTTGAACGAGCAACCGACACTACCTGATCAACGATGTTGGCTTTGCGGATGTCA 2580
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Db 2641 CCTCTGGAGGCTGGAGCCACCCCGTCCACATTCACCTTTGTTGACTTCAAGATCTCTCAAGC 2700
QY 2701 GAACTGGTGTGTCGGCAGGTCATGCCCTACGAGTCTGCTGGCTTAAAGATGTCGTCT 2760
Db 2701 GAACTGGTGTGTCGGCAGGTCATGCCCTACGAGTCTGCTGGCTTAAAGATGTCGTCT 2760

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Db 2701 GAACCTGGTGTGTCGTGGCCAGGCTCATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCGTCT 2760
Qy 2761 GGTGGGCGAGGGTGAGACCTCGACCTACCAATCGAGGCCCTACTACCAACCTGGAGCTGAGCTT 2820
Db 2761 GGTGGGCGAGGGTGAGACCTCGACCTACCAATCGAGGCCCTACTACCAACCTGGAGCTGAGCTT 2820
Qy 2821 ACATGTGCACTGTGCACAACTCTTACGAGGATGAGAGGATGAGAGGATGAGAGGATGAGAGG 2880
Db 2821 ACATGTGCACTGTGCACAACTCTTACGAGGATGAGAGGATGAGAGGATGAGAGGATGAGAGG 2880
Qy 2881 TCACGGCATGGAGAGGAGGATGATCTTCAGAGGAGCTTCGAGAGCCCATGAACCCCA 2940
Db 2881 TCACGGCATGGAGAGGAGGATGATCTTCAGAGGAGCTTCGAGAGCCCATGAACCCCA 2940
Qy 2941 AGTGGCGCGCTTCTTACAAACGACACGACTTCCATGCTCGCGCTGGAAACTTCTCCG 3000
Db 2941 AGTGGCGCGCTTCTTACAAACGACACGACTTCCATGCTCGCGCTGGAAACTTCTCCG 3000
Qy 3001 CCGAGTCCATCAGTCCCGAGTGGAGGAGTGGCGGAGCAGGAGCCGTACAAACCGCCCTCG 3060
Db 3001 CCGAGTCCATCAGTCCCGAGTGGAGGAGTGGCGGAGCAGGAGCCGTACAAACCGCCCTCG 3060
Qy 3061 ATGAGATCCTGGAGATCTTGGAAATCGAGGAGTAAACCCCGAGGACCAAGCTCTACAATC 3120
Db 3061 ATGAGATCCTGGAGATCTTGGAAATCGAGGAGTAAACCCCGAGGACCAAGCTCTACAATC 3120
Qy 3121 GTTTTGAGTCTTAAGACGAGGCTCTGGTGGGTATCTTTTCTTCCCTACGGGAACTCC 3180
Db 3121 GTTTTGAGTCTTAAGACGAGGCTCTGGTGGGTATCTTTTCTTCCCTACGGGAACTCC 3180
Qy 3181 GCTGTCCACTCGGATGTGAAGGACCATCACAAAGCAGTATATATTTGGACTCACCACTG 3240
Db 3181 GCTGTCCACTCGGATGTGAAGGACCATCACAAAGCAGTATATATTTGGACTCACCACTG 3240
Qy 3241 TCATTACGCCCACTGTGACCTATTGATCTTCTGTTCAAACTTTCTAGTGGGAGAGTGT 3300
Db 3241 TCATTACGCCCACTGTGACCTATTGATCTTCTGTTCAAACTTTCTAGTGGGAGAGTGT 3300
Qy 3301 CCATAGTCAAGAAACGCCCATAGGCTATCGTCTAACTGAACCTATTGTGGTCTGTGA 3360
Db 3301 CCATAGTCAAGAAACGCCCATAGGCTATCGTCTAACTGAACCTATTGTGGTCTGTGA 3360
Qy 3361 CGTGAGCTAGATGTCAATGTGATGAGACACAGTAAATACCGGTATATCTTTTCTTAGGAC 3420
Db 3361 CGTGAGCTAGATGTCAATGTGATGAGACACAGTAAATACCGGTATATCTTTTCTTAGGAC 3420
Qy 3421 TACAGGATCAGTTTCTCATGAGATTTACATCCGTCATATGTTTGTCCATGAGAGTCTAGCT 3480
Db 3421 TACAGGATCAGTTTCTCATGAGATTTACATCCGTCATATGTTTGTCCATGAGAGTCTAGCT 3480
Qy 3481 AAGGTTGAGATGATCAGACGGGAATCAATTTGATGCTCTCAGCTCGATTACCGATGTAA 3540
Db 3481 AAGGTTGAGATGATCAGACGGGAATCAATTTGATGCTCTCAGCTCGATTACCGATGTAA 3540
Qy 3541 GACAAGTTAGTAAAGTTGCTTGGTATCCGAAATGACTTCAGGCTCCCTCATTTAGGTTGCA 3600
Db 3541 GACAAGTTAGTAAAGTTGCTTGGTATCCGAAATGACTTCAGGCTCCCTCATTTAGGTTGCA 3600
Qy 3601 TGTGAAACCTTCAGCAACTCATGGGTGTTGGGACCAAAATCATCCATACCTGATTTGAT 3660
Db 3601 TGTGAAACCTTCAGCAACTCATGGGTGTTGGGACCAAAATCATCCATACCTGATTTGAT 3660
Qy 3661 AACTGACCTGGGTCAAT 3677
Db 3661 AACTGACCTGGGTCAAT 3677
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RESULT 5
AAZ25728
ID AAZ25728 standard; DNA; 3676 BP.
XX
AC AAZ25728;
XX

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05-JAN-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidising enzyme genomic DNA.
XX
KW Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
XX detergent; anti-dye transfer; stain removal; bleaching; ds.
XX
OS Stachybotrys chartarum.
XX
PN WO9949010-A2.
XX
PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-EP02042.
XX
PR 24-MAR-1998; 98US-0046969.
XX
PR 22-DEC-1998; 98US-0218702.
XX
PA (UNIL ) UNILEVER NV.
XX (UNIL ) UNILEVER PLC.
XX
PI Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;
PI Wang C;
XX
DR WPI; 1999-601211/51.
XX
DR P-PSDB; AAY45222.
XX
XX
PT Detergent composition containing phenol oxidase from Stachybotrys, used
PT to bleach stains and prevent dye transfer -
XX
XX Example 14; Fig 6; 56pp; English.
XX
CC The present invention describes a detergent composition containing a
CC purified phenol oxidising enzyme derived from Stachybotrys. The present
CC sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The
CC enzyme can be used to modify the colour of dyes and other coloured
CC compounds (e.g. for use in pulp and paper bleaching also for removing
CC stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
CC transfer during fabric washing.
XX
SQ Sequence 3676 BP; 822 A; 1056 C; 849 G; 948 T; 1 other;
Query Match 99.7%; Score 3664.6; DB 20; Length 3676;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3676; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CTGGCTAGCCTCACTTGGTAGACAGCCCTGACAGCCTCACTGGGTGGGGTTCGAAAGGCC 60
Db 1 CTGGCTAGCCTCACTTGGTAGACAGCCCTGACAGCCTCACTGGGTGGGGTTCGAAAGGCC 60
Qy 61 AGTCAATATCTTGGTCACTGCTAATAGTTCCTTGTACGCCCAAAAGCTCCTTCCCGAA 120
Db 61 AGTCAATATCTTGGTCACTGCTAATAGTTCCTTGTACGCCCAAAAGCTCCTTCCCGAA 120
Qy 121 GGGGCACAGACTATCAAGTAGACATATAGGATGCATGCTTTCATAGCCACAGTTAGGG 180
Db 121 GGGGCACAGACTATCAAGTAGACATATAGGATGCATGCTTTCATAGCCACAGTTAGGG 180
Qy 181 TGGTGACCTACTCGAAGAGGCCCGACTTGCATGCATACGACATGTCGCTTCCATGCAAC 240
Db 181 TGGTGACCTACTCGAAGAGGCCCGACTTGCATGCATACGACATGTCGCTTCCATGCAAC 240
Qy 241 ATGTATGGCAGATCGGCGATCAGGCACCCCTCTGCATGCAGAAATAGAACCCCTGGTTT 300
Db 241 ATGTATGGCAGATCGGCGATCAGGCACCCCTCTGCATGCAGAAATAGAACCCCTGGTTT 300
Qy 301 CCTTTTGTCTTTTCTTCTCAACGACGCTGAGCGTGGTGAACCTGAGCAAGGCCGA 360
Db 301 CCTTTTGTCTTTTCTTCTCAACGACGCTGAGCGTGGTGAACCTGAGCAAGGCCGA 360
Qy 361 GTGGTCTGTTTACAGAGGTTACCATCGAACTCTCTCTTTTCCCAATCATGACCTGCCCC 420
Db 361 GTGGTCTGTTTACAGAGGTTACCATCGAACTCTCTCTTTTCCCAATCATGACCTGCCCC 420
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Qy 421 GAGTTTAGCCCCATCAGGCTGTGAATCCACCTTCGATATCCTAGCCTAGTCTACTC 480
Db 421 GAGTTTAGCCCCATCAGGCTGTGAATCCACCTTCGATATCCTAGCCTAGTCTACTC 480
Qy 481 TTCATAGTTGCTCCTGATGGGCACATTGGTCACATTGGCTTGGTYCTCCTACCTCGT 540
Db 481 TTCATAGTTGCTCCTGATGGGCACATTGGTCACATTGGCTTGGTYCTCCTACCTCGT 540
Qy 541 TCTCTTCCGCATCAAGCTCTATGCCGACGACACACCTCATTTGGCCGGACCACTTTG 600
Db 541 TCTCTTCCGCATCAAGCTCTATGCCGACGACACACCTCATTTGGCCGGACCACTTTG 600
Qy 601 AGCGGCACGACCTTCGCGCCGGAAGAGTTGATAACACCTTCACCCCTTGGCCCAATGAT 660
Db 601 AGCGGCACGACCTTCGCGCCGGAAGAGTTGATAACACCTTCACCCCTTGGCCCAATGAT 660
Qy 661 GGAGTTTGGTCTATTTGTCATGATCACCTCACATTCATAGATCAGGATCCCTGGGAAGA 720
Db 661 GGAGTTTGGTCTATTTGTCATGATCACCTCACATTCATAGATCAGGATCCCTGGGAAGA 720
Qy 721 GGGTGTGGAAGCCAGACAGCTTGTCCCTGTTCTTTCAGACTCAGGTCAGCTCCTAGCGG 780
Db 721 GGGTGTGGAAGCCAGACAGCTTGTCCCTGTTCTTTCAGACTCAGGTCAGCTCCTAGCGG 780
Qy 781 CTATCACAGCTCAGATTATCAAGTCCCGTAAAGTCCAGACCCCTTTCATTGTATGATGC 840
Db 781 CTATCACAGCTCAGATTATCAAGTCCCGTAAAGTCCAGACCCCTTTCATTGTATGATGC 840
Qy 841 TGCCTAATTTGGCTATCTCTATGCCGTAGCAGCGGCTTGGCTACAACTGGCTGCCATG 900
Db 841 TGCCTAATTTGGCTATCTCTATGCCGTAGCAGCGGCTTGGCTACAACTGGCTGCCATG 900
Qy 901 GCTGAAGCATCGTGAGATCTATAAAGTCTCCGAATCCCTGGTGAAGTCAAGTCCGCTC 960
Db 901 GCTGAAGCATCGTGAGATCTATAAAGTCTCCGAATCCCTGGTGAAGTCAAGTCCGCTC 960
Qy 961 TCCACACAGTCAACAACAAGCTCTTTCTCTTACAGCTTAGCCTGAGCACATTCACAGA 1020
Db 961 TCCACACAGTCAACAACAAGCTCTTTCTCTTACAGCTTAGCCTGAGCACATTCACAGA 1020
Qy 1021 ACTCTTCCCTCTTTTTCGTCATATGCTGTTCAAGTCATGCAACTGGCAGCAGCCTCCG 1080
Db 1021 ACTCTTCCCTCTTTTTCGTCATATGCTGTTCAAGTCATGCAACTGGCAGCAGCCTCCG 1080
Qy 1081 GGCTCCTGCTGGAGTCTCTCGGCATCCCGATGGACACGGCAGCACCCCATTTGAGGCTG 1140
Db 1081 GGCTCCTGCTGGAGTCTCTCGGCATCCCGATGGACACGGCAGCACCCCATTTGAGGCTG 1140
Qy 1141 TTGATCCGGAAGTGAAGACTGAGGTCTTTCGCTGACTCCCTCTTGGCTGACGAGCGGATG 1200
Db 1141 TTGATCCGGAAGTGAAGACTGAGGTCTTTCGCTGACTCCCTCTTGGCTGACGAGCGGATG 1200
Qy 1201 ACGACTGGAGTCACTCCATACAACTTGCCTTACAGTGAGACACCTGTCCCACCTGTT 1260
Db 1201 ACGACTGGAGTCACTCCATACAACTTGCCTTACAGTGAGACACCTGTCCCACCTGTT 1260
Qy 1261 TTCCTCGATAAATAACTCTTATAGGAATGCCCTGCCAAATTCACCTCTCAAGCAGCCCA 1320
Db 1261 TTCCTCGATAAATAACTCTTATAGGAATGCCCTGCCAAATTCACCTCTCAAGCAGCCCA 1320
Qy 1321 AGATGATGCTTTGATTTTCTAGGAAGCAACTCGGCCCGCCGACTAATGATTTCTAGGATC 1380
Db 1321 AGATGATGCTTTGATTTTCTAGGAAGCAACTCGGCCCGCCGACTAATGATTTCTAGGATC 1380
Qy 1381 ATTACCAACCTGTCCACGGCAAGGACATTTGGTACTATGATCGAGATCAAGCCATTT 1440
Db 1381 ATTACCAACCTGTCCACGGCAAGGACATTTGGTACTATGATCGAGATCAAGCCATTT 1440
Qy 1441 CAGCAAGGGTGAGTTTCTCAGAAACCTTCTGGTAAATTAATCATTTTACTGACCCCTTT 1500
Db 1441 CAGCAAGGGTGAGTTTCTCAGAAACCTTCTGGTAAATTAATCATTTTACTGACCCCTTT 1500

Qy 1501 CAGATTTACCACCACCTTCGGCCCTGCCACTCTCTGTCGGCTAGCATGGCATGAGCCCTGGT 1560
Db 1501 CAGATTTACCACCACCTTCGGCCCTGCCACTCTCTGTCGGCTAGCATGGCATGAGCCCTGGT 1560
Qy 1561 CCTACTTTCAATGTTCCAGAGGACACAGACTGTAGTTAGTTTTCATCAACAATGCCACC 1620
Db 1561 CCTACTTTCAATGTTCCAGAGGACACAGACTGTAGTTAGTTTTCATCAACAATGCCACC 1620
Qy 1621 GTGAGAACTCGGTCCATCTCTGCACGGCTCCCATCGCGTGGCCCTTTTGCATGTTGGGCT 1680
Db 1621 GTGAGAACTCGGTCCATCTCTGCACGGCTCCCATCGCGTGGCCCTTTTGCATGTTGGGCT 1680
Qy 1681 GAAGATGTAGCTTCCCTGGGAGTACAAAGATTAATACTTTTCCCACTACCAATCCGGC 1740
Db 1681 GAAGATGTAGCTTCCCTGGGAGTACAAAGATTAATACTTTTCCCACTACCAATCCGGC 1740
Qy 1741 CGCCTTCTGTGTTACCATGACACGCTTTTCATGAAGGTATGCTACGAGCCTTTATCTTTTC 1800
Db 1741 CGCCTTCTGTGTTACCATGACACGCTTTTCATGAAGGTATGCTACGAGCCTTTATCTTTTC 1800
Qy 1801 TTGGCTACTTTTGGCTAACCAACTTCTTTCGTAGACTGCTGAGAAATGCTACTTTTGGTC 1860
Db 1801 TTGGCTACTTTTGGCTAACCAACTTCTTTCGTAGACTGCTGAGAAATGCTACTTTTGGTC 1860
Qy 1861 AGGCTGGGCCCTACATTAACAGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCT 1920
Db 1861 AGGCTGGGCCCTACATTAACAGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCT 1920
Qy 1921 ATGGGAGTTGATATCCCTCTGATCCTGAGGCCCAAGTACTATAACGCCGATGTACCC 1980
Db 1921 ATGGGAGTTGATATCCCTCTGATCCTGAGGCCCAAGTACTATAACGCCGATGTACCC 1980
Qy 1981 TGCCTTCCAGCCAGGGTGAGGACCAGGACCTGTGGGAGATGTCATCCATGTCAACGGAC 2040
Db 1981 TGCCTTCCAGCCAGGGTGAGGACCAGGACCTGTGGGAGATGTCATCCATGTCAACGGAC 2040
Qy 2041 AGCATGCGCTTTCCTTAACGTCCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTG 2100
Db 2041 AGCATGCGCTTTCCTTAACGTCCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTG 2100
Qy 2101 CCGTCTCTGCTGCTGGCTCTACCTCTAGCTGTCAGACACAGCTCTCCCAAGTCAAAATTC 2160
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Qy 2161 CTTTCCAAAGTCATTGCTCTGATGCTGCTCTCTTCAAGCCCCCGTTTCAGACCTCTAACC 2220
Db 2161 CTTTCCAAAGTCATTGCTCTGATGCTGCTCTCTTCAAGCCCCCGTTTCAGACCTCTAACC 2220
Qy 2221 TCTACCTTGTCTTGGCCAGGCTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCAAGA 2280
Db 2221 TCTACCTTGTCTTGGCCAGGCTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCAAGA 2280
Qy 2281 ATGAGTCAAGAACTCTAAGACTTAACACTTTAGACTTCCACAACTTTTGTGGCCAGACTC 2340
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Qy 2401 CTCTCGAGGTGATGGCTTCTGCTGACCTCTGGGACCTTGTGAGGACAAACGCCAGGTCC 2460
Db 2401 CTCTCGAGGTGATGGCTTCTGCTGACCTCTGGGACCTTGTGAGGACAAACGCCAGGTCC 2460
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Db 2461 CCTCCACTCTCCGTGACCTTCTTTCCTCTCAAGAAAGGCCCGCCGCAAGCACT 2520
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Db 2521 TCAAGTTTGAACGAGCAACGACACTACCTGATCAACGATTTGGCTTTGCCGATGTCA 2580
Qy 2581 ATGAGCGTGTCTCTGGCCAAAGCCCGAGCTCGGACCGTTGAGGTCTGGGAGTCTGAGAACT 2640

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Db 2581 ATGAGCGTGTCTTGCCAAAGCCCGAGCTGGCACCGTTGAGGTCTGGAGCTCGAGAAGT 2640
Qy CCTCTGAGGCGTGGAGCCACCCCTGCACATTTCACCTTGTGTGACCTTCAAGATCCTCAAGC 2700
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Db 2641 CCTCTGAGGCGTGGAGCCACCCCTGCACATTTCACCTTGTGTGACCTTCAAGATCCTCAAGC 2700
Qy 2701 GAAGTGGTGGTGGCGAGGTATGCCCTACGAGTGTGCTGGTCTTTAAGGATGCTCGTCT 2760
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Db 2701 GAAGTGGTGGTGGCGAGGTATGCCCTACGAGTGTGCTGGTCTTTAAGGATGCTCGTCT 2760
Qy 2761 GGTGGGAGGGGTGAGACCTTACCATTCGAGGCGCCACTACCAACCCCTGGAGCTGAGGCTT 2820
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Qy 2821 ACATGTGGCACTGTCAACAACCTCATTACGAGGATACGACATGATGGCTGTATTCAACG 2880
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Qy 3001 CCGAGTCCATCACTGCCGAGTGCAGGAGTGGCGGAGCAGGAGCCGTACAAACCGCCTCG 3060
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Db 3001 CCGAGTCCATCACTGCCGAGTGCAGGAGTGGCGGAGCAGGAGCCGTACAAACCGCCTCG 3060
Qy 3061 ATGAGATCCTGGAGGATCTTGGAACTGAGGAGTAAACCCCGAGCAGCAAGCTCTACAATC 3120
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Db 3061 ATGAGATCCTGGAGGATCTTGGAACTGAGGAGTAAACCCCGAGCAGCAAGCTCTACAATC 3119
Qy 3121 GTTTTGTAGCTTAAGACGAGGCTCTTGGTGGTATCTTTTCCCTACCGGGAAGTCC 3180
|||||
Db 3120 GTTTTGTAGCTTAAGACGAGGCTCTTGGTGGTATCTTTTCTTCTTCCCTACCGGGAAGTCC 3179
Qy 3181 GCTGTCCACTCGGATGTGAAGGACCATCAACAAGCAGTATATATGGACTCACCACTG 3240
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Db 3180 GCTGTCCACTCGGATGTGAAGGACCATCAACAAGCAGTATATATGGACTCACCACTG 3239
Qy 3241 TCATTACCGCCCACTGTGTACCTATTTCGATCTTCTTCAAACTTTTCTAGTGGAGAGTGT 3300
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Db 3240 TCATTACCGCCCACTGTGTACCTATTTCGATCTTCTTCAAACTTTTCTAGTGGAGAGTGT 3299
Qy 3301 CCATAGTCAAGAAAGCCCATAGGCTATCGTCTAAACTGAACATATGTGTGGTCTGTGA 3360
|||||
Db 3300 CCATAGTCAAGAAAGCCCATAGGCTATCGTCTAAACTGAACATATGTGTGGTCTGTGA 3359
Qy 3361 CGTGGAGTAGATGTCAATTGTGTGAGACACAGTAAATACGGTATATCTTTTCTTAGGAC 3420
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Db 3360 CGTGGAGTAGATGTCAATTGTGTGAGACACAGTAAATACGGTATATCTTTTCTTAGGAC 3419
Qy 3421 TACAGGATCAGTTTCTCATGAGATTACATCGTCTTAATGTGTGTCTCCATGAGAGTCTAGCT 3480
|||||
Db 3420 TACAGGATCAGTTTCTCATGAGATTACATCGTCTTAATGTGTGTCTCCATGAGAGTCTAGCT 3479
Qy 3481 AAGGTTGAGAAATGATCAGACGGGAATCATATTTGATGCTCTCAGCTCGTATATACGAGTGA 3540
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Db 3480 AAGGTTGAGAAATGATCAGACGGGAATCATATTTGATGCTCTCAGCTCGTATATACGAGTGA 3539
Qy 3541 GACAAGTTAGGTAAAGTGTGTTGTTATCCGAAATACACTCAGGCTCCCTCATTTAGGTTGCA 3600
|||||
Db 3540 GACAAGTTAGGTAAAGTGTGTTGTTATCCGAAATGACTCAGGCTCCCTCATTTAGGTTGCA 3599
Qy 3601 TGTGAAACCTTTCAGCAACTCATGGGTGTTGGGACCAAAATCATCCATACCTGATTTTGTAT 3660
|||||
Db 3600 TGTGAAACCTTTCAGCAACTCATGGGTGTTGGGACCAAAATCATCCATACCTGATTTTGTAT 3659
Qy 3661 AACTGACCTGGGTCAAT 3677
|||||

Db 3660 AACTGACCTGGGTCAAT 3676
RESULT 6
AAZ25735
ID AAZ25735 standard; DNA; 2067 BP.
XX
XX AAZ25735;
XX AC
XX 05-JAN-2000 (first entry)
XX
XX Stachybotrys chartarum phenol oxidising enzyme PCR fragment.
DE Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
XX Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
KW detergent; anti-dye transfer; stain removal; bleaching; PCR primer; ss.
XX
XX Synthetic.
OS Stachybotrys chartarum.
XX
XX WO9949010-A2.
XX
XX 30-SEP-1999.
XX
XX 23-MAR-1999; 99WO-EP02042.
PF
XX 24-MAR-1998; 98US-0046969.
PR
XX 22-DEC-1998; 98US-0218702.
PR
XX (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
XX
XX Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;
PI Wang C;
PI
XX WPI; 1999-601211/51.
DR
XX Detergent composition containing phenol oxidase from Stachybotrys, used
PT to bleach stains and prevent dye transfer -
PT
XX
PS Example 17; Fig 9; 56pp; English.
CC
CC The present invention describes a detergent composition containing a
CC purified phenol oxidising enzyme derived from stachybotrys. The present
CC sequence represents a PCR fragment of stachybotrys chartarum phenol
CC oxidising enzyme. The enzyme can be used to modify the colour of dyes
CC and other coloured compounds (e.g. for use in pulp and paper bleaching
CC also for removing stains, e.g. food, tea, blood etc., from fabrics) and
CC for preventing dye transfer during fabric washing.
XX
XX Sequence 2067 BP; 445 A; 621 C; 500 G; 501 T; 0 other;
SQ
Query Match 55.9%; Score 2054; DB 20; Length 2067;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1041 AATATGCTGTTCAAGTCATGCAACTGGCAGCAGCTCCGGGCTCCTGTCTGGAGTCCCTC 1100
|||||
Db 7 AATATGCTGTTCAAGTCATGCAACTGGCAGCAGCTCCGGGCTCCTGTCTGGAGTCCCTC 66
Qy 1101 GGCATCCCGATGGACACCGGAGCCACCCCATTTGAGGCTGTTGATCCCGAAGTGAAGACT 1160
|||||
Db 67 GGCATCCCGATGGACACCGGAGCCACCCCATTTGAGGCTGTTGATCCCGAAGTGAAGACT 126
Qy 1161 GAGGTCTTCGCTGACTCCCTCTTCTGCTCAGCAGCGATGACGACTGGAGTCACTCCA 1220
|||||
Db 127 GAGGTCTTCGCTGACTCCCTCTTCTGCTCAGCAGCGATGACGACTGGAGTCACTCCA 186
Qy 1221 TACAACCTTGCCTTTTACAGGTGAGACACCTGTCCCACTGTTTTCCTCGATAACTACTCT 1280
|||||
Db 187 TACAACCTTGCCTTTACAGGTGAGACACCTGTCCCACTGTTTTCCTCGATAACTACTCT 246
Qy 1281 TATAGGAATGCCCTGCCCAATTTCCACCTCTCAAGCAGCCCAAGATGATGTCTTTGATTTT 1340
|||||

Db 247 TATAGGAATGCCCTGCCAAATTCACACCTGCTCAAGCAGCCCAAGATGTATGCTTTGATTTT 306
Qy 1341 CTACGAACAACCTCGGCCCGCACTAATATCTTAGGATCATTTACCAACCCCTGTACACGG 1400
Db 307 CTACGAACAACCTCGGCCCGCACTAATATCTTAGGATCATTTACCAACCCCTGTACACGG 366
Qy 1401 CAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAGGGTGAGTTGCT 1460
Db 367 CAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAGGGTGAGTTGCT 426
Qy 1461 CAGAAACCTTGTGGTAAATTAATCTATGCTTACTGACCCCTTTTCAGATTTTACCCCACTTCGG 1520
Db 427 CAGAAACCTTGTGGTAAATTAATCTATGCTTACTGACCCCTTTTCAGATTTTACCCCACTTCGG 486
Qy 1521 CCCTGCCACTCTCGCTCGCTACGATGGCATGAGCCCTCGTCTACTTTCAATGTTTCCAG 1580
Db 487 CCCTGCCACTCTCGCTCGCTACGATGGCATGAGCCCTCGTCTACTTTCAATGTTTCCAG 546
Qy 1581 AGGAACAGAGACTGTAGTTAGTTAGTTTCATCAACAATGCCACCTGGAGAACTCGGTCATCT 1640
Db 547 AGGAACAGAGACTGTAGTTAGTTAGTTTCATCAACAATGCCACCTGGAGAACTCGGTCATCT 606
Qy 1641 GCACGGCTCCCATCGCTGCGCTTTCGATGGTTGGGCTGAAGATGTGACCTTCCCTGG 1700
Db 607 GCACGGCTCCCATCGCTGCGCTTTCGATGGTTGGGCTGAAGATGTGACCTTCCCTGG 666
Qy 1701 CGAGTACAAGGATTACTACTTTCCCACTACCAATFCCCGCCCTTCTGTGTACCATGA 1760
Db 667 CGAGTACAAGGATTACTACTTTCCCACTACCAATFCCCGCCCTTCTGTGTACCATGA 726
Qy 1761 CCAGCTTTTCATGAAAGTATGCTACGAGCCCTTATCTTTCTTGGCTACCTTTGGCTAAC 1820
Db 727 CCAGCTTTTCATGAAAGTATGCTACGAGCCCTTATCTTTCTTGGCTACCTTTGGCTAAC 786
Qy 1821 AACTTCCCTTTCGTAGACTGCTGAGATGCTTACTTGTGAGGCTGGCGCTACATTTAC 1880
Db 787 AACTTCCCTTTCGTAGACTGCTGAGATGCTTACTTGTGAGGCTGGCGCTACATTTAC 846
Qy 1881 AACGACGAGGCTGAGGATGCTCTCGGCTTCTAGTGTGCTATGCGAGTTTCGATATCCCT 1940
Db 847 AACGACGAGGCTGAGGATGCTCTCGGCTTCTAGTGTGCTATGCGAGTTTCGATATCCCT 906
Qy 1941 CTGATCTGAGCGCAAGTACTATAACCCGATGGTACCCTGCGTTTCGACCGAGGTGAG 2000
Db 907 CTGATCTGAGCGCAAGTACTATAACCCGATGGTACCCTGCGTTTCGACCGAGGTGAG 966
Qy 2001 GACCAGGACCTGTGGGAGATGTCATCCATGTCAACGACAGCCATGGCTTTCCTTAAC 2060
Db 967 GACCAGGACCTGTGGGAGATGTCATCCATGTCAACGACAGCCATGGCTTTCCTTAAC 1026
Qy 2061 GTCCAGCCCGCAAGTACCGTTTCCGATTTCCTCAACGCTGCGGCTCTCGTGTGGCTC 2120
Db 1027 GTCCAGCCCGCAAGTACCGTTTCCGATTTCCTCAACGCTGCGGCTCTCGTGTGGCTC 1086
Qy 2121 CTCACCTCTGTAGGACAGCTCTCCCAAGCTCAGAAATTCCTTTCCAAAGTCAATTCGCT 2180
Db 1087 CTCACCTCTGTAGGACAGCTCTCCCAAGCTCAGAAATTCCTTTCCAAAGTCAATTCGCT 1146
Qy 2181 GATGCTGTCTCTTCAAGCCCGCTTACGACCTTACCTTACCTTGTGTCGGCAG 2240
Db 1147 GATGCTGTCTCTTCAAGCCCGCTTACGACCTTACCTTACCTTGTGTCGGCAG 1206
Qy 2241 CGTTACGAGATCATTTATGTTATGCCCTCCCTCTCAGCAATGAGTCAAGAACTCTAGA 2300
Db 1207 CGTTACGAGATCATTTATGTTATGCCCTCCCTCTCAGCAATGAGTCAAGAACTCTAGA 1266
Qy 2301 CTAACACTTGTAGACTTCACCAACTTTTGTGCGCAGACTTGTGACCTGCGCAAGGTTGCT 2360
Db 1267 CTAACACTTGTAGACTTCACCAACTTTTGTGCGCAGACTTGTGACCTGCGCAAGGTTGCT 1326
Qy 2361 GAGACCAACGATGTGCGGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATCGGCTTC 2420
Db 1327 GAGACCAACGATGTGCGGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATCGGCTTC 1386

Qy 2421 GTCGTACGCTCTGACACTGTTTGAGGACAACAGCCAGGTCCTCTCCACTCTCGTGACGTT 2480
Db 1387 GTCGTACGCTCTGACACTGTTTGAGGACAACAGCCAGGTCCTCTCCACTCTCGTGACGTT 1446
Qy 2481 CTTTCCCTCTCTACAGAAGAGGCCCGCCGACAAAGCACTTCAAGTTTGAACGCCAGAAC 2540
Db 1447 CTTTCCCTCTCTACAGAAGAGGCCCGCCGACAAAGCACTTCAAGTTTGAACGCCAGAAC 1506
Qy 2541 GGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCAATGACGCTGCTCTGCGCCAG 2600
Db 1507 GGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCAATGACGCTGCTCTGCGCCAG 1566
Qy 2601 CCCGAGCTCGCACCGTTGAGGCTCTGGAGCTTCGAGAACTCCTCTGAGGCTTGGAGCCAC 2660
Db 1567 CCCGAGCTCGCACCGTTGAGGCTCTGGAGCTTCGAGAACTCCTCTGAGGCTTGGAGCCAC 1626
Qy 2661 CCCGTCACATTTACCTTGTGACTTCAAGATCTCAAGCGAACTGGTGGTGGCCAG 2720
Db 1627 CCCGTCACATTTACCTTGTGACTTCAAGATCTCAAGCGAACTGGTGGTGGCCAG 1686
Qy 2721 GTCATGCCCTACGAGTCTGCTTAAAGGATGCTGCTGGTGGGAGGGGTCAGACC 2780
Db 1687 GTCATGCCCTACGAGTCTGCTTAAAGGATGCTGCTGGTGGGAGGGGTCAGACC 1746
Qy 2781 CTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTTACATGTGGCACTGTCCACAC 2840
Db 1747 CTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTTACATGTGGCACTGTCCACAC 1806
Qy 2841 CTCATTACAGAGGATAACGACATGATGGCTGTATTCAACGTCACGCCCATGGAGGAGAG 2900
Db 1807 CTCATTACAGAGGATAACGACATGATGGCTGTATTCAACGTCACGCCCATGGAGGAGAG 1866
Qy 2901 GGATATCTTCAGGAGGACTTCGAGACCCCATGAACCCCAAGTGGCGCGCTTCCCTTAC 2960
Db 1867 GGATATCTTCAGGAGGACTTCGAGACCCCATGAACCCCAAGTGGCGCGCTTCCCTTAC 1926
Qy 2961 AACCGCAACGACTTCCATGCTCGGCTGGAACCTTCTCCGCGAGTCCATCACTGCCCGA 3020
Db 1927 AACCGCAACGACTTCCATGCTCGGCTGGAACCTTCTCCGCGAGTCCATCACTGCCCGA 1986
Qy 3021 GTGAGGAGCTGGCGGAGCAGAGCCGTTACACCCCTCGATGAGATCCTGAGGATCTT 3080
Db 1987 GTGAGGAGCTGGCGGAGCAGAGCCGTTACACCCCTCGATGAGATCCTGAGGATCTT 2046
Qy 3081 GGAATCGAGGAGTA 3094
Db 2047 GGAATCGAGGAGTA 2060

RESULT 7

AZ27609
ID AZ27609 standard; DNA; 2067 BP.
XX
XX AC
XX AC
DF 16-DEC-1999 (first entry)
XX
DE Stachybotrys phenol oxidase coding sequence.
KW Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
KW fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
OS Stachybotrys chartarum.
XX WO9949020-A2.
PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-US06327.
XX
PR 24-MAR-1998; 98US-0046969.
PR 22-DEC-1998; 98US-0218702.

PR 22-MAR-1999; 99US-0273957.
XX (GEMV) GENENCOR INT INC.
XX Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;
XX WPI; 1999-591088/50.
XX Novel enzyme for modifying coloured compounds used to prevent
XX dye-transfer -
XX Example 17; Fig 9; 64pp; English.
XX This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
CC of the invention. The invention is used to modify a coloured compound and
CC prevent dye transfer during fabric washing, or for stain bleaching or
CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC and food industries.
XX Sequence 2067 BP; 445 A; 621 C; 500 G; 501 T; 0 other;
SQ
Query Match 55.9%; Score 2054; DB 20; Length 2067;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1041 AATATGCTGTTCAAGTCATGSCAACTGGCAGCAGCCCTCCGGGCTCCTGTCTGGAGTCCTC 1100
Db 7 AATATGCTGTTCAAGTCATGSCAACTGGCAGCAGCCCTCCGGGCTCCTGTCTGGAGTCCTC 66
Qy 1101 GGCATCCGGATGGACACGGGAGCCACCCCATTTGAGGCTGTTGATCCGGAAGTGAAGACT 1160
Db 67 GGCATCCGGATGGACACGGGAGCCACCCCATTTGAGGCTGTTGATCCGGAAGTGAAGACT 126
Qy 1161 GAGGCTCTTCGCTGACTCCCTCCTTGGCTGACGAGCGGATGACGACTGGGAGTCACTCCA 1220
Db 127 GAGGCTCTTCGCTGACTCCCTCCTTGGCTGACGAGCGGATGACGACTGGGAGTCACTCCA 186
Qy 1221 TACAACCTTGCTTTACAGGTGAGACACCTGTCCACCTGTTTTCCTCGATAAATCTCT 1280
Db 187 TACAACCTTGCTTTACAGGTGAGACACCTGTCCACCTGTTTTCCTCGATAAATCTCT 246
Qy 1281 TATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTTTGATTTT 1340
Db 247 TATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTTTGATTTT 306
Qy 1341 CTACGAAGCAACTCGGCCCGGACCTAAATGTAATCTAGGATCATTTACCAACCTGTCAACCGG 1400
Db 307 CTACGAAGCAACTCGGCCCGGACCTAAATGTAATCTAGGATCATTTACCAACCTGTCAACCGG 366
Qy 1401 CAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAAAGGGTGAGTTTGCT 1460
Db 367 CAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAAAGGGTGAGTTTGCT 426
Qy 1461 CAGAAACCTTGCGTAAATTAATCATTTGTTACTGACCCCTTCAGATTTACCCACCTGTGCG 1520
Db 427 CAGAAACCTTGCGTAAATTAATCATTTGTTACTGACCCCTTCAGATTTACCCACCTGTGCG 486
Qy 1521 CCCTGCCACTCTCGCTACGATGGATGACCGCTGCTACTTTCAATGTTCCACG 1580
Db 487 CCCTGCCACTCTCGCTACGATGGATGACCGCTGCTACTTTCAATGTTCCACG 546
Qy 1581 AGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGAGAACTCGGTCCTACT 1640
Db 547 AGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGAGAACTCGGTCCTACT 606
Qy 1641 GCAGGCTCCCATCGCGTCCCTTTGATGTTGGCTGAAGATGTGACCTTCCTCCG 1700
Db 607 GCAGGCTCCCATCGCGTCCCTTTGATGTTGGCTGAAGATGTGACCTTCCTCCG 666
Qy 1701 CGAGTACAGGATTACTACTTTTCCCACTACCAATCCGCCCGCTTCTGTGGTACCATGA 1760
Db 667 CGAGTACAGGATTACTACTTTTCCCACTACCAATCCGCCCGCTTCTGTGGTACCATGA 726

Qy 1761 CCACGCTTTTCATGAAGGTATGCTACGAGCCCTTATATCTTTCTTGCTACCTTTGGCTTAACC 1820
Db CCACGCTTTTCATGAAGGTATGCTACGAGCCCTTATATCTTTCTTGCTACCTTTGGCTTAACC 786
Qy 1821 AACCTCCTTTGCTAGACTGCTGAGAATGCCCTACTTTGCTCAGGCTGGCGCTACATATATC 1880
Db AACCTCCTTTGCTAGACTGCTGAGAATGCCCTACTTTGCTCAGGCTGGCGCTACATATATC 846
Qy 1881 AACGACGAGGCTGAGGATGCTCTCGGCTTTCTAGTGGCTATGGCGAGTTCCGATATCCCT 1940
Db AACGACGAGGCTGAGGATGCTCTCGGCTTTCTAGTGGCTATGGCGAGTTCCGATATCCCT 906
Qy 1941 CTGATCTGACGGCCAAAGTACTATAACGCCGATGGTACCCCTGCTTCGACGAGGGTGAG 2000
Db CTGATCTGACGGCCAAAGTACTATAACGCCGATGGTACCCCTGCTTCGACGAGGGTGAG 966
Qy 2001 GACGAGACCTGTGGGAGATGTCATCCATGCTCAACGACAGCCATGGCCCTTTCCTTAAC 2060
Db GACGAGACCTGTGGGAGATGTCATCCATGCTCAACGACAGCCATGGCCCTTTCCTTAAC 1026
Qy 2061 GTCCAGCCCGCAAGTACCCTTTCCGATTTCTCAACGCTGCCGTGCTCTCGTGGCTC 2120
Db GTCCAGCCCGCAAGTACCCTTTCCGATTTCTCAACGCTGCCGTGCTCTCGTGGCTC 1086
Qy 2121 CTCCTACCTGTCAGACACGACTCTCCCAACGTCAGAAATTCCTTTCCAAAGTCATTTGCCCT 2180
Db CTCCTACCTGTCAGACACGACTCTCCCAACGTCAGAAATTCCTTTCCAAAGTCATTTGCCCT 1146
Qy 2181 GATCCTGCTCCTCTCAAGCCCGCTTCAGACCTCTACCTCTACCTTGCTGTTGCCGAG 2240
Db GATCCTGCTCCTCTCAAGCCCGCTTCAGACCTCTACCTCTACCTTGCTGTTGCCGAG 1206
Qy 2241 CGTTACGAGATCATTTATGTTGATGCCCTCCCTCTCAAGAAATGAGTCAAGAACTCTAAGA 2300
Db CGTTACGAGATCATTTATGTTGATGCCCTCCCTCTCAAGAAATGAGTCAAGAACTCTAAGA 1266
Qy 2301 CTAACTTTGTAGACTTCAACCACTTTGCTGGCAGACTCTTGACCTCGCAAGCTTGCT 2360
Db CTAACTTTGTAGACTTCAACCACTTTGCTGGCAGACTCTTGACCTCGCAAGCTTGCT 1326
Qy 2361 GAGACCAAGATGTCGGCGAGGAGTACGCTCGCACTCTCGAGGTGATGGCTC 2420
Db GAGACCAAGATGTCGGCGAGGAGTACGCTCGCACTCTCGAGGTGATGGCTC 1386
Qy 2421 GTCGTCAGCTCTGGCACTGTTTGAGGACAAACGAGGTCCTCCCTCCACTCTCCGTCGACT 2480
Db GTCGTCAGCTCTGGCACTGTTTGAGGACAAACGAGGTCCTCCCTCCACTCTCCGTCGACT 1446
Qy 2481 CCTTTCCCTCTCAAGAAAGGCCCGCCGACAACTTTCAAGTTTGAACGCAAGCAAC 2540
Db CCTTTCCCTCTCAAGAAAGGCCCGCCGACAACTTTCAAGTTTGAACGCAAGCAAC 1506
Qy 2541 GGACACTACCTGATCAAGGATGTTGGCTTTGCCGATGTCATAGGCTGCTCGGCCAAG 2600
Db GGACACTACCTGATCAAGGATGTTGGCTTTGCCGATGTCATAGGCTGCTCGGCCAAG 1566
Qy 2601 CCCGAGCTCGGACCGTTGAGGCTCTGGAGCTCGAGAACTCCTCTGGAGGCTGGAGCCAC 2660
Db CCCGAGCTCGGACCGTTGAGGCTCTGGAGCTCGAGAACTCCTCTGGAGGCTGGAGCCAC 1626
Qy 2661 CCCGTCCCACTTACCTTTGTTGACTTCAAGATCCTCAAGCGAACTGGTGGTGGCCAG 2720
Db CCCGTCCCACTTACCTTTGTTGACTTCAAGATCCTCAAGCGAACTGGTGGTGGCCAG 1686
Qy 2721 GTCATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCGCTCTGGTGGGCGAGGGTGAGCC 2780
Db GTCATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCGCTCTGGTGGGCGAGGGTGAGCC 1746
Qy 2781 CTGACCATCGAGGCCCACTACCAACCTCGAGCTTGAGCTTACATGTGCACTGTCCACAC 2840
Db CTGACCATCGAGGCCCACTACCAACCTCGAGCTTGAGCTTACATGTGCACTGTCCACAC 1806
Qy 2841 CTCATTACGAGGATAACGACATGATGGCTGTATTCAACGTCACGCCCATGGAGGAGAAG 2900

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Db 1807 CTCATTTCAGGAGTAACGACATGATGGCTGATTCAACGTCACCGCCATGGAGGAG 1866
Qy 2901 GGATATCTTCAGGAGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCCCTTCTTAC 2960
Db 1867 GGATATCTTCAGGAGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCCCTTCTTAC 1926
Qy 2961 AACCGACGACTTCATGCTCGCGCTGGAACTTCTCGCGGAGTGCATCACTGCCGA 3020
Db 1927 AACCGACGACTTCATGCTCGCGCTGGAACTTCTCGCGGAGTGCATCACTGCCGA 1986
Qy 3021 GTGAGGAGCTGGCGAGCAGGACCGGTACACCGCCTCGATGAGATCCTGAGGATCTT 3080
Db 1987 GTGAGGAGCTGGCGAGCAGGACCGGTACACCGCCTCGATGAGATCCTGAGGATCTT 2046
Qy 3081 GGAATCGAGGAGTA 3094
Db 2047 GGAATCGAGGAGTA 2060

RESULT 8
ABA92911
ID ABA92911 standard; DNA; 7248 BP.
XX
AC ABA92911;
DT
09-APR-2002 (first entry)
XX
Stachybotrys chartarum laccase gene.
XX
Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;
KW copper; metal cofactor; gene; plant; ds.
XX
Stachybotrys chartarum.
OS
PN WO200196543-A2.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US19174.
XX
PR 15-JUN-2000; 2000US-211732P.
XX
PA (PROD-) PRODIGENE INC.
XX (GENM) GENENCOR INC.
XX
PI Hood E, Howard JA, Bailey M, Van Gastel FJC, Ward M, Wang H;
PI Woodward S;
XX
XX WPI; 2002-090204/12.
XX
XX Improving recovery of active enzyme e.g. laccase, which requires
PT transitional metal cofactor e.g. copper for activity, from a plant, by
PT introducing plant nucleotide sequences encoding the enzyme and exposing
PT it to cofactor -
XX
XX Example 5; Fig 16A-E; 81pp; English.
PS
XX
XX The present invention describes a method for improving the recovery of
CC an active enzyme from a plant where the enzyme requires a transitional
CC metal cofactor for activity. The method comprises introducing into the
CC plant nucleotide sequences encoding the enzyme and exposing the enzyme
CC to the metal cofactor. The method is useful for improving recovery of
CC active enzyme which requires a transitional metal cofactor for activity,
CC preferably for improving recovery of active laccase which requires
CC copper for activity. The method can be used for improving recovery of
CC active organophosphate hydrolase (OPH, E.C. 3.1.8.1) which requires
CC zinc, nickel, cobalt or manganese for activity, where the method further
CC comprises adding bicarbonate ion salt. The present sequence encodes the
CC fungal Stachybotrys chartarum laccase enzyme. Laccases are also called
CC blue copper oxidases and use copper to accept and donate electrons in
CC the oxidation and reduction of substrates.
XX

SQ Sequence 7248 BP; 1928 A; 1744 C; 1579 G; 1997 T; 0 other;
Query Match 40.1%; Score 1474.6; DB 24; Length 7248;
Best Local Similarity 86.1%; Pred. No. 0;
Matches 1806; Conservative 0; Mismatches 24; Indels 267; Gaps 5;

Qy 1030 TTCCTTTTCGTCATATGCTTCAAGTTCATGGCACTGCGCAGCAGCCTCCGGGCTCCTGT 1089
Db 5184 TTCGGCTTTGTCATATGCTTCAAGTTCATGGCACTGCGCAGCAGCCTCCGGGCTCCTGT 5243
Qy 1090 CTGGAGTCTCCGGCATCCGATGGACACCGGACGCCACCCATTGAGGCTGTGATCCCG 1149
Db 5244 CTGGAGTCTCCGGCATCCGATGGACACCGGACGCCACCCATTGAGGCTGTGATCCCG 5303
Qy 1150 AAGTGAAGACTGAGGTCTTCGCTGACTCCCTCTCTGCTGACGAGCGCATGACGACTGG 1209
Db 5304 AAGTGAAGACTGAGGTCTTCGCTGACTCCCTCTCTGCTGACGAGCGCATGACGACTGG 5363
Qy 1210 AGTCACCTCCATACAACTTGCTTTACAGGTGAGACACCTGTCCACCTGTTTCCCTCGA 1269
Db 5364 AGTCACCTCCATACAACTTGCTTTAC- - - - - 5389
Qy 1270 TAACTAACTCTTTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATCTATG 1329
Db 5390 - - - - - AGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGAT- - - - - 5430
Qy 1330 TCCTTTGATTTTCTACGAAGCAACTCGGCCCGGCACTAATGATTTAGGATCAATTACCAAC 1389
Db 5431 - - - - - GATCATTACCAAC 5443
Qy 1390 CCGTGCACCGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAGG 1449
Db 5444 CCTGTACCGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAG- 5502
Qy 1450 GTGAGTTTGTCTCAGAAACCTTTGTGGTAATTAATCATTTGTACTGACCCCTTCAGATTAC 1509
Db 5503 - - - - - GATTTAC 5509
Qy 1510 CCCACCTTGGCGCCCTGCCACTCTCGTCCGCTACGATGGCATGAGCCCTGGTCTCTACTTTC 1569
Db 5510 CCCACCTTGGCGCCCTGCCACTCTCGTCCGCTACGATGGCATGAGCCCTGGTCTCTACTTTC 5569
Qy 1570 AATGTTCCAGAGAACACAGAGACTGTAGTTAGTTTCATCAACAATGCCACCGTGGAGAAC 1629
Db 5570 AATGTTCCAGAGAACACAGAGACTGTAGTTAGTTTCATCAACAATGCCACCGTGGAGAAC 5629
Qy 1630 TCGGTCCATCTGCACGGCTCCCATCGCTGCCCTTCGATGGTTGGCTGNAGATGTG 1689
Db 5630 TCGGTCCATCTGCACGGCTCCCATCGCTGCCCTTCGATGGTTGGCTGAAGATGTG 5689
Qy 1690 ACCTTCCCTGGCGAGTACAAGGATTACTACTTTCCCACTACCAATCCGCCCGCTTCG 1749
Db 5690 ACCTTCCCTGGCGAGTACAAGGATTACTACTTTCCCACTACCAATCCGCCCGCTTCG 5749
Qy 1750 TGGTACCATGACCGCTTTTCATGAAGGTATGCTACGAGCCCTTATCTTTCTTGGCTACC 1809
Db 5750 TGGTACCATGACCGCTTTTCATGA- - - - - 5774
Qy 1810 TTTGGCTAACCAACTTCCTTTCGTAGACTGCTGAGATGCCCTACTTTGCTCAGGCTGGCG 1869
Db 5775 - - - - - AGACTGCTGAGAAATGCCCTACTTTGCTCAGGCTGGCG 5810
Qy 1870 CCTACATTATCAACACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGT 1929
Db 5811 CCTACATTATCAACACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGT 5870
Qy 1930 TCGATATCCCTCTGATCTCGACGGCCAAAGTACTATAACCCGATGTAACCTCCGTTCCA 1989
Db 5871 TCGATATCCCTCTGATCTCGACGGCCAAAGTACTATAACCCGATGTAACCTCCGTTCCA 5930
Qy 1990 CCGAGGGTGAGGACACGAGCCTGTGGGGAGATGTCATCCATGTCAACGAGCAGCATGGC 2049
Db 5931 CCGAGGGTGAGGACACGAGCCTGTGGGGAGATGTCATCCATGTCAACGAGCAGCATGGC 5990

Qy 2050 CTTTCCTTTAAGCTCCAGCCCGCAAGTACCCTTTCCGATTCTTCAACGCTCCCGTGTCTC 2109
Db 5991 CTTTCCTTTAAGCTCCAGCCCGCAAGTACCCTTTCCGATTCTTCAACGCTCCCGTGTCTC 6050
Qy 2110 GTGCTTGGCTCCTCTACCTCTGTCAGGACCAGCTCTCCCAAGTCAGAAATTCCTTTCCAA 2169
Db 6051 GTGCTTGGCTCCTCTACCTCTGTCAGGACCAGCTCTCCCAAGTCAGAAATTCCTTTCCAA 6110
Qy 2170 TCATTGCCCTGTAGTCTGCTCTTCAAGCCCGGTTTCAGACCTCTAACTCTACCTTGC 2229
Db 6111 TCATTGCCCTGTAGTCTGCTCTTCAAGCCCGGTTTCAGACCTCTAACTCTACCTTGC 6170
Qy 2230 CTGTTGCCGAGCGTTACGAGATCATTTATTGGTATGCCCTCCCTCTCACGAATGAGTCAA 2289
Db 6171 CTGTTGCCGAGCGTTACGAGATCATTTATTGGTATGCCCTCCCTCTCACGAATGAGTCAA 6199
Qy 2290 GAACCTCTAAGACTTAACACTTTGTAGACTTACCAACTTTGCTGGCCAGACTCTTTGACCTGC 2349
Db 6200 -----GACTTTCACCAACTTTGCTGGCCAGACTCTTTGACCTGC 6236
Qy 2350 GCAAGCTTGTGAGACCAACATGTCGGCGAGGAGTACGCTCGCACTCTCGAGG 2409
Db 6237 GCAAGCTTGTGAGACCAACATGTCGGCGAGGAGTACGCTCGCACTCTCGAGG 6296
Qy 2410 TGATGCGCTTCTGCTCAGCTCTGSCACTGTTGAGGACAACAGCAGTCCCTCCACTC 2469
Db 6297 TGATGCGCTTCTGCTCAGCTCTGSCACTGTTGAGGACAACAGCAGTCCCTCCACTC 6356
Qy 2470 TCCGTGAGCTTCTTTCCCTCTCTCAAGGAAGGCCCGCGCAAGCAACTTCAAGTTTG 2529
Db 6357 TCCGTGAGCTTCTTTCCCTCTCTCAAGGAAGGCCCGCGCAAGCAACTTCAAGTTTG 6416
Qy 2530 AACGAGCAAGCGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCATGAGCGTG 2589
Db 6417 AACGAGCAAGCGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCATGAGCGTG 6476
Qy 2590 TCCTGGCCAAAGCCGAGCTCGGCACCGTTGAGGCTGGGAGCTCGAGAATCCTCTGGAG 2649
Db 6477 TCCTGGCCAAAGCCGAGCTCGGCACCGTTGAGGCTGGGAGCTCGAGAATCCTCTGGAG 6536
Qy 2650 GCTGAGGACCCCGTCCACATTCACCTTTGAGTTCGAAGTCTCAAGGAACTGGTG 2709
Db 6537 GCTGAGGACCCCGTCCACATTCACCTTTGAGTTCGAAGTCTCAAGGAACTGGTG 6596
Qy 2710 GTCGTGGCCAGTCAATGCTACGAGTCTGCTGGTCTTAAGGATGTCGCTGGTTGGCA 2769
Db 6597 GTCGTGGCCAGTCAATGCTACGAGTCTGCTGGTCTTAAGGATGTCGCTGGTTGGCA 6656
Qy 2770 GGGGTGAGACCCCTGACCATCGAGGCCCCACTACCAACCCCTGGACTGGAGCTTACATGTGGC 2829
Db 6657 GGGGTGAGACCCCTGACCATCGAGGCCCCACTACCAACCCCTGGACTGGAGCTTACATGTGGC 6716
Qy 2830 ACTGTCAACCTTATTCAGAGGATACGACATGATGGCTGTTATTCAGCTCAGCGCA 2889
Db 6717 ACTGTCAACCTTATTCAGAGGATACGACATGATGGCTGTTATTCAGCTCAGCGCA 6776
Qy 2890 TGGAGGAGAGGATATCTTCAGGAGACTTCGAGGAGCCCATGAACCCCAAGTGGCGG 2949
Db 6777 TGGAGGAGAGGATATCTTCAGGAGACTTCGAGGAGCCCATGAACCCCAAGTGGCGG 6836
Qy 2950 CCGTTCTTACAACCCGCAACGACTTCTCCATGCTCGCGCTGGAACTTCTCCGCGGAGTCCA 3009
Db 6837 CCGTTCTTACAACCCGCAACGACTTCTCCATGCTCGCGCTGGAACTTCTCCGCGGAGTCCA 6896
Qy 3010 TCACGTCCCGAGTCAGAGTGGCCGAGCAGGAGCCGTACACCCGCTCGATGAGATCC 3069
Db 6897 TCACGTCCCGAGTCAGAGTGGCCGAGCAGGAGCCGTACACCCGCTCGATGAGATCC 6956
Qy 3070 TGGAGATCTTGGATCGAGGATTAACCCCGAGCCCAAGCTCTACATCGTTTG 3126
Db 6957 TGGAGATCTTGGATCGAGGATTAACCCCGAGCCCAAGCTCTACATCGTTTG 7013

RESULT 9
AAZ27601
ID AAZ27601 standard; DNA; 1791 BP.
XX
AC AAZ27601;
XX
DT 16-DEC-1999 (first entry)
XX
DE Stachybotrys phenol oxidase coding sequence.
XX
KW Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
XX fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
OS Stachybotrys chartarum.
XX
PN WO9949020-A2.
XX
PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-US06327.
XX
PR 24-MAR-1998; 98US-0046969.
PR 22-DEC-1998; 98US-0218702.
PR 22-MAR-1999; 99US-0273957.
XX
PA (GEMV) GENENCOR INT INC.
XX
PI Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;
XX
DR WPI; 1999-591088/50.
DR P-PSDB; AAY39992.
XX
PT Novel enzyme for modifying coloured compounds used to prevent
PT dye-transfer -
XX
PS Claim 21; Fig 5; 64pp; English.
XX
CC This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
CC of the invention. The invention is used to modify a coloured compound and
CC prevent dye transfer during fabric washing, or for stain bleaching or
CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC and food industries.
XX
SQ Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;
Query Match 40.1%; Score 1474; DB 20; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
Qy 1038 GTCATATGCTGTTCAAGTCAATGCAACTGGCAGCAGCTCCGGGCTCCTGCTGGAGTC 1097
Db 1 GTCATATGCTGTTCAAGTCAATGCAACTGGCAGCAGCTCCGGGCTCCTGCTGGAGTC 60
Qy 1098 CTCGCATCCCGATGGACACCGGCAGCCACCCTTTGAGGCTGTTGATCCCGAAGTGAAG 1157
Db 61 CTCGCATCCCGATGGACACCGGCAGCCACCCTTTGAGGCTGTTGATCCCGAAGTGAAG 120
Qy 1158 ACTGAGGCTTCGCTGACTCCCTCCTTCTGTCAGCAGCGGATGACGACTGGGAGTCACCT 1217
Db 121 ACTGAGGCTTCGCTGACTCCCTCCTTCTGTCAGCAGCGGATGACGACTGGGAGTCACCT 180
Qy 1218 CCATACAACTTCTTTACAGGTGAGACACCTGTCCACCTGTTTTCCTCGATAACTAAC 1277
Db 181 CCATACAACTTCTTTAC----- 198
Qy 1278 TCTTTATGGAATGCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGATGCTTTGAT 1337
Db 199 -----AGGAATGCCTGCCAATTCACCTGTCAAGCAGCCCAAGAT----- 239
Qy 1338 TTTCTACGAGCAACTCGCCCCGAGCTAATGATTTCTAGGATCATTACCACCCCTGTAC 1397
Db 240 -----GATCATTACCACCCCTGTAC 260

Qy 1398 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTGAGCAAAAGGTGAGTTT 1457
Dy 261 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTGAGCAAAAG- 311
Qy 1458 GCTCAGAACCTTGTGGTAAATTAATCATTTACTGACCCCTTTTCAGATTTACCCACCTT 1517
Dy 312 -----GATTTACCCACCTT 326
Qy 1518 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGTCTACTTTCAATGTTCC 1577
Dy 327 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGTCTACTTTCAATGTTCC 386
Qy 1578 CAGAGGAACAGAGACTGATGTTAGTTAGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 1637
Dy 387 CAGAGGAACAGAGACTGATGTTAGTTAGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 446
Qy 1638 TCTGCACGGCTCCCATCGCTGCCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCC 1697
Dy 447 TCTGCACGGCTCCCATCGCTGCCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCC 506
Qy 1698 TGGCGAGTACAAGGATTAATCTTTCCCACTACCAATGCCCGCCCTCTGTGGTACCA 1757
Dy 507 TGGCGAGTACAAGGATTAATCTTTCCCACTACCAATGCCCGCCCTCTGTGGTACCA 566
Qy 1758 TGACCAACGCTTTCATGAAGGATGCTACGAGCCCTTATCTTTCTTGGCTACCTTTGGCTA 1817
Dy 567 TGACCACGCTTTCATGA----- 583
Qy 1818 ACCAATCTCTTTGCTAGACTGCTGAGAAATGCTTACTTTGGTAGGCTGGCGCTTACATTT 1877
Dy 584 -----AGACTGCTGAGAAATGCTTACTTTGGTAGGCTGGCGCTTACATTT 627
Qy 1878 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTCGATATC 1937
Dy 628 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTCGATATC 687
Qy 1938 CCTCTGATCTTACGAGGCAAGTACTATTAACCGCGATGTAACCTGCGTTTCGACCGAGGTT 1997
Dy 688 CCTCTGATCTTACGAGGCAAGTACTATTAACCGCGATGTAACCTGCGTTTCGACCGAGGTT 747
Qy 1998 GAGGACGAGGACCTTGGGGAGATGCTATCCATGCTCAACGACGACCCATGGCTTTCCTT 2057
Dy 748 GAGGACGAGGACCTTGGGGAGATGCTATCCATGCTCAACGACGACCCATGGCTTTCCTT 807
Qy 2058 AACGTCCAGCCCGCAAGTACCGTTTCCGATTTCTCAACGCTGCGTCTCTGCTTTGG 2117
Dy 808 AACGTCCAGCCCGCAAGTACCGTTTCCGATTTCTCAACGCTGCGTCTCTGCTTTGG 867
Qy 2118 CTCCTCTACCTCGTCAGGACGAGCTCTCCCAACGCTCAGAATTCCTTTCCAAAGTCATTCGC 2177
Dy 868 CTCCTCTACCTCGTCAGGACGAGCTCTCCCAACGCTCAGAATTCCTTTCCAAAGTCATTCGC 927
Qy 2178 TCTGATGCTGCTCCTTCAAGCCCGCTTCAAGCCCTTAACCTCTACCTTGTGTTGCC 2237
Dy 928 TCTGATGCTGCTCCTTCAAGCCCGCTTCAAGCCCTTAACCTCTACCTTGTGTTGCC 987
Qy 2238 GAGCGTTACGAGATCATTTATTTGGTATGCCCCCTCTCAGCAATGAGTCAAGAAGTCTA 2297
Dy 988 GAGCGTTACGAGATCATTTATTT----- 1008
Qy 2298 AGACTTAACACTTTGTAGACTTCAACCACTTTGCTGGCCAGACTCTTGACCTCGCAACGTT 2357
Dy 1009 -----GACTTCAACCACTTTGCTGGCCAGACTCTTGACCTCGCAACGTT 1053
Qy 2358 GCTGAGACCAACGATGTCGGGACGAGAGATGAGTACGCTTCGCACTCTCGAGTGATGGCC 2417
Dy 1054 GCTGAGACCAACGATGTCGGGACGAGAGATGAGTACGCTTCGCACTCTCGAGTGATGGCC 1113
Qy 2418 TTCGTGCTGAGCTCTGGCACTGTTGAGGACAAACGACGAGTCCCTCCACTCTCCGTGAC 2477
Dy 1114 TTCGTGCTGAGCTCTGGCACTGTTGAGGACAAACGACGAGTCCCTCCACTCTCCGTGAC 1173

Qy 2478 GTTCCTTTTCCCTCTCAAGAAGAGGCCCCCGGACAGCACTTCAAGTTTGAACGCAGC 2537
Dy 1174 GTTCCTTTTCCCTCTCAAGAAGAGGCCCCCGGACAGCACTTCAAGTTTGAACGCAGC 1233
Qy 2538 AACGACACTACCTGATCAACGATGTTGGCTTTGCGGATGTCAATGACGCTGCTCGTGCC 2597
Dy 1234 AACGACACTACCTGATCAACGATGTTGGCTTTGCGGATGTCAATGACGCTGCTCGTGCC 1293
Qy 2598 AAGCCCGAGCTCGGCACCGTTGAGTCTGGAGCTCGAGAACTCCTCTGGAGGCTGGAGC 2657
Dy 1294 AAGCCCGAGCTCGGCACCGTTGAGTCTGGAGCTCGAGAACTCCTCTGGAGGCTGGAGC 1353
Qy 2658 CACCCGCTCCACATTCACCTTTGACTTCAAGATCTCAAGCGAACTGGTGGTGGTGGC 2717
Dy 1354 CACCCGCTCCACATTCACCTTTGACTTCAAGATCTCAAGCGAACTGGTGGTGGTGGC 1413
Qy 2718 CAGGTCAATGAGCTTACGAGTCTGCTGCTTAAGGATGCTGCTGGGAGGGGTGAG 2777
Dy 1414 CAGGTCAATGAGCTTACGAGTCTGCTGCTTAAGGATGCTGCTGGGAGGGGTGAG 1473
Qy 2778 ACCCTGACCATCGAGGCCCCACTTACCAACCCCTGGACTGGAGCTTACATGTGGCACTGTGCAC 2837
Dy 1474 ACCCTGACCATCGAGGCCCCACTTACCAACCCCTGGACTGGAGCTTACATGTGGCACTGTGCAC 1533
Qy 2838 AACCTCAATTCAGGAGTAACGACATGATGCTGCTTCAAGCTCACCGCCCATGGAGGAG 2897
Dy 1534 AACCTCAATTCAGGAGTAACGACATGATGCTGCTTCAAGCTCACCGCCCATGGAGGAG 1593
Qy 2898 AAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCCCTTCCCT 2957
Dy 1594 AAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCCCTTCCCT 1653
Qy 2958 TACAACCCCAACGACTTCCATGCTCGCGCTGGAATTTCTCGCGCGAGTCCATCACTGCC 3017
Dy 1654 TACAACCCCAACGACTTCCATGCTCGCGCTGGAATTTCTCGCGCGAGTCCATCACTGCC 1713
Qy 3018 CGAGTGCAGGAGCTGGCGGAGGAGGAGCGGTACAACCCCTCGATGAGATCCTCGAGGAT 3077
Dy 1714 CGAGTGCAGGAGCTGGCGGAGGAGGAGCGGTACAACCCCTCGATGAGATCCTCGAGGAT 1773
Qy 3078 CTGGAATCGAGGAGTAA 3095
Dy 1774 CTGGAATCGAGGAGTAA 1791
RESULT 10
AAA50019
ID AAA50019 standard; DNA; 1791 BP.
XX
AC AAA50019;
XX
XX
DT 10-OCT-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidising enzyme cDNA.
XX
KW Phenol oxidising enzyme; detergent; bleaching; ss.
XX
OS Stachybotrys chartarum.
XX
FH Key
FT CDS Location/Qualifiers
FT 7..1791
XX /*tag= a
XX
PN WO200039306-A2.
XX
PD 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-EP10287.
XX
PR 23-DEC-1998; 98US-0220871.
XX 23-JUN-1999; 99US-0338723.
PA (UNIL) UNILEVER NV.

PA (UNIL) UNILEVER PLC.
XX (HIND-) HINDUSTAN LEVER LTD.
FI Bodie EA, Van Der Velden S, De Vries CH, Wang H;
XX WPI: 2000-514528/46.
DR P-PSDB; AAY95537.
XX Detergent composition comprising novel phenol oxidising enzyme obtained
PT from fungus or bacteria, useful for pulp and paper bleaching, bleaching
PT color of stains on fabric and for anti-dye redeposition
XX Disclosure; Fig 5A-B; 45pp; English.
XX
CC The present sequence is that of the Stachybotrys chartarum MUCL 38898
CC cDNA encoding a phenol oxidising enzyme (see AAY95537). The invention
CC relates to detergent compositions comprising novel phenol oxidising
CC enzymes that are encoded by nucleic acids capable of hybridising to
CC the S. chartarum phenol oxidising enzyme gene (see AAA50018), provided
CC the enzymes are capable of modifying the colour associated with dyes
CC or coloured compounds, and are produced from a bacterium, yeast or
CC fungus (see AAY95538-40). The phenol oxidising enzymes can be used
CC for pulp and paper bleaching, for bleaching the colour of stains on
CC fabric and for anti-dye transfer in detergent and textile
CC applications. They may also be capable of modifying the colour in
CC the absence or presence of an enhancer. Expression vectors and host
CC cells comprising a nucleic acid encoding a phenol oxidising enzyme,
CC methods for producing the phenol oxidising enzyme, and methods for
CC constructing expression hosts are provided.
XX
SQ Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

Query Match 40.1%; Score 1474; DB 21; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

Qy 1038 GTCATATGCTGTTCAAGTCATGCGCACTGGCAGCAGCCTCCGGCTCCTGCTGGAGTC 1097
Db 1 GTCATATGCTGTTCAAGTCATGCGCACTGGCAGCAGCCTCCGGCTCCTGCTGGAGTC 60

Qy 1098 CTCGGCATCCGATGGACACCGGAGCCACCCCATTTGAGGCTGTGATCCCGAAGTGAAG 1157
Db 61 CTCGGCATCCGATGGACACCGGAGCCACCCCATTTGAGGCTGTGATCCCGAAGTGAAG 120

Qy 1158 ACTGAGGCTTCGCTGACTCCCTCCTGCTGCAGCAGCGATGACGACTGGGAGTCACT 1217
Db 121 ACTGAGGCTTCGCTGACTCCCTCCTGCTGCAGCAGCGATGACGACTGGGAGTCACT 180

Qy 1218 CCATACAACTTGCCTTTACAGGTGAGACACCTGTCCACCTGTTTCCCTCGATAACTAAC 1277
Db 181 CCATACAACTTGCCTTTAC----- 198

Qy 1278 TCTATAGGAATGCCCTGCCAATTCACCTGTCAAGCAGGCCAAGATGATGCTTTGAT 1337
Db 199 -----AGGAATGCCCTGCCAATTCACCTGTCAAGCAGGCCAAGAT----- 239

Qy 1338 TTTCTACGAAGCAACTCGGCCCGGACTTAATGTTTCTAGGATCATACCAACCTGTCTAC 1397
Db 240 -----GATCATTACCAACCTGTCTAC----- 260

Qy 1398 CGGAAGGACATTTGGTACTATGATGCGAGATCAAGCCATTTTCAGAAAGGAGTCACTTT 1457
Db 261 CGGAAGGACATTTGGTACTATGATGCGAGATCAAGCCATTTTCAGAAAG----- 311

Qy 1458 GCTCAGAAACCTTGTGGTAATTAATCATGTTACTGACCCCTTTTCAGATTTACCCACCTT 1517
Db 312 -----GATTTACCCACCTT----- 326

Qy 1518 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGCTACTCTTTCAATGTTC 1577
Db 327 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGCTACTCTTTCAATGTTC 386

Qy 1578 CAGAGGAACAGAGACTGTAGTTAGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 1637

Db 387 CAGAGGAACAGAGACTGTAGTTAGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 446
Qy 1638 TCTGCACGGCTCCCATCGCTGCCCTTTCGATGTTGGCTGAAAGATGTGACTTCC 1697
Db 447 TCTGCACGGCTCCCATCGCTGCCCTTTCGATGTTGGCTGAAAGATGTGACTTCC 506
Qy 1698 TGGGAGTACAAAGGATTACTACTTTTCCCACTACCAATCCGCCCGCCCTTCTGTGTGATCA 1757
Db 507 TGGGAGTACAAAGGATTACTACTTTTCCCACTACCAATCCGCCCGCCCTTCTGTGTGATCA 566
Qy 1758 TGACCAAGCTTTTCATGAAGGATGCTAGCAGGCCCTTATCTTCTTGGCTACTCTTGGCTA 1817
Db 567 TGACCAAGCTTTTCATGA----- 583
Qy 1818 ACCAACTTCCTTTTCGTAGTACGCTGAGAATGCCCTACTTTTGGTACGGCTGGCGCCTACATT 1877
Db 584 -----AGACTGCTGAGAATGCCCTACTTTTGGTACGGCTGGCGCCTACATT 627
Qy 1878 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTGGATATC 1937
Db 628 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTGGATATC 687
Qy 1938 CCTCTGATCTGAGCGCAAGTACTATTAACCCGATGTTACCCCTGCGTTTCGACGAGGGT 1997
Db 688 CCTCTGATCTCTGAGCGCAAGTACTATAACGCCGATGGTACCCCTGCGTTTCGACGAGGGT 747
Qy 1998 GAGGACGAGGAGCTGTGGGAGATGTCATCCATGTCACAGGACAGCCATGGCCCTTCCCT 2057
Db 748 GAGGACGAGGAGCTGTGGGAGATGTCATCCATGTCACAGGACAGCCATGGCCCTTCCCT 807
Qy 2058 AACGTCCAGCCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCCGTCTGCTGCTTGG 2117
Db 808 AACGTCCAGCCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCCGTCTGCTGCTTGG 867
Qy 2118 CTCCTCTACCTCTGTCAGGACAGCTCTCCCAACGTCAGAATTCCTTTCGAAGTCAATGCC 2177
Db 868 CTCCTCTACCTCTGTCAGGACAGCTCTCCCAACGTCAGAATTCCTTTCGAAGTCAATGCC 927
Qy 2178 TCTGATGCTGCTCTCTTCAAGCCCCCGTTTCAGACCTCTAACCTCTACCTTGTGTTGCC 2237
Db 928 TCTGATGCTGCTCTCTTCAAGCCCCCGTTTCAGACCTCTAACCTCTACCTTGTGTTGCC 987
Qy 2238 GAGGTTTACGAGATCAATTATTGGTATGCCCCCTCTCAGCAATGAGTCAAGAATCTA 2297
Db 988 GAGGTTTACGAGATCAATTAT----- 1008
Qy 2298 AGACTAACCTTTGATAGCTTCACCAACTTTTGTGCGCAGACTCTTGACCTCGCAAGCTT 2357
Db 1009 -----GACTTCACCAACTTTTGTGCGCAGACTCTTGACCTCGCAAGCTT 1053
Qy 2358 GCTGAGACCAACGATGTCCGGCAGGAGATGAGTACGCTCCGACTCTCGAGGTGATGGC 2417
Db 1054 GCTGAGACCAACGATGTCCGGCAGGAGATGAGTACGCTCCGACTCTCGAGGTGATGGC 1113
Qy 2418 TTCGTGTCGCTGCTGCTGCTGTTGAGGACAAACGAGGTCCTCCACTCTCCGCTGAC 2477
Db 1114 TTCGTGTCGCTGCTGCTGCTGTTGAGGACAAACGAGGTCCTCCACTCTCCGCTGAC 1173
Qy 2478 GTTCTTTTCCCTCTCAAGAAAGGCCCCCGCAGAACGACTTCAAGTTTGAACGACG 2537
Db 1174 GTTCTTTTCCCTCTCAAGAAAGGCCCCCGCAGAACGACTTCAAGTTTGAACGACG 1233
Qy 2538 AACGGACACTACCTTGATCAACGATGTTGGCTTTGCGGATGTCATGAGCGTCTCTGGCC 2597
Db 1234 AACGGACACTACCTTGATCAACGATGTTGGCTTTGCGGATGTCATGAGCGTGTCTGGCC 1293
Qy 2598 AAGCCCGAGCTCGCACGCTTGGAGTCTGGGAGCTCGAGAACTCCTCTGGAGGCTGGAGC 2657
Db 1294 AAGCCCGAGCTCGCACGCTTGGAGTCTGGGAGCTCGAGAACTCCTCTGGAGGCTGGAGC 1353
Qy 2658 CACCCCGTCCACATTCACCTTGTGACTTCAAGATTCCTCAAGCGAACTGSGTGTGCTGGC 2717
Db 2658 CACCCCGTCCACATTCACCTTGTGACTTCAAGATTCCTCAAGCGAACTGSGTGTGCTGGC 2717

Db 1354 CACCCGTCACATTCACCTTGTGACTTCAAGATCCTCAACGGAACTGGTGGTGGC 1413
Qy 2718 CAGGTATGCCCTACGAGTCTCTGGTCTTAAGGATGCTGTGGTGGCAGGGGTGAG 2777
Db 1414 CAGGTATGCCCTACGAGTCTCTGGTCTTAAGGATGCTGTGGTGGCAGGGGTGAG 1473
Qy 2778 ACCCTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTTACATGTGGCACTGTAC 2837
Db 1474 ACCCTGACCATCGAGGCCCACTACCAACCCCTGGACTGGAGCTTACATGTGGCACTGTAC 1533
Qy 2838 AACCTCATTCACGAGGATTAACGACATGATGGCTGTATTCAAGTCCACGCCCATGGAGGAG 2897
Db 1534 AACCTCATTCACGAGGATTAACGACATGATGGCTGTATTCAAGTCCACGCCCATGGAGGAG 1593
Qy 2898 AAGGATATCTTTCAGGAGGACTTCGAGGACCCCACTGAACCCCAAGTGGCGGCCCTTCT 2957
Db 1594 AAGGATATCTTTCAGGAGGACTTCGAGGACCCCACTGAACCCCAAGTGGCGGCCCTTCT 1653
Qy 2958 TACAACCCGACGACTTCCATGCTCGCGTGGAACTTCTCGCGCGAGTCCATCACTGCC 3017
Db 1654 TACAACCCGACGACTTCCATGCTCGCGTGGAACTTCTCGCGCGAGTCCATCACTGCC 1713
Qy 3018 CGAGTGCAGGAGCTGGCGGAGGAGCGGTACAACCGCTCGATGAGATCCTGGAGGAT 3077
Db 1714 CGAGTGCAGGAGCTGGCGGAGGAGCGGTACAACCGCTCGATGAGATCCTGGAGGAT 1773
Qy 3078 CTTGGAATCGAGGAGTAA 3095
Db 1774 CTTGGAATCGAGGAGTAA 1791

RESULT 11
ID AAA51314 standard; DNA; 1791 BP.
XX
AC AAA51314;
XX
DT 09-OCT-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidizing enzyme cDNA.
XX
KW Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
KW pulp; paper bleaching; ss.
XX
OS Stachybotrys chartarum.
XX
FH Key Location/Qualifiers
FT CDS 7..1791
FT /*tag= a
FT /product= phenol_Oxidizing_Enzyme
XX
PN WO200037654-A2.
XX
PD 29-JUN-2000.
XX
PF 20-DEC-1999; 99WO-US31009.
XX
PR 23-DEC-1998; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.
XX
PA (GENW) GENENCOR INT INC.
XX
PI Wang H, Bodie EA;
XX
DR WPI: 2000-452191/39.
DR P-PSDB: AAY96761.
XX
PT New phenol oxidizing enzyme for modifying colors associated with dyes
PT or colored compounds, is obtained from fungus and is encoded by a
PT nucleic acid comprising a specific nucleotide sequence
XX
PS Disclosure; Fig 5A-B; 45pp; English.
XX

CC This cDNA encodes Stachybotrys chartarum phenol oxidizing enzyme.
CC Phenol oxidizing enzymes encoded by nucleic acid sequences which
CC hybridize to this DNA are claimed, as long as the enzyme is capable of
CC modifying the colour associated with dyes or coloured compounds. The
CC enzymes are useful in detergent compositions and for modifying colors
CC associated with dyes or colored compounds which occur in stains in a
CC sample. The enzymes are also useful for pulp and paper bleaching,
CC anti-dye transfer in detergent and other textile applications.
XX
SQ Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

Query Match 40.1%; Score 1474; DB 21; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

Qy 1038 GTCATATGCTTCAAGTCATGCAACTGGCAGAGCCTCCGGCTCCTGCTCGAGTC 1097
Db 1 GTCATATGCTTCAAGTCATGCAACTGGCAGAGCCTCCGGCTCCTGCTCGAGTC 60

Qy 1098 CTCGGCATCCCGATGGACACCGGACGCCCACTTGAAGCTTGTATCCCCGAAGTGAAG 1157
Db 61 CTCGGCATCCCGATGGACACCGGACGCCCACTTGAAGCTTGTATCCCCGAAGTGAAG 120

Qy 1158 ACTGAGGTCTTCGCTGACTCCTCCTTGTGTCAGCAGGCGATGACACTGGGAGTCACT 1217
Db 121 ACTGAGGTCTTCGCTGACTCCTCCTTGTGTCAGCAGGCGATGACACTGGGAGTCACT 180

Qy 1218 CCATACAACTTGCCTTACAGGTGAGACACCTGTGCCACCTGTTTCCCTCGATACATAC 1277
Db 181 CCATACAACTTGCCTTAC----- 198

Qy 1278 TCTTATAGGAATGCCCTGCCCAATCCACCTGTCAAGCAGCCCCAAGATGTATGCTTTGAT 1337
Db 199 -----AGGAATGCCCTGCCCAATCCACCTGTCAAGCAGCCCCAAGAT----- 239

Qy 1338 TTTCTACGAAGCAACTCGGCCCGGACTAATGTATTCTTAGGATCATTACCAACCCCTGTGAC 1397
Db 240 -----GATCATTACCAACCCCTGTGAC 260

Qy 1398 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAGGGTGATTT 1457
Db 261 CGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAG----- 311

Qy 1458 GCTCAGAAACCTTGTGTGTAATTAATCATTGTTACTGAGCCCTTTCAGATTTACCCACCTTT 1517
Db 312 -----GATTTACCCACCTTT 326

Qy 1518 GGGCCCTGCCACTCTCGTGGCTAGCATGGCATAGCCCTGGTCTCTACTTTCAATGTTCC 1577
Db 327 GGGCCCTGCCACTCTCGTGGCTAGCATGGCATAGCCCTGGTCTCTACTTTCAATGTTCC 386

Qy 1578 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 1637
Db 387 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 446

Qy 1638 TCTGCACGGCTCCCATCGCGTGGCCCTTTTCATGTTGGGTGAAGATGTGACCTTCC 1697
Db 447 TCTGCACGGCTCCCATCGCGTGGCCCTTTTCATGTTGGGTGAAGATGTGACCTTCC 506

Qy 1698 TGGCGAGTACAAGGATTAATCTTTCCCAACTTACCAATCCGCCGCCCTTCTCTGGTACCA 1757
Db 507 TGGCGAGTACAAGGATTAATCTTTCCCAACTTACCAATCCGCCGCCCTTCTCTGGTACCA 566

Qy 1758 TCACCACGCTTTCATGAAGGTATGCTACGAGCCTTTATCTTCTTGGCTACCTTTGGCTA 1817
Db 567 TCACCACGCTTTCATGA----- 583

Qy 1818 ACCAACTTCTCTTCGTAGACTGCTGAGAACTGCTACTTTGGTCAGGCTGGGCCCTACATTT 1877
Db 584 -----AGACTGCTGAGAACTGCTACTTTGGTCAGGCTGGGCCCTACATTT 627

Qy 1878 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCTATGGCGAGTTCGATATC 1937
Db 1937

Db 628 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCTATGCGGAGTTTCAATATC 687
Qy 1938 CCTCTGATCCTGACGGCCAACTACTATAAACCGCATGTATCCCTGCGTTCGACGAGGGT 1997
Db 688 CCTCTGATCCTGACGGCCAACTACTATAAACCGCATGTATCCCTGCGTTCGACGAGGGT 747
Qy 1998 GAGGACCAAGGACCTGTGTGGGAGATGTATCATCATGTCAACGACGAGCCATGGCTTTCCTT 2057
Db 748 GAGGACCAAGGACCTGTGTGGGAGATGTATCATCATGTCAACGACGAGCCATGGCTTTCCTT 807
Qy 2058 AACGTCCAGCCCGCCGAACTACCGTTTCCGATTCCTCAACGCTGCGGTGCTCTCGTCTTGG 2117
Db 808 AACGTCCAGCCCGCCGAACTACCGTTTCCGATTCCTCAACGCTGCGGTGCTCTCGTCTTGG 867
Qy 2118 CTCCTCTACCTCTGTCAGACAGCTCTCCCAACGTCAGAAATTCCTTTCCAAAGTCATTGCC 2177
Db 868 CTCCTCTACCTCTGTCAGACAGCTCTCCCAACGTCAGAAATTCCTTTCCAAAGTCATTGCC 927
Qy 2178 TCTGATGCTGGTCTCTTCAAGCCCCCGTTTCAGACCTCTAACCTCTACCTTTGCTGTGGCC 2237
Db 928 TCTGATGCTGGTCTCTTCAAGCCCCCGTTTCAGACCTCTAACCTCTACCTTTGCTGTGGCC 987
Qy 2238 GAGCCTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCAGCAATGAGTCAAGAACTCTA 2297
Db 988 GAGCCTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCAGCAATGAGTCAAGAACTCTA 1008
Qy 2298 AGACTTAACACTTGTATGACTTTCACCAACTTTGCTGCCAGACTTTGACCTGCGCAACGTT 2357
Db 1009 -----GACTTCACCAACTTTGCTGCCAGACTTTGACCTGCGCAACGTT 1053
Qy 2358 GCTGAGACAACGATGTGCGGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATGGC 2417
Db 1054 GCTGAGACAACGATGTGCGGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATGGC 1113
Qy 2418 TTCGTGCTGAGCTTGGCACTGTTGAGGACAACAGCCAGGTCCCTCCACTCTCCGTGAC 2477
Db 1114 TTCGTGCTGAGCTTGGCACTGTTGAGGACAACAGCCAGGTCCCTCCACTCTCCGTGAC 1173
Qy 2478 GTTCCTTTCCCTCCTCAAGAAGGCCCGCCGACAGCACTTCAAGTTTGAACGCAGC 2537
Db 1174 GTTCCTTTCCCTCCTCAAGAAGGCCCGCCGACAGCACTTCAAGTTTGAACGCAGC 1233
Qy 2538 AACGGACACTACTGATCAACGATTTGGCTTTGCCGATGTCAATGAGCGTCTCCTGGCC 2597
Db 1234 AACGGACACTACTGATCAACGATTTGGCTTTGCCGATGTCAATGAGCGTCTCCTGGCC 1293
Qy 2598 AAGCCCGAGCTCGGACACCGTTGAGTCTGGGAGCTCGAGAACTCTCTGGAGCTGGAGC 2657
Db 1294 AAGCCCGAGCTCGGACACCGTTGAGTCTGGGAGCTCGAGAACTCTCTGGAGCTGGAGC 1353
Qy 2658 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCCTCAAGCGAACTGGTGGTCTGTGC 2717
Db 1354 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCCTCAAGCGAACTGGTGGTCTGTGC 1413
Qy 2718 GAGGTATGCCCTAGAGTCTGCTGGCTTTAAGGATGTGCTGTGGTGGGACGAGGTGAG 2777
Db 1414 GAGGTATGCCCTAGAGTCTGCTGGCTTTAAGGATGTGCTGTGGTGGGACGAGGTGAG 1473
Qy 2778 ACCCTGACATCGAGGCCCACTACCAACCTCGACTGGAGCTTACATGTGGCACTGTAC 2837
Db 1474 ACCCTGACATCGAGGCCCACTACCAACCTCGACTGGAGCTTACATGTGGCACTGTAC 1533
Qy 2838 AACCTCATTCACGAGGATACACATGATGGCTGTATTCAAGCTCACGCCCATGAGGAG 2897
Db 1534 AACCTCATTCACGAGGATACACATGATGGCTGTATTCAAGCTCACGCCCATGAGGAG 1593
Qy 2898 AAGGGATATCTTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCCGCTTCT 2957
Db 1594 AAGGGATATCTTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCCGCTTCT 1653
Qy 2958 TACACCGCAACGACTTTCATGCTCGCGTGGAAACTTCTCCGCGAGTCCATCACTGCC 3017
Db 1654 TACACCGCAACGACTTTCATGCTCGCGTGGAAACTTCTCCGCGAGTCCATCACTGCC 1713

Qy 3018 CGAGTGCAGGAGCTGGCCGACGAGGACCGTACAAACCGCTCGATGAGATCCTGGAGAT 3077
Db 1714 CGAGTGCAGGAGCTGGCCGACGAGGACCGTACAAACCGCTCGATGAGATCCTGGAGAT 1773
Qy 3078 CTTGGAATCGAGGAGTAA 3095
Db 1774 CTTGGAATCGAGGAGTAA 1791
RESULT 12
AAL47584
ID AAL47584 standard; cDNA; 1791 BP.
XX
AC AAL47584;
XX
DT 13-SEP-2002 (first entry)
XX
S chartarum phenol oxidising enzyme cDNA.
DE
XX Phenol oxidising enzyme; enzyme; fungus; redox reaction; detergent;
KW paper industry; pulp industry; textile; food industry; gene; ss.
XX
OS Stachybotrys chartarum.
XX
FH Key Location/Qualifiers
FT CDS 7..1791
ET /*tag= a
ET /product= "phenol oxidising enzyme"
XX
PN US6399329-B1.
PD 04-JUN-2002.
XX
PF 21-DEC-1999; 99US-0468578.
XX
PR 12-DEC-1998; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.
XX
PA (GEMV) GENENCOR INT INC.
XX
PI Wang H, Bodie EA;
XX
DR WPI; 2002-498835/53.
DR P-PSDB; AAO18210.
XX
PT New polynucleotides encoding phenol oxidizing enzymes, useful for
PT preventing the transfer of dyes in solution from one textile to another
PT during detergent washing -
XX
PS Disclosure; Fig 5; 37pp; English.
XX
CC The present invention provides the protein and coding sequences of phenol
CC oxidising enzymes from Stachybotrys chartarum, Bipolaris spicifera and
CC Curvularia pallescens. These enzymes are useful in the textiles, paper,
CC pulp, detergent and food industries. In particular they are useful for
CC preventing the transfer of dyes in solution from one textile to another
CC during detergent washing (dye transfer inhibition). The present sequence
CC is the S. chartarum phenol oxidising enzyme cDNA.
SQ
Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;
Query Match 40.1%; Score 1474; DB 24; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
Qy 1038 GTCAATATGCTGTTCAAGTCAATGGCAACTGGCAGAGCTCCGGGCTCTGTCTGGAGTC 1097
Db 1 GTCAATATGCTGTTCAAGTCAATGGCAACTGGCAGAGCTCCGGGCTCTGTCTGGAGTC 60
Qy 1098 CTCGGCATCCCGATGGACACACCGGACCCACCATTTAGGCTGTTGATCCCGAAGTGAAG 1157
Db 61 CTCGGCATCCCGATGGACACACCGGACCCACCATTTAGGCTGTTGATCCCGAAGTGAAG 120

QY 1158 ACTGAGGCTTCGCTGACTCCCTCCTTGTGTCAGACGAGGCGATGACGACTGGGAGTCACCT 1217
|||||
Db 121 ACTGAGGCTTCGCTGACTCCCTCCTTGTGTCAGACGAGGCGATGACGACTGGGAGTCACCT 180
|||||
QY 1218 CCATACAACCTTGCCTTTACAGGTGAGACACCTGTGCCACCTGTTTCCCTCGATAACTAC 1277
|||||
Db 181 CCATACAACCTTGCCTTTAC----- 198
|||||
QY 1278 TCTTATAGGAATGCCCTGCGCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTTTTGAT 1337
|||||
Db 199 -----AGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGAT----- 239
|||||
QY 1338 TTTCTACGAAGCACTCGGCCCGGACTAATGTATCTAGGATCATTTACCAACCTGTCTAC 1397
|||||
Db 240 -----GATCATTTACCAACCTGTCTAC 260
|||||
QY 1398 CGCAAGGACATTTGGTACTATGATGATCAGATCAGCCATTTCAAGCAAGGCTGAGTTT 1457
|||||
Db 261 CGCAAGGACATTTGGTACTATGATGATCAGATCAGCCATTTCAAGCAAG----- 311
|||||
QY 1458 GCTCAAAAACCTTGTGGTAATTAATCATTTGTTACTGACCCCTTTTCAGATTTACCCACCTT 1517
|||||
Db 312 -----GATTTACCCACCTT 326
|||||
QY 1518 GGGCCCTGCCACTCTCGTCGGGTACGATGGCATGAGCCCTGGTCTACTTTTCAATGTTCC 1577
|||||
Db 327 GGGCCCTGCCACTCTCGTCGGGTACGATGGCATGAGCCCTGGTCTACTTTTCAATGTTCC 386
|||||
QY 1578 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACATGCCACCGTGGAGAACTCGGTCCA 1637
|||||
Db 387 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACATGCCACCGTGGAGAACTCGGTCCA 446
|||||
QY 1638 TCTGCACGGCTCCCATCGCGTCCCTTTTCGATGGTTGGGTGAAGATGTGACCTTCC 1697
|||||
Db 447 TCTGCACGGCTCCCATCGCGTCCCTTTTCGATGGTTGGGTGAAGATGTGACCTTCC 506
|||||
QY 1698 TGGCGAGTACAGGATTAATTTCCCAACTACCAATCGCCCGCCTTCTGTGGTACCA 1757
|||||
Db 507 TGGCGAGTACAGGATTAATTTCCCAACTACCAATCGCCCGCCTTCTGTGGTACCA 566
|||||
QY 1758 TGACCACGCTTTTCAAGGTATGCTACGAGCGCTTTATCTTTCTTGGCTACCTTTGGCTA 1817
|||||
Db 567 TGACCACGCTTTTCAAG----- 583
|||||
QY 1818 ACCAACTTCTCTTCTGTPAGACTGCTGAGATGCTACTTTGGTCAGGCTGGCGCCTACATT 1877
|||||
Db 584 -----AGACTGCTGAGATGCCTACTTTTGGTCAGGCTGGCGCCTACATT 627
|||||
QY 1878 ATCAAGCAGAGGCTGAGGATGCTTCGGTCTTCTTAGTGGCTATGGCGAGTTCGATATC 1937
|||||
Db 628 ATCAAGCAGAGGCTGAGGATGCTTCGGTCTTCTTAGTGGCTATGGCGAGTTCGATATC 687
|||||
QY 1938 CCTCTGATCCTGACGGCCAAAGTACTATAACGGCGATGTTACCTCGTTCGACCGAGGCT 1997
|||||
Db 688 CCTCTGATCCTGACGGCCAAAGTACTATAACGGCGATGTTACCTCGTTCGACCGAGGCT 747
|||||
QY 1998 GAGGACAGGACCTGTGGGAGATGTCATCCATGTCAACGGCAGCCATGGCTTTCCCTT 2057
|||||
Db 748 GAGGACAGGACCTGTGGGAGATGTCATCCATGTCAACGGCAGCCATGGCTTTCCCTT 807
|||||
QY 2058 AAGTCCAGCCCGCAAGTACCGTTCGATTCCTCAACGCTGCCGTGCTCTGCTGGTTGG 2117
|||||
Db 808 AAGTCCAGCCCGCAAGTACCGTTCGATTCCTCAACGCTGCCGTGCTCTGCTGGTTGG 867
|||||
QY 2118 CTCCTCTACTCTGCTCAGGACCAAGCTCTCCCAAGCTCAGATTCCTTTCCAAAGTCATGGC 2177
|||||
Db 868 CTCCTCTACTCTGCTCAGGACCAAGCTCTCCCAAGCTCAGATTCCTTTCCAAAGTCATGGC 927
|||||
QY 2178 TCTGATGCTGGTCTCCTTCAAGCCCGCTTCAGACCTCTAACCTCTACCTTCTGCTGTGCC 2237
|||||
Db 928 TCTGATGCTGGTCTCCTTCAAGCCCGCTTCAGACCTCTAACCTCTACCTTCTGCTGTGCC 987
|||||

QY 2238 GAGCGTTACGAGATCATTTATTTGGTATGCCCTCCCTCTCACGAATGAGTCAAGAAGCTCTA 2297
|||||
Db 988 GAGCGTTACGAGATCATTTATTT----- 1008
|||||
QY 2298 AGACTAAACACTTTGTAGACTTACCAACTTTGCTGGCAGACTCTTGACCTGGCAACGTT 2357
|||||
Db 1009 -----GACTTACCAACTTTGCTGGCAGACTCTTGACCTGGCAACGTT 1053
|||||
QY 2358 GGTGAGACCAACGATGTTCGGCGACGAGGATGATAGCTCGCACTCTCGAGGTGATGCGC 2417
|||||
Db 1054 GCTGAGACCAACGATGTTCGGCGACGAGGATGATAGCTCGCACTCTCGAGGTGATGCGC 1113
|||||
QY 2418 TTCGTCGTGAGCTCTGGCACTGTTCGAGGACACAGCCAGGTCCCTTCCACTCTCCGTGAC 2477
|||||
Db 1114 TTCGTCGTGAGCTCTGGCACTGTTCGAGGACACAGCCAGGTCCCTTCCACTCTCCGTGAC 1173
|||||
QY 2478 GTTCTCTTCCCTCCCTCACAAAGGAAGCCCGCGACAGCACTTCAAGTTTGAACGACG 2537
|||||
Db 1174 GTTCTCTTCCCTCCCTCACAAAGGAAGCCCGCGACAGCACTTCAAGTTTGAACGACG 1233
|||||
QY 2538 AACGGACACTACTGTATCAACGATGTTCGCTTTGCGGATGTCAATGAGCGTGTCTTGCC 2597
|||||
Db 1234 AACGGACACTACTGTATCAACGATGTTCGCTTTGCGGATGTCAATGAGCGTGTCTTGCC 1293
|||||
QY 2598 AAGCCGGAGCTCGGCACCGTTGAGGTCTGGAGCTCGAAGCTCTCTTGAGGCTGGAGC 2657
|||||
Db 1294 AAGCCGGAGCTCGGCACCGTTGAGGTCTGGAGCTCGAAGCTCTCTTGAGGCTGGAGC 1353
|||||
QY 2658 CACCCGCTCCACATTCACCTTTGTTGACTTCAAGATCCTCAAGGAACTGTTGCTGTGCG 2717
|||||
Db 1354 CACCCGCTCCACATTCACCTTTGTTGACTTCAAGATCCTCAAGGAACTGTTGCTGTGCG 1413
|||||
QY 2718 CAGGTATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCTCTGTTGGCAGGGGTGAG 2777
|||||
Db 1414 CAGGTATGCCCTACGAGTCTGCTGGTCTTAAGGATGTCTCTGTTGGCAGGGGTGAG 1473
|||||
QY 2778 ACCGTGACCATCGAGGCCCACTACCAACCTTGAGCTTGAGCTTACATGTGGCACTGTGAC 2837
|||||
Db 1474 ACCGTGACCATCGAGGCCCACTACCAACCTTGAGCTTGAGCTTACATGTGGCACTGTGAC 1533
|||||
QY 2838 AACCTCATTTCAGGAGGATAACGACATGATGGCTGTATTCAACGTCAACGCCATGGAGGAG 2897
|||||
Db 1534 AACCTCATTTCAGGAGGATAACGACATGATGGCTGTATTCAACGTCAACGCCATGGAGGAG 1593
|||||
QY 2898 AAGGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCGTTCTCT 2957
|||||
Db 1594 AAGGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCGTTCTCT 1653
|||||
QY 2958 TACAACCGCAACGACTTCCATGCTCGCGTGGAAACTTCTCCGCCAGTCCATCACTGCC 3017
|||||
Db 1654 TACAACCGCAACGACTTCCATGCTCGCGTGGAAACTTCTCCGCCAGTCCATCACTGCC 1713
|||||
QY 3018 CGAGTCAAGAGCTGGCCGAGGAGGCGGTACAACGCTCGATCAGATCCTGAGGAGAT 3077
|||||
Db 1714 CGAGTCAAGAGCTGGCCGAGGAGGCGGTACAACGCTCGATCAGATCCTGAGGAGAT 3077
|||||
QY 3078 CTTGGAATCGAGGAGTAA 3095
|||||
Db 1774 CTTGGAATCGAGGAGTAA 1791
|||||

RESULT 13
AAZ25727
ID AAZ25727 standard; cDNA; 1791 BP.
XX
AC AAZ25727;
XX
DT 05-JAN-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidising enzyme encoding cDNA.
XX Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
KW detergent; anti-dye transfer; stain removal; bleaching; ss.

XX Stachybotrys chartarum.
XX WO9949010-A2.
XX PN
XX PD 30-SEP-1999.
XX PF 23-MAR-1999; 99WO-EP02042.
XX PR 24-MAR-1998; 98US-0046969.
XX PR 22-DEC-1998; 98US-0218702.
XX PA (UNIL) UNILEVER NV.
XX PA (UNIL) UNILEVER PLC.
XX Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;
XX Wang C;
XX WPI; 1999-601211/51.
XX DR P-PSDB; AAY45222.
XX PT Detergent composition containing phenol oxidase from Stachybotrys, used
XX PT to bleach stains and prevent dye transfer -
XX PS Example 15; Fig 5; 56pp; English.
XX CC The present invention describes a detergent composition containing a
XX CC purified phenol oxidising enzyme derived from Stachybotrys. The present
XX CC sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The
XX CC enzyme can be used to modify the colour of dyes and other coloured
XX CC compounds (e.g. for use in pulp and paper bleaching also for removing
XX CC stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
XX CC transfer during fabric washing.
XX SQ Sequence 1791 BP; 380 A; 554 C; 448 G; 409 T; 0 other;

Query Match 40.0%; Score 1469.2; DB 20; Length 1791;
Best Local Similarity 86.9%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 3; Indels 267; Gaps 5;

QY 1038 GTCATATGCTCTCAAGTCATGGCACTGGCAGAGCTCGGGCTCCTGTCGAGTC 1097
DB 1 GTCATATGCTCTCAAGTCATGGCACTGGCAGAGCTCGGGCTCCTGTCGAGTC 60
QY 1098 CTCGGCATCCCGATGGACACCGCGACCCACCATTTAGGCTGTTGATCCCGAAGTGAAG 1157
DB 61 CTCGGCATCCCGATGGACACCGCGACCCACCATTTAGGCTGTTGATCCCGAAGTGAAG 120
QY 1158 ACTGAGGCTTCGCTGACTCCCTCCTTGGTCGAGGGGATGAGACTGGGAGTCACTT 1217
DB 121 ACTGAGGCTTCGCTGACTCCCTCCTTGGTCGAGGGGATGAGACTGGGAGTCACTT 180
QY 1218 CCATACAACTTCTTACAGGTGAGACACCTGTCCACCTGTTTCCCTCGATACTAAC 1277
DB 181 CCATACAACTTCTTAC----- 198
QY 1278 TCTTATAGAATGCGCTGCCAATTCACCTGTCAAGCAGCCCAAGATGATGCTTTGAT 1337
DB 199 -----AGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGAT----- 239
QY 1338 TTTCTACGAAGCAACTCGGCCCCGACTAATGATTTCTAGGATCATTAACAACCCGTGAC 1397
DB 240 -----GATCATTAACAACCCGTGAC 260
QY 1398 CGGCAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTACGAAGGGTGAATTT 1457
DB 261 CGGCAGGACATTTGGTACTATGAGATCGAGATCAAGCCATTTACGAAG----- 311
QY 1458 GCTCAGAAACCTTGTGGTAATTAATCATTTGTTACTGACCCCTTCAGATTTACCCCACTTT 1517
DB 312 -----GATTTACCCCACTTT 326
QY 1518 GCGCCCTGCCACTCTCGTCGGGTACGATGGCATGAGCCCTGGTCCTACTTTCAATGTTCC 1577

DB 327 GCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGTCCTACTTTCAATGTTCC 386
QY 1578 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTTGGAGAACTCGGTCCA 1637
DB 387 CAGAGGAACAGAGACTGTAGTTAGTTCATCAACAATGCCACCGTTGGAGAACTCGGTCCA 446
QY 1638 TCTGACGGCTCCCATCGCATCGCCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCC 1697
DB 447 TCTGACGGCTCCCATCGCATCGCCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCC 506
QY 1698 TGGGAGTACAGGATTAATACTTTCCAACTACCAATCCCGCCCTTCTGTGTATACA 1757
DB 507 TGGGAGTACAGGATTAATACTTTCCAACTACCAATCCCGCCCTTCTGTGTATACA 566
QY 1758 TGACCACCTTTTCATGAAGGTATGCTACGAGCCTTTATCTTTCTTGGCTACCTTTGGCTA 1817
DB 567 TGACCACGCTTTCATGA----- 583
QY 1818 ACCAACTTCTTTTCGTAGACTGCTGAGAAATGCTACTTTTGGTCAGGCTGGCGCCTACATTT 1877
DB 584 -----AGACTGCTGAGAAATGCTACTTTTGGTCAGGCTGGCGCCTACATTT 627
QY 1878 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCTATGCGAGTTCGATATC 1937
DB 628 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTCTAGTGGCTATGCGAGTTCGATATC 687
QY 1938 CTTCTGATCTCTGACGGCCCAAGTACTATTAACGCCGATGTACCTCGTTTCGACCCAGGGT 1997
DB 688 CTTCTGATCTCTGACGGCCCAAGTACTATTAACGCCGATGTACCTCGTTTCGACCCAGGGT 747
QY 1998 GAGGACGAGGACCTGTGGGAGATGTATCATGATGTAACGAGACGATGGCTTTTCCTT 2057
DB 748 GAGGACGAGGACCTGTGGGAGATGTATCATGATGTAACGAGACGATGGCTTTTCCTT 807
QY 2058 AACGTCGAGCCCGCAAGTACCGTTTCGATTTCCATGATTCCTCAAGCTGCGCTCTCGTCTTGG 2117
DB 808 AACGTCGAGCCCGCAAGTACCGTTTCGATTTCCATGATTCCTCAAGCTGCGCTCTCGTCTTGG 867
QY 2118 CTCCTCTACCTCTGTCAGGACCAAGCTCTCCCAACGTCAGAAATTCCTTCCAAAGTCAATGCC 2177
DB 868 CTCCTCTACCTCTGTCAGGACCAAGCTCTCCCAACGTCAGAAATTCCTTCCAAAGTCAATGCC 927
QY 2178 TCTGATGCTGGTCTCTTCAAGCCCGCTTCAAGCTCTAACCTCTACCTTGTCTTGTGCTTGGC 2237
DB 928 TCTGATGCTGGTCTCTTCAAGCCCGCTTCAAGCTCTAACCTCTACCTTGTCTTGTGCTTGGC 987
QY 2238 GAGCCTTACGAGATCATTTATGGTATGCCCTCTCACGAATGAGTCAAGAATCTCTA 2297
DB 988 GAGCCTTACGAGATCATTTAT----- 1008
QY 2298 AGACTAAACACTTGTAGACTTTCACCAACTTTGCTGGCCAGACTCTTTGAGCTGCGCAACGTT 2357
DB 1009 -----GACTTCACCAACTTTGCTGGCCAGACTCTTTGAGCTGCGCAACGTT 1053
QY 2358 GCTGAGACCAAGATGTCTGGGACGAGGATGATGAGTACGCTTCGCACTCTCGAGGTGATGGC 2417
DB 1054 GCTGAGACCAAGATGTCTGGGACGAGGATGATGAGTACGCTTCGCACTCTCGAGGTGATGGC 1113
QY 2418 TTCGTCGTGAGTCTTGGCACTGTTGAGGACACAGCCAGGTCCTCCCTCCACTCTCGGTGAC 2477
DB 1114 TTCGTCGTGAGTCTTGGCACTGTTGAGGACACAGCCAGGTCCTCCCTCCACTCTCGGTGAC 1173
QY 2478 GTTCTCTTCCCTCTCAAGAAGGAGCCCGCCGCAAGCAAGCACTTCAAGTTTCAAGCGCAGC 2537
DB 1174 GTTCTCTTCCCTCTCAAGAAGGAGCCCGCCGCAAGCACTTCAAGTTTCAAGCGCAGC 1233
QY 2538 AACGACACTTACCTGATCAACGATGTGGCTTTGCCGATGTCAATGAGGCTGTCTGTGGCC 2597
DB 1234 AACGACACTTACCTGATCAACGATGTGGCTTTGCCGATGTCAATGAGGCTGTCTGTGGCC 1293
QY 2598 AAGCCCGAGCTCGGCACCGCTTGAAGTCTGGGAGCTCGAGAACTCTCTCGAGGCTGGAGC 2657

Db 1294 AAGCCGAGCTCGGCACCGTTGAGGCTCTGGGAGCTCGAGAACTCTCTGGAGGCTGGACC 1353
QY 2658 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCCCTCAAGCGAAGCTGGTGGTCTGGGC 2717
Db 1354 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCCCTCAAGCGAAGCTGGTGGTCTGGGC 1413
QY 2718 CAGGTACGCTCAGGAGTCTGCTGGTCTTAAGGATGCTGCTGGTGGGAGGAGTGGAG 2777
Db 1414 CAGGTACGCTCAGGAGTCTGCTGGTCTTAAGGATGCTGCTGGTGGGAGGAGTGGAG 1473
QY 2778 ACCCTGACCATCGAGGCCACCTACCAACCCCTGGAGCTTACATGTGGCACTGTCTAC 2837
Db 1474 ACCCTGACCATCGAGGCCACCTACCAACCCCTGGAGCTTACATGTGGCACTGTCTAC 1533
QY 2838 AACCTATTACGAGGATAACGACATGATGTCTGATTAACGTCACCGCCCATGGAGGAG 2897
Db 1534 AACCTATTACGAGGATAACGACATGATGTCTGATTAACGTCACCGCCCATGGAGGAG 1593
QY 2898 AAGGATATCTTCAGGAGGACTTCGAGGACCCATGAACCCCAAGTGGCGCCGCTTCTT 2957
Db 1594 AAGGATATCTTCAGGAGGACTTCGAGGACCCATGAACCCCAAGTGGCGCCGCTTCTT 1653
QY 2958 TACAACCGCAAGCACTTCCATGCTGGCGCTGGAACCTTCTCGCGCGAGTCCATCACTGCC 3017
Db 1654 TACAACCGCAAGCACTTCCATGCTGGCGCTGGAACCTTCTCGCGCGAGTCCATCACTGCC 1713
QY 3018 CGAGTGCAGGAGCTGGCGGAGCAGGAGCGGTACAACCGCTCGATGAGATCCTGGAGGAT 3077
Db 1714 CGAGTGCAGGAGCTGGCGGAGCAGGAGCGGTACAACCGCTCGATGAGATCCTGGAGGAT 1773
QY 3078 CTTGGAATCGAGGAGTAA 3095
Db 1774 CTTGGAATCGAGGAGTAA 1791

RESULT 14
AAZ61243
ID AAZ61243 standard; DNA; 2110 BP.
XX
AC AAZ61243;
XX
DT 30-MAY-2000 (first entry)
XX
DE DNA encoding a phenol oxidising enzyme.
XX
KW Phenol oxidizing enzyme; fungus; redox reaction; detergent; bleaching;
KW fabric; pulp; paper; decolourisation; plant-derived food product;
KW coloured compound; porphyrin; tannin; polyphenol; carotenoid;
KW anthocyanin; Maillard reaction product; ss.
XX
OS Acremonium murorum.
XX
FH Key Location/Qualifiers
FT CDS 135..1943
FT /tag= a
FT /product= "phenol oxidising enzyme"
XX
PN WO200005349-A1.
XX
PD 03-FEB-2000.
XX
PF 13-JUL-1999; 99WO-EP04922.
XX
PR 21-JUL-1998; 98EP-0202454.
XX
PA (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
XX
PI (HIND-) HINDUSTAN LEVER LTD.
XX
DR Convents D, Gouka RJ, Van Der Heiden M, Swarthoff T, Verrips CT;
WPI: 2000-195101/17.
DR P-PSDB: AAY69204.

XX Phenol-oxidizing enzyme from Acremonium, used in detergent compositions
PT for bleaching stains on fabrics -
XX
PS Example 2; Page 37-40; 45pp; English.
XX
CC The present sequence encodes a phenol oxidizing enzyme from the
CC fungus Acremonium murorum. The enzyme has the CBS accession number
CC 157.72. The enzyme catalyses redox reactions and is specific for
CC molecular oxygen as the electron acceptor. The phenol oxidising enzyme
CC is specifically used in detergents for bleaching strains on fabrics,
CC but also for bleaching pulp and paper and for decolourisation of
CC plant-derived food products. The enzyme has a pH optimum in the
CC alkaline to neutral range and can bleach a wide variety of coloured
CC compounds, e.g. porphyrins, tannins, polyphenols, carotenoids,
CC anthocyanins and Maillard reaction products.
XX
SQ Sequence 2110 BP; 400 A; 732 C; 556 G; 422 T; 0 other;

Query Match 13.8%; Score 507.6; DB 21; Length 2110;
Best Local Similarity 61.3%; Pred. NO. 1.2e-139;
Matches 969; Conservative 0; Mismatches 479; Indels 134; Gaps 4;

QY 1501 CAGATTATCCCACTTGGCCCTGCCACTCTCTCGGCTACGATGGCATGAGCCCTGT 1560
Db 459 CAGGTCTTCCCTGACCTGGGGCTCTGACCTCTGGGCTACGAGCGCATCTCGCCCGGT 518
QY 1561 CCTACTTCAATGTTCCCAAGAGAACAGAGCTGTAGTTAGTTTCATCAACAATGCCAC 1620
Db 519 CCTACTTCAATGTTCCCAAGAGAACAGAGCTGTAGTTAGTTTCATCAACAATGCCAC 1620
QY 1621 GTGGAGAACTCGGTCATCTGCACGGCTCCCATCGGTCGCCCTTTCGATGTTGGGCT 1680
Db 579 GTGGAGAACTCGGTCATCTGCACGGCTCCCATCGGTCGCCCTTTCGATGTTGGGCT 638
QY 1681 GAAGATGTGACCTTCCCTGGCGAGTACAAGGATTACTACTTCCCAACTACCAATCCGCC 1740
Db 639 GAGGATGTGACCAACCCCGGCGAGTACAAGGATTACTACTTCCCAACTACCAATCCGCC 698
QY 1741 CGCCTTCTGTGTACATGACCAACCTTTCATGAAGTATGCTACGAGCTTTATCTTTC 1800
Db 699 CGCTTCTGTGTACATGACCAACCTTTCATGAAGTATGCTACGAGCTTTATCTTTC 725
QY 1801 TTGGTACTTTGGCTAACCAACTTCTTCTGTAGACTGCTGAGAATGCTTACTTTGGTTC 1860
Db 726 TTGGTACTTTGGCTAACCAACTTCTTCTGTAGACTGCTGAGAATGCTTACTTTGGTTC 1860
QY 1861 AGGCTGGCGCTTACATTTATCAACGAGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCT 1920
Db 760 AGGCTGGCGCTTACATTTATCAACGAGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCT 819
QY 1921 ATGGCGAGTTGATATCCCTCTGTGATCGCGGCAAGTACTATAAGCGCGATGTACCC 1980
Db 820 ATGGAGAGTACGACATCCCTCTCATCTGACTTTCGAGAGGATGAGGATGAGGATGAG 879
QY 1981 TCGGTTCCGAGGAGGTGAGGACGAGGAGTGTGGGAGATGCTATCCATGTCACGAGAC 2040
Db 880 TCGGTTCCGAGGAGGTGAGGACGAGGAGTGTGGGAGATGCTATCCATGTCACGAGGAG 939
QY 2041 ACCCATGGCGCTTTCCTTAACGTCGAGCGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTG 2100
Db 940 TCCCGTGGCGCTTTCCTTAACGTCGAGCGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTG 999
QY 2101 CCGTGTCTGCTGGCTTCTCTACCTCGTCAGGACGAGCTCTCCCAACGTCAGAAATTC 2160
Db 1000 CCGTGTCTGCTGGCTTCTCTACCTCGTCAGGACGAGCTCTCCCAACGTCAGAAATTC 1059
QY 2161 CTTTCCAAAGTCAATGCCCTCTGATGCTGGTCTCTTCAAGCCCCCGGTTGAGACCTTAACC 2220
Db 1060 CTTTCCAAAGTCAATGCCCTCTGATGCTGGTCTCTTCAAGCCCCCGGTTGAGACCTTAACC 1119
QY 2221 TCTACCTTGTGTTGGCGAGGCTTACGAGATCATATTGTTGTTATGCCCTTCCCTTCTCACA 2280
Db 2221 TCTACCTTGTGTTGGCGAGGCTTACGAGATCATATTGTTGTTATGCCCTTCCCTTCTCACA 2280

Db 1120 TCGTCTCTCCATTGCTGAGCGCTACGAGATCA----- 1152
Qy 2281 ATGAGTCAAGAACTCTAAGACTAAGACTTTGTAGACTTCACCAACTTTTCTGCTGGCGAGACTC 2340
Db 1153 -----TCCTCGACTTCTCCGACTTCGAGGGCAAGACCA 1185
Qy 2341 TTGACCTCGCAACGTTTGTCTGAGACCAACAGATGTCGGCGAGCAGGATGAGTACGCTCCCA 2400
Db 1186 TCGAGCTCCGCAACGAGCCCGGTCGGCGGCTCGGCATCAGAGTCAACTACGACGACA 1245
Qy 2401 CTCTCGAGGTGATGGGCTTCGTCTGCTGACCTCTGGACTGTT-----GAGACACACGCC 2454
Db 1246 CCGACAAGGTCTATCGGCTTCAACGTCGCGAGGGCCCCCTCTCCTCGCGCCGACACCTCCG 1305
Qy 2455 AGGTCCCTCCACTCTCGCTGACGTTCTTTCCTCTCACAAGGAAGGCCCGCCGACCA 2514
Db 1306 TCGTCCCCCTCCACCTCCGTCGAGTGCCCTTCCCTCCAGCACCTCGACCACCTCGACC 1365
Qy 2515 AGCACTTCAAGTTTGAACGCAAGCAACGACACTACTCTGATCAACGATGTTGGCTTTGGCG 2574
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RESULT 15
AAA50020
ID AAA50020 standard; DNA; 2905 BP.

XX AC AAA50020;
XX XX
DT 10-OCT-2000 (first entry)
XX Bipolaris spicifera phenol oxidising enzyme gene.
DE Phenol oxidising enzyme; detergent; bleaching; ds.
KW Bipolaris spicifera.
XX OS
XX

PH Key Location/Qualifiers
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FT 890..2179
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XX 06-JUL-2000.
XX 20-DEC-1999; 99WO-EP10287.
XX 23-DEC-1998; 98US-0220871.
XX 23-JUN-1999; 99US-0338723.
XX (UNIL) UNILEVER NV.
XX (UNIL) UNILEVER PLC.
XX (HIND-) HINDUSTAN LEVER LTD.
XX Bodie EA, Van Der Velden S, De Vries CH, Wang H;
XX WPI: 2000-514528/46.
XX P-PSDB; AAY95538.
XX Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition -
XX Example 5; Fig 2; 45pp; English.
XX The present sequence is that of the Bipolaris spicifera phenol oxidising enzyme gene. The gene was isolated from genomic DNA using primers (see AAA50025-26) based on the phenol oxidising enzyme of Stachybotrys chartarum (see AAY95537) and the bilirubin oxidase of Myrothecium verrucaria. The invention relates to detergent compositions comprising novel phenol oxidising enzymes that have at least 60% identity with the phenol oxidising enzymes of Stachybotrys chartarum, and which are obtained from a bacterium, yeast or non-Stachybotrys fungus, especially B. spicifera, Curvularia pallescens (see AAY95539) and Amerosporium atrum (see AAY95540). The phenol oxidising enzyme is capable of modifying the colour associated with dyes or coloured compounds, and can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. It may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidising enzyme, methods for producing the phenol oxidising enzyme, and methods for constructing expression hosts are provided.
XX Sequence 2905 BP; 714 A; 792 C; 664 G; 734 T; 1 other;

Query Match 12.5%; Score 460.8; DB 21; Length 2905;
Best Local Similarity 59.3%; Pred. No. 1.2e-125;
Matches 976; Conservative 0; Mismatches 537; Indels 133; Gaps 6;
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Job time : 771.875 secs

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; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3677
; TYPE: DNA
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US-09-218-702-3

Query Match 100.0%; Score 3676.6; DB 4; Length 3677;
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Db 241 ATGATGCGACATCGCGGATCAGGACCCCTCTGATGATGATGATGATGATGATGATGATGAT 300
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US-09-218-702-5
; Sequence 5, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huang
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218.702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2067
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid
US-09-218-702-5
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Query Match 55.9%; Score 2054; DB 4; Length 2067;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 5, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA
US-09-468-578-5
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Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;
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RESULT 5
US-09-218-702-1
; Sequence 1, Application US/09218702
; Patent No. 6426410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Stachybotrys sp.
US-09-218-702-1

Query Match 40.1%; Score 1474; DB 4; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

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Db 988 GAGCGTTACGAGATCATTTATTT ----- 1008
Qy 2298 AGACTAAACACTTGTAGACTTCAACCACTTGTGTCGCCAGACTTTTGACTGCGCAACGTT 2357
Db 1009 -----GACTTCAACCAACTTGTGTCGCCAGACTTTTGACTGCGCAACGTT 1053
Qy 2358 GCTGAGACCAACGATGTGCGGCACGAGGATGAGTACGCTCGCACTCTCGAGGTGATGGC 2417
Db 1054 GCTGAGACCAACGATGTGCGGCACGAGGATGAGTACGCTCGCACTCTCGAGGTGATGGC 1113
Qy 2418 TTCGTCGTAGCTCTGGCACTGTTGAGGACACACCGAGTCCCTCCACTCTCCGTGAC 2477
Db 1114 TTCGTCGTAGCTCTGGCACTGTTGAGGACACACCGAGTCCCTCCACTCTCCGTGAC 1173

Qy 2478 GTTCCTTTCCCTCCTCACAAGGAAGCCCGCCACAAAGCACTTCAAGTTTGAACGCAGC 2537
Db 1174 GTTCCTTTCCCTCCTCACAAGGAAGCCCGCCACAAAGCACTTCAAGTTTGAACGCAGC 1233
Qy 2538 AACGGACACTACCTGATCAACGATGTTTGGCTTTCGCCATGTCAATGAGCGTGTCTCTGGCC 2597
Db 1234 AACGGACACTACCTGATCAACGATGTTTGGCTTTCGCCATGTCAATGAGCGTGTCTCTGGCC 1293
Qy 2598 AAGCCCGAGCTCGCACCGTGTGAGTCTGGAGCTCGAGAACTCCTCTGGAGGTGAGC 2657
Db 1294 AAGCCCGAGCTCGCACCGTGTGAGTCTGGAGCTCGAGAACTCCTCTGGAGGTGAGC 1353
Qy 2658 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCTCAAGCGAACTGGTGGTCTGGC 2717
Db 1354 CACCCCGTCCACATTCACCTTGTGACTTCAAGATCTCAAGCGAACTGGTGGTCTGGC 1413
Qy 2718 CAGTCAATGCCCTACGAGTCTGCTGCTTAAAGATGTCTGCTTGGGCGAGGGTGG 2777
Db 1414 CAGTCAATGCCCTACGAGTCTGCTGCTTAAAGATGTCTGCTTGGGCGAGGGTGG 1473
Qy 2778 ACCCTGACCATCGAGGGCCACTACCAACCCCTGGAGCTTACATGTGGCACTGTAC 2837
Db 1474 ACCCTGACCATCGAGGGCCACTACCAACCCCTGGAGCTTACATGTGGCACTGTAC 1533
Qy 2838 AACCTCATTACGAGGATAACGACATGATGGCTGTATTTCACGCTCACGCCCATGGAGG 2897
Db 1534 AACCTCATTACGAGGATAACGACATGATGGCTGTATTTCACGCTCACGCCCATGGAGG 1593
Qy 2898 AAGGATATCTTCAGGAGGACTTCGAGGACCCCTGAACCCCAAGTGGCGCGCTTCT 2957
Db 1594 AAGGATATCTTCAGGAGGACTTCGAGGACCCCTGAACCCCAAGTGGCGCGCTTCT 1653
Qy 2958 TACAACCCCAACGACTTCCATCTCGCGCTGGAACCTTCTCCGCCGAGTCCATCACTGCC 3017
Db 1654 TACAACCCCAACGACTTCCATCTCGCGCTGGAACCTTCTCCGCCGAGTCCATCACTGCC 1713
Qy 3018 CGAGTGCAGGAGCTGGCGGACGAGGACCGTACAAACCCCTCGATGAGATCCTGGAGGAT 3077
Db 1714 CGAGTGCAGGAGCTGGCGGACGAGGACCGTACAAACCCCTCGATGAGATCCTGGAGGAT 1773
Qy 3078 CTTGGAATCGAGGAGTAA 3095
Db 1774 CTTGGAATCGAGGAGTAA 1791

RESULT 6
US-09-468-578-3
; Sequence 3, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Bipolaris spicifera
US-09-468-578-3

Query Match 12.5%; Score 460.8; DB 4; Length 2905;
Best Local Similarity 59.3%; Pred. No. 6,3e-129;
Matches 976; Conservative 0; Mismatches 537; Indels 133; Gaps 6;

Qy 1491 CTGACCCCTTCAGATTTACCCACACCTTCGGCCCTGCCACTCTCGTCGGCTACGATGGCAT 1550
Db 478 CTTACCCAGCAGCGCTATCCAAAGCTTCGGCCCTCGCTCGTTAGGTAGCTATGACGGCAT 537
Qy 1551 GAGCCCTGCTCTACTTTCATGTTCACAGAGAACAGAGACTGTAGTTAGTTATCAACAA 1610
Db 538 CTCCCAAGGTCTACGATCATAGTCCGAGAGAACAGAGACTGTGTACCGTTTATAAA 597
Qy 1611 CAATGCCACCGTGGAGAACTCGGTCCATCTGCACGGCTCCCATCGCTGCCCTTTTCGA 1670
Db 598 CCAGGGTATCGGAAAGCTCCATCCATCTCCACGGCTCCCTCCCTCGCTCCCTTTTGA 657
Qy 1671 TGGTTGGCTGAAGATGTGACCTTCCCTCGGCGAGTACAA----- 1709
Db 658 CGGATGGCTGATGATATGATCATGAAGGGGGAATACAAAGGTACGATAGCGTGTGATTC 717
Qy 1710 -----GGATTACTACTTTCCC 1725
Db 718 TACGATCAGGAAGCCTCTATCATACTAACAGGACTTTCTTCACAGACTACTACTACCGG 777
Qy 1726 AACTACCAATCCGCCCTCTCTGTGTGTTACCATGACCAAGCTTTTCATGAAGGTA--TGCT 1783
Db 778 AACAAACCAAGCTGCCAGATTTTGTGGTACCAGGATCATGCTATGCTATGTTGTAAGTCTT 837
Qy 1784 AGGAGCCTTTATCTTCTTGGCTACCTTTGGCTAACCAACTTCCCTTCGTAGACTGTGA 1843
Db 838 TACGACTTTTATGTTAGTGAACGGAAGGATTAAGCTAACATCTGTGCAGACCGCAGA 897
Qy 1844 GAATSCCTACTTGTGAGGCTGGCGCTACATATATCAACAGCAGGCTGAGGATGCTCT 1903
Db 898 AAATGCCCTATTTCGGCAAGCGCGGCTACTCTGATCACAGCCGGCTGAGGATGCTCT 957
Qy 1904 CGGTCTTCTAGTGGCTATGCGAGTTGATATCCCTCTGATCTGACGGCCAAAGTACTA 1963
Db 958 CGGCTTCTCAGGTTACGGAATAACGACATTCGCGTGGTCTCAGTTCCAAAGTACTA 1017
Qy 1964 TAACCCGATGGTACCTTCGGTTCGACCGAGGTGAGAACAGGACCTGTGGGAGATGT 2023
Db 1018 CAACCCGATGGAATCTTTAAGACCAGTGTGGGAGAACGAAGAGTGTTCGGGCGACAT 1077
Qy 2024 CATCATGCTCAACGACAGCATGCTCTTCAACGCTCCAGCCCGCAAGTACCGTTT 2083
Db 1078 CATCATGCTCAACGCTGAGCCCTGCGCAATCTTAATGTTGAGCCTCGAAAGTATGCTCT 1137
Qy 2084 CCGATTCTCAACGCTGCGGTCTGCTGCTTGGCTCTCTACCTCTGTCAGGACGAGCTC 2143
Db 1138 TCGATTCTCAACGCGGCTGTTTCTAGGAATTTGCGCTTACTTCGTCAAGCAAGACAA 1197
Qy 2144 TCCCAACGCTCAGATTCCTTTCCAAAGTCAATTCGCTCTGATGCTGTCTTCCTCAAGCCCC 2203
Db 1198 CACTGCGCACTAGGCTTCCTTTCCAGGTCAATTCGCTCTGATGCGGGCTACTCACACACCC 1257
Qy 2204 CGTTCAGACCTCTAACCTCTACCTTGTGTTGGCGAGGTTACGAGATCATTTGGTAT 2263
Db 1258 GGTTCAAACCTCAGATATGATGTGTGACCGCGAAGCGCTACAGAT----- 1305
Qy 2264 GCCCTCCCTCTCAGGAATGAGTCAAGAAGTCTAAGACTAAGACTGTGATGATCTACCAA 2323
Db 1306 -----TGTTTCGATTTCCGCC 1323
Qy 2324 CTTTGTCTGCCAGACTCTTGACCTGCGCAAGCTGTCTGAGACCAACAGATGTGGCGGAGA 2383
Db 1324 CTATGCCGCAAAAGTTGGATCTGCGCAATTCGCAAGGCAATGATGATCTACCGA 1383
Qy 2384 GGATGAGTACCTCGCACTCTCGAGGTGATGGCTTCGTCGCTGAGCTCTGCGACTGTGA 2443
Db 1384 CGACGACTACCGAAACACTGACAAGGTATGCGTTTCACCTGACGAGCCAAACAGTCTG 1443
Qy 2444 GGACAACAGCAGGTCCTCCACTCTCCGTGAGCTTCTTCTTCCCTCTCTCAAGGAAGG 2503
Db 1444 CGATAACTCCGTGTACCGGAGCAGCTATCTCAGATCCAGTTCCCGCGGAGACA---AAAC 1500
Qy 2504 CCCCGCGACAAAGCACTTCAAGTTTGAACGCAAGCAAGCACTACCTGATCAACGATGT 2563

Db 1501 CGACATAGACCATCACCTTCCGTTTCCATCGTACCAACGGCGAGTGGCGCATCAACGGCAT 1560
Qy 2564 TGGTTTTCCCATGTCAATGAGCGTCTCTGCGCAAGCCGAGCTCGGCACCGCTTTGAGGT 2623
Db 1561 CGGTTTGCAGACGCTCGAGAACCCTGTTCTTGGCAAGGTACCGCGCGTACTGTGCGAGCT 1620
Qy 2624 CTGGAGCTCGAGAACTCCTCTGGAGGCTGGAGCGACCCCTCCACATTCACCTTTGTTGA 2683
Db 1621 TTGGAACTTGAGAACAGCTCCGGCGGCTGTGTACACCCCATCCACGTCACCTAGTAGA 1680
Qy 2684 CTTCAAGATCTCAAGCGAACTGG-----TGGTCTGGCCAGGTTCATGCCCTACGAGTC 2737
Db 1681 CTTCCGAGTCTGTCGACGCTACGCGAGCAAGGCACTCGCGCGCTCATGCCCTATGAGGC 1740
Qy 2738 TGCTGGTCTTAAGGATGCTCTGTTGGCAGGCGGTGAGACCTTGACATCGAGGCCCA 2797
Db 1741 CGCGGTCTCAAGGACGCTGTGTGCTGCGCGCTACAGAGCGGTCTCTGTCGAAGCACA 1800
Qy 2798 CTACCAACCCCTGGACTGGAGCTTACATGTGCACTGTTCACAACCTCATTCACGAGGATAA 2857
Db 1801 TTACGCCCCATGGGACGAGTCTACATGTTCCACTGCCACAACCTCATCCACGAAGACCA 1860
Qy 2858 CGACATGATGCTGTATTCAACGCTCACCGCCATGGAGGAGAGGATATCTTCAGAG-- 2915
Db 1861 AGACATGATGCGCGCTTCGACGCTGACTTAACTCCAGAACTTTGGGTACAACGAGACAC 1920
Qy 2916 -GACTTCCGAGGACCCCATGAACCCCAAGTGGCGCGCTTCTTACAAACCGCAACGACTT 2974
Db 1921 TGATTTCCACGATCTGAGGATCTCTGCTGCTGTCAGCAAGACCTTTACCGCGGGTGATCT 1980
Qy 2975 CCATGCTCGCGCTGAAACTTCTCCGCGAGTCCATCACTGCCCCGAGTGCAGGAGCTGGC 3034
Db 1981 CACGCGCGATCGGGTATCTTTTTCAGAAAGATCCATCAGGCTAGAGTAAATGAGTTGGC 2040
Qy 3035 CGAGCAGGAGCGGTACAAACCGCTCG 3060
Db 2041 GCTCGAGCAGCTTACACGCAACTCG 2066

RESULT 7
US-09-468-578-6
; Sequence 6, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Curvularia pallescens
us-09-468-578-6

Query Match 12.4%; Score 455.6; DB 4; Length 2063;
Best Local Similarity 59.1%; Pred. No. 1.9e-127;
Matches 971; Conservative 0; Mismatches 544; Indels 129; Gaps 6;
Qy 1501 CAGATTTACCCACCATTCGCGCCCTGCCACTCTCGTCGGCTACGATGGCATGAGCCCTGGT 1560
Db 376 CAGGCTCATCCAAAGTCTACGTCCTGCTGCTTGGTAGCTATGATGGCATTTCCACGAGC 435
Qy 1561 CCTACTTTTCAATGTTCCAGAGGAACAGAGACTGTGTAGTTAGTTTTCATCAACAATGCCACC 1620

Db 436 CCTACGATCATCGTGCCGAGAGGAACAGAACCCGTTGTACGATTCGTAAACACCGGATGAT 495
Qy 1621 GTGGAGAACTCGGTCCATCTGACACGGCTCCCATCGCTGCCCTTTTCGATGGTGGGCT 1680
Db 496 CCGAGAGATTGATTCATCTCATGTGTTCTCCCTCCCGTGCCTTTGACGGATGGGCT 555
Qy 1681 GAAGATGTGACCTTCCCTGGGAGTACAAAGT----- 1713
Db 556 GAAGATTTGATTATGAAGGGCCAAATCAAAAGTACAAACAGAACAAATCTTATGCATCAGG 615
Qy 1714 ----- 1714
Db 616 TGCCCTCTTTTATCTAAACAGACTCGTTCTTAGAGACTACTACCCGAAACAAACAGGCTG 675
Qy 1739 CCCGCTTCTGTGGTACCATGACACAGCT-TTCATGAAGGTATGCTACGAGCCTTATCT 1797
Db 676 CCAGATTCCTGTGGTACCACGATCATGCTATGCATGTTGTAGCTTTCGACGACTAATCAT 735
Qy 1798 TTCTTTGGCTACCTTTGGCTAACCAACTTCTTTCGTAGACTGCTGAGAAATGCTACTTTG 1857
Db 736 GGGAGCGAAACGGAAGATCGGGCTGACACTTATGCAGACTCGGAAATGCCTATTTTG 795
Qy 1858 GTCAGGCTGGGCGCTACATTTATCAAGCAGAGGCTGAGGATGCTCTCGGTCTTCCTAGTG 1917
Db 796 GACAGGCTGGGCGCTTACCTGATACAGACCAGGCTGAGAGCGGCTCGGCGCTTCCTTCGG 855
Qy 1918 GCTATGGCGAGTTGATATCCCTCTGATCTCTGACGGCCAAAGTACTATAACGCCGATGTA 1977
Db 856 GTTACGGAAATACGACATCCCACTGGTGTCTGCTCAGTTTCCAGTTTCTACAAACAGTGATGAA 915
Qy 1978 CCTCGGTTTCGACGAGGTTGAGGACCAAGGACCTGTGGGAGATGTCATCCATGTCACAG 2037
Db 916 CTCCTCAGACCACTGTGGGAAAGAACACAGTCTCTGGGCGAGCTCATCCATGTCAACG 975
Qy 2038 GACAGCCATGGCTTTCCTTAACGTCAGGCCCGGCAAGTACGAGTTTCCGATTCCTCAACG 2097
Db 976 GTACGCCCTGGCCATTTCTCAACGTTGAGCCTCGAAAGATATCGCCTTCGATTTCTTCAATG 1035
Qy 2098 CTGCGCTGCTCGTCTGGCTTCCCTACTCTACCTGCTCAGACCAAGCTCTCCCAACGTCAGAA 2157
Db 1036 CGGTGTTTCTCGGNACTTTGCCCTCTATTTCGTCAACACACAGCCACTGCTACTAGAC 1095
Qy 2158 TTCCTTTCCAAAGTCAATGCCCTCTGATGCTGCTCTTCAAGCCCGGCTTCAGACCTCTA 2217
Db 1096 TTCCCTTCAGGTCTATGCCCTCTGATGACGGCTACTCACGACCCGCTTCCAAACCTCAG 1155
Qy 2218 ACCTCTACTTGTGCTTGGCGAGCGTTACGAGATCAATTTATGGTATGCCCTCCCTCTCA 2277
Db 1156 ATATTACGTTGGCAGCAGCAGCGCTACGAGAT----- 1189
Qy 2278 CGAATGAGTCAAGAACTCTAAGACTTAACACTTTGTAGACTTCACCAACTTTGCTGGCCAGA 2337
Db 1190 -----TGATTCGACTTTGGCGCTTATGAGGCCAGA 1221
Qy 2338 CTCCTTGACCTGGCAACGCTTGTGAGACCAACGATGTGGGCGACGAGGATGAGTACGCTC 2397
Db 1222 CGATAGATTTGCGTAACCTTTGCAAAAGGCCAATGGGGTCGGCCGATGACGATTAATGCAA 1281
Qy 2398 GCACCTCTCGAGGTGATGGCTTCTGCTGCTACGCTTGGGCACTGTTGAGGACAAACGCCAGG 2457
Db 1282 ACATCGAAGGTATGATGGCTTCTTCCATGTGTCAGCAGCAAGCAGTGTGCTGATTAACCTCGGTGG 1341
Qy 2458 TCCCTCTCACCTCCGTCACGTTCTCTTTCCCTCTCTCAAGGAAGGCCCGCCGACAAAGC 2517
Db 1342 TACCGGCACAGCTATCTCAGATTCAGTTTCCCGCGGACA---AAACCGGCTATCGACCAAC 1398
Qy 2518 ACTTCAAGTTTGAAGCGCAGCAACGGACACTACCTGATCAACGATGTTGGCTTTGCGCGATG 2577
Db 1399 ACTTCCCGCTTCCATCGCACCAACAGCGAGTGGCGATCAACGGCATCGGTTTCGACAGC 1458
Qy 2578 TCAATGACGCTGTCTGTGCCAAGCCCGAGCTCGGACCGGTTGAGGTCGTGGGAGCTCGAGA 2637
Db 1459 TCCAGAACCGTATCCTGTGCCAAGGTACCGCGCGGCACTGTGCGAGCTATGCGAACTCGAGA 1518

Qy 2638 ACTCCTCTGGAGGCTGGAGCCACCCCGTCCACATTCACATTTGTTGACTTCAAGATCCTCA 2697
Db 1519 ACAGCTCGCGGGCTGTGTCGACCCCATCCAGTCCACCTGGTCGACTTCGAGTCGTGCG 1578
Qy 2698 AGCGAACTGGTG-----GTGCTGGCCAGGTCTATGCCCTACGAGTCTGCTGTCTTAAG 2751
Db 1579 CACGCTACGGTGACGAAAGCACTCGCGCGTCTATGCCCTACGAGTCCGCGGCTCTCAAG 1638
Qy 2752 ATGCTGCTGTGGTGGGAGGGTGAGACCTCTGACCATCGAGGCCACCTACCAACCTCGA 2811
Db 1639 ACGTCTGTGCTGCGCGCCACGAGAGCGTCTGCTGGAAGCACACTACGCCCCCTGGG 1698
Qy 2812 CTGGAGCTTACATGTCGACCTGTACACACTTATTCACGAGGATACACATGATGGCTG 2871
Db 1699 ACGGAGTCTACATGTTCCACTGCCACAACTGATCCAGAAAGCAACATGATGGCGG 1758
Qy 2872 TATTCAAGCTCACCCCATGGAGGAGGATATCTTCA---GGAGGACTTCGAGGACC 2928
Db 1759 CGTTTGACGTGACTAAGCTCCAGAACTTTGGCTACACGAGACGAGGATTTCCACGACC 1818
Qy 2929 CCATGAACCCAAAGTGGCGCGCTTCTTACAAACCGCAACGACTTCCATGCTCGCGTG 2988
Db 1819 CGGAAGATTCTCGCTGCTGTGCAAGACCTTTCACCGCGCTGACTTGACGGCGGATCGG 1878
Qy 2989 GAACTTCTCGCGGAGTCCATCTACTGCCGCTGACAGTGCAGAGCTGGCCGAGGAGCGCT 3048
Db 1879 GTATCTCTCAGAGCATCCATCAGGCTAGAGTGAACGAGTTGGCGCTGGAACAGCGCT 1938
Qy 3049 ACAACCGCTCGATGAGATCCTGG 3072
Db 1939 ACAGCGAATGSCACAGGTCAAGG 1962

RESULT 8
US-09-401-476-1
; Sequence 1, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401.476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ. ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1958
; TYPE: DNA
; ORGANISM: Stachybotrys chararum
US-09-401-476-1

Query Match 8.2%; Score 300.4; DB 4; Length 1958;
Best Local Similarity 55.2%; Pred. No. 1.7e-80;
Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;

Qy 1491 CTGACCCCTTTTCAGATTTACCCCACTTGGCGCCTGCCACTCTCGTCGCTACGATGGCAT 1550
Db 316 CTTCTCCCAAGATCTATCCCTGATCTGGAGCGGCCCAACATGGTTGGATACGATGGCAT 375
Qy 1551 GAGCCCTGGTCTACTTTTCAATGTTTCCAGAGAAACAGAGACTGTAGTTAGTTTCATCAA 1610
Db 376 GTCCCAAGGACTTACCATCATCTCTCTCGTGGCACTGAGAGTGTGTCCGCTTCGTGAA 435
Qy 1611 CA-----ATGCCACCGTGGAGAACTCGGTCCATCTGCACGGCTCCCATCGGTGCC 1664
Db 436 CAGCGGAGAGAACCACTCTCCCAACAGCGTCCACTTGCACGGCTCTTCTCTCGAGCTCC 495
Qy 1665 TTTGATGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAGGATTTACTACTTTC 1724
Db 496 CTTTGTGTTGGGCTGAGGACACTTACCCAGCCTGGCGAGTACAGGATTTACTATACC 555
Qy 1725 CAACTACCAATCCGCGCCCTTCTGTGTACCATGACCACGCTTTTCATGAAGGTATGCTA 1784

Db 556 CAACAGGAGGCTGCCCGATGCTTTGGTACCATGACCATGC----- 597
Qy 1785 CGAGCCTTATCTTTCTTGGCTACCTTTTGGCTAACCAACTTCTTCTAGACTGCTGAC 1844
Db 598 -----CATGTCCATCACCGCCGAG 616
Qy 1845 AATGCTACTTTGGTCAGGCTGGCGCCTACATATTATCAACGAGGAGGCTGAGATGCTCTC 1904
Db 617 AACGCCATACATGGGTACGGCTGGTGTCTACATGATCCAGAGACCCGGCTGAGGATGCCCTG 676
Qy 1905 GGTCTTCTAGTGGCTATGGGAGTTTCGATATCCCTCTGATCTCCAGCGCAAGTACTAT 1964
Db 677 AACCTCCCGAGGGCTACGGGAGTTTGAATCCCTTGGTCTGACTGCCAAGCGATAC 736
Qy 1965 AACGCCATGTGTACCTTCGTTCCAGGAGGTGAGACCAAGACCTGTGGGGAGATGTC 2024
Db 737 AACGCAGAGCGACATCTCTTCTCCACCAATGAGAGGTTTCCAGCTTCTGGGGTACGTT 796
Qy 2025 ATCCATGT----- 2032
Db 797 ATTCAAGTGGTAAAGTTGAGCCCATTTGAGATGCTTCAGATCCTAGAAATATGATATGA 856
Qy 2033 -----CAACGGAGACCGCATGGCTTTTCTTAAACG 2061
Db 857 AATGTGTGATGCTCTAACCAAGTGTATCACAGAACGGTTCAGCCTTGGCCTATGCTCAACG 916
Qy 2062 TCCAGCCCCGAAGTACCGTTCCGATTCCCTCAACGGCTGCCGTGTCTGCTTGGCTTCC 2121
Db 917 TGCAGCCGCGAAGTACCGCTTCGCTTCCCTCAACGGCTGCCGTCTCAGCGCTTTTCGGCTC 976
Qy 2122 TCTACCTCGTCAGGACCAAGCTCTCCCAACGGTCAGAAATTCCTTTTCCAAAGTCAATGCGCTG 2181
Db 977 TGTATCTTGTACCTCTGAGGATTCAGAGACCAAGTTCCTTCCAGGTCTATGCGCGTG 1036
Qy 2182 ATGCTGGTCTCCTCAACGCCCGTTACAGCTCTAACTCTACCTTCTGCTTCCCGAGC 2241
Db 1037 ACGTGGTCTGCTTGGGGCCCTGTGTACACTGACACTCTGTACATCTCTATGGCCGAGC 1096
Qy 2242 GTTAGGATCATATTATGATGGCTATGCCCTCCCTCTCACGAATGAGTCAAGAACTCTAAGAC 2301
Db 1097 GCTGGGAGTTGTATC----- 1113
Qy 2302 TAACACTTGTAGACTTACCAACTTTTGTGCGCAGACTCTTGCCTGGCGAACGTTGCTG 2361
Db 1114 -----GACTTCTCCACCTTCGCTGCGTGGCCAGTCTCATGATCGCAACCTTTCCTG 1162
Qy 2362 AGACCAACGATGTCGGCGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATGCGCTTCG 2421
Db 1163 GTGCTGACGGTCTCGGTGTTGAGCGCTGAGTTGTGATAACACTGACAAAGTCTATGGGATTCG 1222
Qy 2422 TCGTCAGCTCTGGCACTGTTGAG---GACAAACAGCCAGGTCCCTTCCACTCTCGGTGAGC 2478
Db 1223 TCGTTGATGAAGTCTCTGAGTGGCCGACACTTCTGAGGTGCTTGCACACCTCCGAGATG 1282
Qy 2479 TTCTTTTCCCTCTCTACAAAGGAAGCCCGCCGCAAGAC-----TTTCA 2523
Db 1283 TTCTTTTCCCGAGGGCGCAACTGGGACCCCGCAACCCCACTGATCAGCAGACTTTCA 1342
Qy 2524 AGTTTGAACGAGCAACGACACTACCTGATCAACGATGTTGGCTTTGCCCATGTCAATG 2583
Db 1343 CTTTGGCGGTGCTAATGGACAGTGGACAATCAACGGAGTTTACCTTCTCGATGTCGAGA 1402
Qy 2584 AGCGTGTCTGGCAAGCCGAGCTGCGCAGCGTTGAGTGTGGGAGTTCGAGAACTCCT 2643
Db 1403 ACCGTCTGCTCGCAATGTGCCCGGACACTGTGTAGATCTGGGCACTTGAGAACAACT 1462
Qy 2644 CTGAGGCTGGAGCACCCCGTCCACATTCACCTTGTGTGACTTCAAGATCCTCAAGCGAA 2703
Db 1463 CCAACGGTTGGACTCACCTCTGTACATTCACCTCTGTTGACTTCCGAGTCTCTTCTCGTT 1522
Qy 2704 CTGGTGGTCTGGCCAGGTCATGCCCTACGAGTCTGTGGTCTTAAAGGATCTGCTGCTGGT 2763

Db 1523 CCACTGCCCGTGG---AGTCGAGCCTTATGAGGCTGTGCTCAAGGATGTTGTCTGCG 1579
Qy 2764 TGGCAGGGGTGAGACCCTGACCATTCGAGGGCCCACTAGCAACCCCTGGAC----- 2812
Db 1580 TGGCTCGTCTGAGGTGTCTATGTTGAGGGCCCACTACGCTCTCTTCCCGTAAGTTCTCG 1639
Qy 2813 -----TGGAGCTTACATGTGGCA 2830
Db 1640 CTTTAACTTAAGTGGTTTTCACATCATGCTAACATCTACAAGTGGTGTCTACATTTGCA 1699
Qy 2831 CTGTCAACAACCTCATTTACGAGGATAACGACATGATGCTGTATTCAACGTCACCGCAT 2890
Db 1700 CTGCCACAACCTGATCCACGAGGACACACATGATGCTGCTTTCAATGTCACTGTCT 1759
Qy 2891 GGAGGAGAAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCG 2950
Db 1760 CGGTGACTATGGCTACAACTACACCGAGTTTCAATTGACCCCATGGAGCCTCTCTGGAGGCC 1819
Qy 2951 GGTTCCTTACAACCGCAACGACTTCCATGCTGCGCTCGAATCTTCTCCGGGAGTCCAT 3010
Db 1820 CCGCCCTTCTCTCGGAGAGTTTGAGAAATGGCTCGGGTGACTTTCAGCGAGCTTGGCAT 1879
Qy 3011 CACTGCCCGAGTGCAGGAGCTGGCGGAGCAGGAGCGGTACAACCGCCTCGATGA 3064
Db 1880 CACTGACCCGATTCAGGAGATGGCTAGCTTCAACCCCTACGCCCAGGCTGATGA 1933

RESULT 9
US-09-401-476-3
; Sequence 3, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401.476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Stachybotrys chararum
US-09-401-476-3

Query Match 8.2%; Score 300.4; DB 4: Length 2095;
Best Local Similarity 55.2%; Pred. No. 1.8e-80;
Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;

Qy 1491 CTGACCCCTTTCAGATTTACCCCACTTTCGCCCTTCCACTCTCGTGGCTACGATGGCAT 1550
Db 380 CTTCCTCCACAGATCTACCTGATCTGGAGCGCCCAACATGTTGGATACGATGGCAT 439
Qy 1551 GAGCGCTGGTCTTACTTTCATGTTTCCAGAGAACAGAGACTGTAGTTAGTTTCATCAA 1610
Db 440 GTCCCCAGGACTACCACTTCCTCTCGTGGCACTGAGAGTGTTCGCCGTTTCGTGAA 499
Qy 1611 CA-----ATGCCACGTTGAGAACTCGTCCATCTGACGCTCCCATCGCTGCCGCC 1664
Db 500 CAGCGGAGAGAACACTCTCCCAACAGCGTCCACTTTCAGCGGCTCTTCTCTCGAGCTCC 559
Qy 1665 TTTCCATGTTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAGGATTTACTACTTTCC 1724
Db 560 CTTTGTGTTTGGGCTGAGGACACTACCCAGCGCTGGCGAGTACAGGATTTACTACTACC 619
Qy 1725 CAACTACCAATCCGCCCGCTTCTGTGTGTACATGACACCGCTTTCATGAAAGGTATGCTA 1784
Db 620 CAACAGGAGGCTGCCCGCATGCTTTGGTACCATGACCATG2----- 661
Qy 1785 CGAGCCTTATCTTCTTGGGTACCTTTTGGCTAACCAACTTCTTTCGTAGACTGCTGAG 1844
Db 662 -----CATGTCCATCACCGCCGAG 680

Db 296 GATGCAAGTGATCAAC-----TTCTCTGTGTCATCGGTGCCGATACCTGGTCTCTTG 346

Qy 2196 CAAGCCCGGTTACAGACCTCTAACCTCTACCTGTGTTGGCGAGCGGTACAGAGATCAAT 2255

Db 347 ACCAAGCCCTGTTACAGCAAGCAACCTTGAGATCTCTATGGCGGAGCGCTGGGAGGTGTT 406

Qy 2256 ATTG 2259

Db 407 TTTG 410

RESULT 11

US-08-232-463-14

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232.463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935.313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: pTZgpt-Fls

US-08-232-463-14

Query Match 1.6%; Score 58; DB 1; Length 7218;

Best Local Similarity 6.1%; Pred. No. 9.le-07;

Matches 26; Conservative 228; Mismatches 174; Indels 0; Gaps 0;

Qy 286 GAACCCCGCTGGTTCCTTTGTTCTTCTTCTCAACGACGCGTGACGGTGTTAA 345

Db 1064 GATYYY 1123

Qy 346 CTTGACGAAGCCGAGTGGTCTGTTACGAGGTTACCACTCTCTCTTCCCAAT 405

Db 1124 YY 1183

Qy 406 CATGACCTGCCCGCGAGTTAGGCCCCCATCAGGCTGTGAATCCACTTCGATAATCCT 465

Db 1184 YY 1243

Qy 466 AGCCTAGTACTCTTCAATAGTTGCTCCTGATGGGCACCTTTGGTCACATTCGCTTGG 525

Db 1244 YY 1303

Qy 526 TTYCTCTACCTGTTCTCTTCCGCATCAAGCCTCTATGCCGAGACACACCTCATG 585

Db 1304 YY 1363

Qy 586 GCCCGGACCACTTTGAGCGCGCACACCTTCGCCGCCGAGAGTTGATAACACCTTCA 645

Db 1364 YY 1423

Qy 646 CCTTGCCCAATGATGAGTGTGTTGCTATTGTCATGATCACCTCACATTCACCTAGATC 705

Db 1424 YYYYYYYYYYGTACCAATCTCTCTATCTCTTTAACTACTTGCATAGATAGTAATTAC 1483

Qy 706 ACGGATCC 713

Db 1484 AGTGATGC 1491

RESULT 12

US-09-535-008-66

; Sequence 66, Application US/09535008

; Patent No. 6465629

; GENERAL INFORMATION:

; APPLICANT: Wong, Alexander K.C.

; APPLICANT: Tavtigian, Sean V.

; APPLICANT: Teng, David H.-F.

; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE

; FILE REFERENCE: 2318-259

; CURRENT APPLICATION NUMBER: US/09/535.008

; CURRENT FILING DATE: 2000-03-23

; EARLIER APPLICATION NUMBER: U.S. 60/125,806

; EARLIER FILING DATE: 1999-03-23

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 66

; LENGTH: 5468

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: CDS

; NAME/KEY: CDS

; LOCATION: (75)..(5012)

; FEATURE:

; NAME/KEY: conflict

; LOCATION: (1780)

; OTHER INFORMATION: GenBank Accession No. 6465629 U29175 shows a C at this

; OTHER INFORMATION: position (position 1784 in GenBank) rather than

; OTHER INFORMATION: the G shown here.

; FEATURE:

; NAME/KEY: allele

; LOCATION: (26)

; OTHER INFORMATION: Polymorphism of either T or C in this noncoding

; OTHER INFORMATION: region.

; FEATURE:

; NAME/KEY: allele

; LOCATION: (1583)

; OTHER INFORMATION: Polymorphism of A or G resulting in a silent

; OTHER INFORMATION: mutation.

; FEATURE:

; NAME/KEY: allele

; LOCATION: (1598)

; OTHER INFORMATION: Polymorphism of T or C resulting in a silent

; OTHER INFORMATION: mutation.

; FEATURE:

; NAME/KEY: allele

; LOCATION: (1892)

; OTHER INFORMATION: Polymorphism of A or G resulting in a silent


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; SEQ ID NO 68
; LENGTH: 5564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(5108)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1780)
; OTHER INFORMATION: GenBank Accession No. 6465629 U29175 shows a C at this
; OTHER INFORMATION: position (position 1784 in GenBank) rather than
; OTHER INFORMATION: the G shown here.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)
; OTHER INFORMATION: Polymorphism of either T or C in this noncoding
; OTHER INFORMATION: region.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1598)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1892)
; OTHER INFORMATION: Polymorphism of T or C resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4245)..(4340)
; OTHER INFORMATION: This is a 96 base insertion compared to SEQ ID
; OTHER INFORMATION: NO:1.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4594)..(4595)
; OTHER INFORMATION: A deletion of CAG occurs between these bases as
; OTHER INFORMATION: compared to SEQ ID NO:1 (bases 4499-4501 of SEQ ID
; OTHER INFORMATION: NO:1).
US-09-535-008-68

Query Match      1.2%; Score 43.2; DB 4; Length 5564;
Best Local Similarity 45.5%; Pred. No. 0.023;
Matches 153; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Qy 2765 GGGCAGGGGTGAGACCTGACCATCGAGGCCCACTACCAACCCCTGGAGCTTGAGCTTACAT 2824
Db 4589 GGACAGCAGTGGACGTCAGCTCAGCGAGGTCTTCATCCAGCTGCCCTCGCGAAGAGGCT 4648
Qy 2825 GTGGCACTGTACACACCTATTCAGAGATTAACGACATGATGGCTGTATTCAACGTCAC 2884
Db 4649 GCGCGAGTACTACGAGCTCATCCGAAGCCCGTGGACTTCAAGAAGATAAAGGAGCGCAT 4708
Qy 2885 CGCCATGGAGGAGAGGGATATCTTCAGAGGACTTCGAGGCCCATCAACCCCAAGTG 2944
Db 4709 TCGCAACCAAGATACCGAGCTCAACGACCTAGAGAAGGAGCTGCTCTCTGTGCA 4768
Qy 2945 GGGCGCGGTTCCTTACAAACCGCAAGACTTCATCTCGCGCTGGAAATCTCTCGCGCA 3004
Db 4769 GAACGCACAGACTTCAACCTGGAGGCTCCCTGATCTATGAAGACTCATGCTTTGCA 4828
Qy 3005 GTCCATCACTGCCAGGTGACGAGCTGGCGAGGAGGCGGTACAAACCGCTTCGATGA 3064
Db 4829 GTCTGCTTCAACCGCTGCGGACAGAAATCGAAGGAGGATGACAGTGAAGGCGAGGA 4888
Qy 3065 GATCTGGAGGATCTTGAATCGAGGATTAACCC 3100
Db 4889 GAGTGAAGGAGGAAGAGGGCGGAGGAGGCTC 4924

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RESULT 15
US-09-535-008-76
; Sequence 76, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; TITLE OF INVENTION: AND OTHER CANCER TYPES
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 5573
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(5117)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1780)
; OTHER INFORMATION: GenBank Accession No. 6465629 U29175 shows a C at this
; OTHER INFORMATION: position (position 1784 in GenBank) rather than
; OTHER INFORMATION: the G shown here.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)
; OTHER INFORMATION: Polymorphism of either T or C in this noncoding
; OTHER INFORMATION: region.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1583)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1598)
; OTHER INFORMATION: Polymorphism of T or C resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1892)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; NAME/KEY: misc_feature
; LOCATION: (4245)..(4349)
; OTHER INFORMATION: Addition of 105 basepairs compared to SEQ ID NO:1.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4603)..(4604)
; OTHER INFORMATION: Deletion of CAG between these two basepairs as
; OTHER INFORMATION: compared to SEQ ID NO:1 (deletion of basepairs
; OTHER INFORMATION: 4499-4501 of SEQ ID NO:1).
US-09-535-008-76

Query Match      1.2%; Score 43.2; DB 4; Length 5573;
Best Local Similarity 45.5%; Pred. No. 0.023;
Matches 153; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Qy 2765 GGGCAGGGGTGAGACCTGACCATCGAGGCCCACTACCAACCCCTGGAGCTTGAGCTTACAT 2824
Db 4598 GGACAGCAGTGGACGTCAGCTCAGCGAGGTCTTCATCCAGCTGCCCTCGCGAAGAGGCT 4657
Qy 2825 GTGGCACTGTACACACCTATTCAGAGGATTAACGACATGATGGCTGTATTCAACGTCAC 2884

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Db	4658	CCCCGAGTACTACGACGCTCATCGCAGCCCGTGACCTTCAGAAAGATAAAGAGGCCAT	4717
Qy	2885	CGCCATGGAGGAAGGGATATCTTCAGGAGCTTCGAGGACCCCAAGTGAACCCCAAGT	2944
Db	4718	TCGCACACCAAGTACCGGAGCCTCAAGCACTCAGAGAAGGACGTCATGCTCTGTGCCA	4777
Qy	2945	GCGGCGCGTTCCTTACACACCGCAAGCACTTCATCCTCGCGCTGAAACTTCTCCGCCGA	3004
Db	4778	GAAGCACAAGACCTTCAACCTGGAGGCTCCCTGATCTATGAAGACTCCATCGCTTTGCA	4837
Qy	3005	GTCCATCACTGCCGAGCTCGAGAGCTGCCGAGCAGAGCGGTACAAACCCCTCGATGA	3064
Db	4838	GTGGTCTTCACACGCGTGGCGAGAAATCAGAGAAGGAGTACACAGTGAAGCGGAGGA	4897
Qy	3065	GATCTGGAGGATCTTTGGAATCGAGAGTAAACCCC	3100
Db	4898	GAGTGGAGGAGGAAGAGGGCGAGGAGGAGGCTC	4933

Search completed: February 13, 2003, 05:12:08
Job time : 193.68 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 20:54:16 ; Search time 166.097 Seconds
(without alignments)
11275.230 Million cell updates/sec

20	37.8	1.0	1872	10	US-09-452-599-17	Sequence 17, Appl
21	37.6	1.0	1512	9	US-10-124-800-31	Sequence 31, Appl
22	37.6	1.0	4509	9	US-10-124-800-5	Sequence 5, Appl
23	37.6	1.0	4512	9	US-10-124-800-27	Sequence 27, Appl
C 24	37.4	1.0	615	9	US-10-125-815-4	Sequence 4, Appl
	37	1.0	2223	9	US-09-984-245-120	Sequence 120, App
25	36.6	1.0	1707	9	US-09-938-842A-186	Sequence 186, App
26	36.2	1.0	2187	9	US-09-984-245-93	Sequence 93, Appl
27	36.2	1.0	500	9	US-10-047-542-33	Sequence 33, Appl
28	35.8	1.0	1642	10	US-09-765-231A-25	Sequence 25, Appl
29	35.8	1.0	651	9	US-09-738-626-2385	Sequence 2385, App
30	35.6	1.0	2148	9	US-09-738-626-2384	Sequence 2384, Ap
C 31	35.6	1.0	698	9	US-09-764-868-156	Sequence 156, App
C 32	35.4	1.0	1002	9	US-09-738-626-1755	Sequence 1755, Ap
33	35.2	1.0	2748	9	US-09-738-626-2853	Sequence 2853, App
34	35.2	1.0	951	9	US-09-975-719-432	Sequence 432, App
35	35	1.0	1050	9	US-09-975-719-428	Sequence 428, App
C 36	35	1.0	1104	10	US-09-815-242-7676	Sequence 7676, Ap
37	35	1.0	42235	9	US-09-975-719-1	Sequence 1, Appl
38	35	1.0	1185	10	US-09-987-576-784	Sequence 784, App
39	34.8	0.9	6442	9	US-09-950-335A-11	Sequence 11, Appl
40	34.8	0.9	2787	10	US-09-815-242-6320	Sequence 6320, Ap
C 41	34.6	0.9	417	10	US-09-960-352-14176	Sequence 14176, A
C 42	34.4	0.9	927	9	US-10-029-180-97	Sequence 97, Appl
43	34.4	0.9	522	10	US-09-980-107-1314	Sequence 1314, Ap
C 44	34.2	0.9	1764	9	US-09-920-923-36	Sequence 36, Appl
45	34.2	0.9				

ALIGNMENTS

```

RESULT 1
US-10-080-210-1
; Sequence 1, Application US/10080210
; Patent No. US2002014243A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-10-080-210-1

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	Query Match	100.0%;	Score	3676.6;	DB 12;	Length	3677;
	Best Local Similarity	100.0%;	Pred. No.	0;	Mismatches	0;	Gaps
	Matches 3677;	Conservative	0;				
QY	1	CTGGCTAGCCCTACTTGGTAGACAGCCCTGACAGCCTCACTGGCTGGGGGTGCGAAAGGCC	60				
Db	1	CTGGCTAGCCCTACTTGGTAGACAGCCCTGACGCCTCACTGGCTGGGGGTGCGAAAGGCC	60				
QY	61	AGTCAATATCTTGGTCACTGCTAATAGTTTCCTTGGTAGCGCAAAGAAGCTCCTTGGCCGA	120				
Db	61	AGTCAATATCTTGGTCACTGCTAATAGTTTCCTTGGTAGCGCAAAGAAGCTCCTTGGCCGA	120				
QY	121	GGGSCACAGACTATCAAGTGAGACATATAGGATGCATGCTTTTCATAGCCACAGATTAGGG	180				
Db	121	GGGSCACAGACTATCAAGTGAGACATATAGGATGCATGCTTTTCATAGCCACAGATTAGGG	180				
QY	181	TGGTGACCTTACTGGAAGAGGCCCGCATTTGCATGCATACGACATGTGCTTCCATGCAAC	240				
Db	181	TGGTGACCTTACTGGAAGAGGCCCGCATTTGCATGCATACGACATGTGCTTCCATGCAAC	240				

Qy	241	ATGTA	TGCGC	ACAT	TCGGC	GATC	AGGC	ACCC	TCTG	CAAT	CGA	ATAG	CAAC	CCCC	CTGG	TTT	300
Db	241	ATGTA	TGCGC	ACAT	TCGGC	GATC	AGGC	ACCC	TCTG	CAAT	CGA	ATAG	CAAC	CCCC	CTGG	TTT	300
Qy	301	CC	TTT	TG	TTT	TC	TTT	CT	CT	CA	CG	GG	GT	GAG	CG	TT	360
Db	301	CC	TTT	TG	TTT	TC	TTT	CT	CT	CA	CG	GG	GT	GAG	CG	TT	360
Qy	361	GT	GT	CT	GT	TT	TC	AG	GT	TAC	CA	TCT	CT	CT	TT	TT	420
Db	361	GT	GT	CT	GT	TT	TC	AG	GT	TAC	CA	TCT	CT	CT	TT	TT	420
Qy	421	GAG	TT	TAG	CCCC	CCAT	CAG	GG	CT	GT	GAA	T	CC	ACT	TC	GC	480
Db	421	GAG	TT	TAG	CCCC	CCAT	CAG	GG	CT	GT	GAA	T	CC	ACT	TC	GC	480
Qy	481	TT	CA	AT	AG	TT	GC	T	CC	AT	T	GG	GC	AC	TT	T	540
Db	481	TT	CA	AT	AG	TT	GC	T	CC	AT	T	GG	GC	AC	TT	T	540
Qy	541	TC	CT	CC	G	CAT	CA	AG	CC	T	AT	G	CC	G	CA	CA	600
Db	541	TC	CT	CC	G	CAT	CA	AG	CC	T	AT	G	CC	G	CA	CA	600
Qy	601	AG	CG	CG	AC	GC	CT	T	CG	CG	CG	AG	GG	TT	GA	T	660
Db	601	AG	CG	CG	AC	GC	CT	T	CG	CG	CG	AG	GG	TT	GA	T	660
Qy	661	GG	AG	TT	T	GT	CT	AT	T	T	GT	CAT	GAT	CAC	CT	CA	720
Db	661	GG	AG	TT	T	GT	CT	AT	T	T	GT	CAT	GAT	CAC	CT	CA	720
Qy	721	GG	GT	G	GA	AG	CC	AG	CA	GC	T	GT	CC	CT	TT	TC	780
Db	721	GG	GT	G	GA	AG	CC	AG	CA	GC	T	GT	CC	CT	TT	TC	780
Qy	781	CT	AT	C	AG	CT	C	AG	GT	T	AT	CA	AG	T	CC	GT	840
Db	781	CT	AT	C	AG	CT	C	AG	GT	T	AT	CA	AG	T	CC	GT	840
Qy	841	TG	CC	T	A	AT	T	T	GC	GT	AT	CT	CT	AT	G	C	900
Db	841	TG	CC	T	A	AT	T	T	GC	GT	AT	CT	CT	AT	G	C	900
Qy	901	G	CT	G	A	G	A	C	T	G	T	C	T	A	A	A	960
Db	901	G	CT	G	A	G	A	C	T	G	T	C	T	A	A	A	960
Qy	961	T	C	C	A	C	AG	TC	A	C	A	AG	CT	T	C	T	1020
Db	961	T	C	C	A	C	AG	TC	A	C	A	AG	CT	T	C	T	1020
Qy	1021	A	C	T	CT	CC	CT	CT	TT	T	C	G	T	CA	A	G	1080
Db	1021	A	C	T	CT	CC	CT	CT	TT	T	C	G	T	CA	A	G	1080
Qy	1081	G	G	CT	C	T	G	T	C	T	G	A	G	T	C	C	1140
Db	1081	G	G	CT	C	T	G	A	G	T	C	C	G	A	T	C	1140
Qy	1141	T	T	G	A	T	C	C	G	A	G	T	C	T	T	C	1200
Db	1141	T	T	G	A	T	C	C	G	A	G	T	C	T	T	C	1200
Qy	1201	A	C	G	A	C	T	G	G	A	G	T	C	T	T	A	1260
Db	1201	A	C	G	A	C	T	G	G	A	G	T	C	T	T	A	1260
Qy	1261	T	T	C	C	T	C	G	A	T	A	C	T	T	A	G	1320
Db	1261	T	T	C	C	T	C	G	A	T	A	C	T	T	A	G	1320

Qy	1321	AGATGATGTC	TTGATTTTCTACGAGCAACTCGGCCCGGAC	TAATGTATTCTAGATC	1381
Db	1321	AGATGATGTC	TTGATTTTCTACGAGCAACTCGGCCCGGAC	TAATGTATTCTAGATC	1381
		AGATGATGTC	TTGATTTTCTACGAGCAACTCGGCCCGGAC	TAATGTATTCTAGATC	1381
Qy	1381	ATTACCAACCCTG	CACGGCAAGGACATTTGGTACTATGAGATCGAGATC	CAAGCCATTT	1440
Db	1381	ATTACCAACCCTG	CACGGCAAGGACATTTGGTACTATGAGATCGAGATC	CAAGCCATTT	1440
Qy	1441	CAGCAAAAGGTG	AGTTTGGTTCAGAAACCTTG	TGGTAAATTAATCATTTGTTACTGACCCCTTT	1500
Db	1441	CAGCAAAAGGTG	AGTTTGGTTCAGAAACCTTG	TGGTAAATTAATCATTTGTTACTGACCCCTTT	1500
Qy	1501	CAGATTTACCCCA	CTTGGCCCTGCCACTCTCTGTCGGCTACGATGGCATG	AGCCCTTGGT	1560
Db	1501	CAGATTTACCCCA	CTTGGCCCTGCCACTCTCTGTCGGCTACGATGGCATG	AGCCCTTGGT	1560
Qy	1561	CCTACTTTCAAT	GTTCCTCCAGAGGAACAGAGACTGTAGTTAGGTTCA	TCAACAATGCCACC	1620
Db	1561	CCTACTTTCAAT	GTTCCTCCAGAGGAACAGAGACTGTAGTTAGGTTCA	TCAACAATGCCACC	1620
Qy	1621	GTGAGAAACTCG	GTCCATCTGCACGGCTCCCCATCGCGTGC	CGCCCTTCGATGGTGGGCT	1680
Db	1621	GTGAGAAACTCG	GTCCATCTGCACGGCTCCCCATCGCGTGC	CGCCCTTCGATGGTGGGCT	1680
Qy	1681	GAGATGTGACCT	TTCCCTCGCGAGTACAAGGATTACTACTTTCCCACT	ACCAATCGGCC	1740
Db	1681	GAGATGTGACCT	TTCCCTCGCGAGTACAAGGATTACTACTTTCCCACT	ACCAATCGGCC	1740
Qy	1741	CGCCTTCCTG	TGTTACCATGACCACGCTTTCATGAAGGTATGCTACG	AGCCCTTTATCTTTC	1800
Db	1741	CGCCTTCCTG	TGTTACCATGACCACGCTTTCATGAAGGTATGCTACG	AGCCCTTTATCTTTC	1800
Qy	1801	TTGGCTACCTTT	GGCTAAACAACCTTCCTTTCTGTAGACTGCTGAGA	ATGCCTACTTTGGCTC	1860
Db	1801	TTGGCTACCTTT	GGCTAAACAACCTTCCTTTCTGTAGACTGCTGAGA	ATGCCTACTTTGGCTC	1860
Qy	1861	AGGCTGCGCCT	TACATATTACAAGACGAGGCTGAGGATGCTCTCG	GTCTTCCCTAGTGGCT	1920
Db	1861	AGGCTGCGCCT	TACATATTACAAGACGAGGCTGAGGATGCTCTCG	GTCTTCCCTAGTGGCT	1920
Qy	1921	ATGGCGAGTT	CGATATCCCTCTGATCCTCAGCGGCCAAGTACTATA	ACGCCGATGGTACCC	1980
Db	1921	ATGGCGAGTT	CGATATCCCTCTGATCCTCAGCGGCCAAGTACTATA	ACGCCGATGGTACCC	1980
Qy	1981	TGCGTTCACCG	CGAGGTGAGGACAGGACCTCTGGGGAGATGTCAT	CTCATCGCTCAACGAC	2040
Db	1981	TGCGTTCACCG	CGAGGTGAGGACAGGACCTCTGGGGAGATGTCAT	CTCATCGCTCAACGAC	2040
Qy	2041	AGCCATGGCCT	TTTCTTAAAGTCCAGCCCGGCAAGTACCGTTTCCG	ATTCTCAACGCTG	2100
Db	2041	AGCCATGGCCT	TTTCTTAAAGTCCAGCCCGGCAAGTACCGTTTCCG	ATTCTCAACGCTG	2100
Qy	2101	CCGTGTCGTG	TCCTCTACCTCGTCAGGACAGCTCTCCCAAGCT	TCAGATTC	2160
Db	2101	CCGTGTCGTG	TCCTCTACCTCGTCAGGACAGCTCTCCCAAGCT	TCAGATTC	2160
Qy	2161	CTTTTCAAGT	CAATGGCTCTGATGGTCTCCTTCAAGCCCGG	TTTCAGACCTTAACC	2220
Db	2161	CTTTTCAAGT	CAATGGCTCTGATGGTCTCCTTCAAGCCCGG	TTTCAGACCTTAACC	2220
Qy	2221	TCTACCTTGT	TGTTGCCGAGCGTTACGAGATCATTTTGGTAT	GTGCCCTCTCAGCA	2280
Db	2221	TCTACCTTGT	TGTTGCCGAGCGTTACGAGATCATTTTGGTAT	GTGCCCTCTCAGCA	2280
Qy	2281	ATGAGTCAAGA	ACTCTAAGACTTAACACTTTGTAGACTTCA	CCAACCTTTGCTGGCCAGACTC	2340
Db	2281	ATGAGTCAAGA	ACTCTAAGACTTAACACTTTGTAGACTTCA	CCAACCTTTGCTGGCCAGACTC	2340
Qy	2341	TTGACCTGCG	CAACGTTGCTGAGACCAACGATGTGCGG	CACGAGGATGAGTACGCTCGCA	2400
Db	2341	TTGACCTGCG	CAACGTTGCTGAGACCAACGATGTGCGG	CACGAGGATGAGTACGCTCGCA	2400
Qy	2401	CTCTCGAGG	TGATGGCGCTTCGTCGTCTGAGCTCTGG	CACTGTTGAGGACAACAGCGGTCC	2460

|||||
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QY 2461 CCTCCACTCTCCGTGACGTTCTCTTCCCTCTCTCAACAAGGAAGGCCCGCCGACAAAGCACT 2520
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US-10-080-233-3
; Sequence 3, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: NO. US20020151450A1el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/10/080.233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-10-080-233-3

Query Match 100.0%; Score 3676.6; DB 12; Length 3677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3

US-09-338-723A-1
; Sequence 1, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huaming, Wang

; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338.723A
; CURRENT FILING DATE: 1999-05-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-338-723A-1

Query Match 100.0%; Score 3675.8; DB 10; Length 3677;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3675; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 1741 CGCCTTCTGTGTACCATGACCACGCTTTTCATGAAGGTATGCTACGAGCCTTTATCTTTTC 1800
QY 1801 TTGGCTACCTTTGGCTAACCAACTCTCTTTCTGATAGCTGCTGAGATGCTACTTTGGTC 1860
DB 1801 TTGGCTACCTTTGGCTAACCAACTCTCTTTCTGATAGCTGCTGAGATGCTACTTTGGTC 1860
QY 1861 AGGCTGGCCCTACATTTATCAACGAGGAGCTGAGATGCTCTCGCTCTTCTAGTGGCT 1920
DB 1861 AGGCTGGCCCTACATTTATCAACGAGGAGCTGAGATGCTCTCGCTCTTCTAGTGGCT 1920

QY 1921 ATGGCAGTTTCGATATCCCTCTGATCCTGACGGCCAAAGTACTATACGCCGATGGTACC 1980
DB 1921 ATGGCAGTTTCGATATCCCTCTGATCCTGACGGCCAAAGTACTATACGCCGATGGTACC 1980
QY 1981 TCGGTTTCGACCAGGGTGAGGACAGGACCTGTGGGAGATGTCTCATGTCAACGGAC 2040
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DB 2041 AGCCATGGCCTTTCTTACGTCACGCGCCGCAAGTACCGTTTCCGATTCCTCAACGGCTG 2100
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DB 2101 CGGTGTCTCGTCTGGCTCTTACCTCGTCAGGACCAAGCTCTCCCAAGCTCAGAAATTC 2160
QY 2161 CTTTCCAAGTCATTTGGCTCTGATGTGTCTCTTCAAGCCCGCTTCAGACCTCTAACC 2220
DB 2161 CTTTCCAAGTCATTTGGCTCTGATGTGTCTCTTCAAGCCCGCTTCAGACCTCTAACC 2220
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DB 2281 ATGAGTCAAGAACTCTAAGACTTAACACTTTGTAGACTTTCACCAACTTTGCTGGCCAGACTC 2340
QY 2341 TTGACTCTGGCAACGTTGCTGAGACCAACGATGTGCGGACAGGATGAGTACGCTCGCA 2400
DB 2341 TTGACTCTGGCAACGTTGCTGAGACCAACGATGTGCGGACAGGATGAGTACGCTCGCA 2400
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DB 2401 CTTCTCAGGTGATGCGCTTTCGTCAGCTTGGCACCTTTGAGGACAAACGCCAGGTCC 2460
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Db 3661 AACTGACCTGGGTCAAT 3677

RESULT 4
US-10-080-233-5
; Sequence 5, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC367
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid
US-10-080-233-5
Query Match 55.9%; Score 2054; DB 12; Length 2067;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1761 CCACGCTTTCATGAAGGATGCTACGAGCCTTTATCTTTCTTGGCTACCTTTGGCTAAC 1820
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QY 3021 GTGCGAGGACTGGCGAGCAGGAGCGGTACAACCGCCTCGATGAGATCTGGAGGATCTT 3080
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QY 3081 GGAATCGAGGAGTA 3094
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RESULT 5

US-09-338-723A-5
; Sequence 5, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huaming, Wang

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; TITLE OF INVENTION: Phenol Oxidizing Enzymes  
; FILE REFERENCE: GC561-2  
; CURRENT APPLICATION NUMBER: US/09/338,723A  
; CURRENT FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 09/220,871  
; FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1791  
; TYPE: DNA  
; ORGANISM: Stachybotrys chartarum  
US-09-338-723A-5
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Query Match 40.1%; Score 1474; DB 10; Length 1791;  
Best Local Similarity 87.0%; Pred. No. 0;  
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;  
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QY 1818 ACCAACTTCTTTTCGTAGACTGCTGAGAAATGCTACTTTGGTCAGGCTGGCGCCTACATT 1877  
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Db 748 GAGGACGAGGACCTGTGGGAGATGTTCATCCATGTCACGCGACAGCCATGGCCCTTTCCTT 807
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Db 1774 CTTGGAATCGAGGAGTAA 1791

RESULT 6
US-10-080-210-5
; Sequence 5, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA
US-10-080-210-5

Query Match 40.1%; Score 1474; DB 12; Length 1791;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps 5;

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Qy 1458 GCTCAGAAACCTTGTGGTAATTAATCATTTACTGACCCCTTTTCAGATTTTACCCACCTT 1517
Db 312 -----GATTTACCCACCTT 326

Qy	1518	GCGCCCTGCCAC	TCTCGT	CGGCTACGATGGC	ATAGCCCTGGT	CCTACTTTCAATG	TTCC	1517
Db	327	GCGCCCTGCCAC	TCTCGT	CGGCTACGATGGC	ATAGCCCTGGT	CCTACTTTCAATG	TTCC	386
Qy	1578	CAGAGGACAGAG	ACTGTAG	TTAGTTTATCAACA	ATGCCACCGTGAG	AACCTCGGTCCA	1637	
Db	387	CAGAGGACAGAG	ACTGTAG	TTAGTTTATCAACA	ATGCCACCGTGAG	AACCTCGGTCCA	446	
Qy	1638	TCCTGCACGGC	TCCCATCCG	CTGCCCTTTCGATGG	TTGGCTCAAGATGTG	ACCTTTCCC	1697	
Db	447	TCCTGCACGGC	TCCCATCCG	CTGCCCTTTCGATGG	TTGGCTCAAGATGTG	ACCTTTCCC	506	
Qy	1698	TGGCGAGTACA	AGGATTA	CTTTCCCACTACCA	ATCCGCCCGCCTTCTGTGG	TACCA	1757	
Db	507	TGGCGAGTACA	AGGATTA	CTTTCCCACTACCA	ATCCGCCCGCCTTCTGTGG	TACCA	566	
Qy	1758	TGACCCAGCTT	TTCATCAAG	STATGCTACGAG	CCCTTATCTTTCTTG	GGCTACCTTTGG	CTA	1817
Db	567	TGACCCAGCTT	TTCATCAAG	STATGCTACGAG	CCCTTATCTTTCTTG	GGCTACCTTTGG	CTA	583
Qy	1818	ACCAACTTCCT	TTTCTGTAG	ACTGCTGAGATG	CTACTTTTGGTCAG	GCTGGCCCTAC	ATT	1877
Db	584	-----	-----	AGACTGCTGAGA	ATGCCCTACTTTTGGT	CAAGCTGGCGCCTAC	ATT	627
Qy	1878	ATCAACGACG	AGGCTGAG	ATGCTCTCGGTCTT	CTCTAGTGGCTATGG	CGGAGTTCCGAT	ATC	1937
Db	628	ATCAACGACG	AGGCTGAG	ATGCTCTCGGTCTT	CTCTAGTGGCTATGG	CGGAGTTCCGAT	ATC	687
Qy	1938	CTCTGTATCT	GTACGGC	CAAGTACTATAAC	GGCGATGTACCC	TGCGTTCCGAC	CGAGGT	1997
Db	688	CTCTGTATCT	GTACGGC	CAAGTACTATAAC	GGCGATGTACCC	TGCGTTCCGAC	CGAGGT	747
Qy	1998	GAGSACCAGG	ACCTGTGG	GAGATGCTATCC	ATGTCAACGACAG	CCATGGCCCTT	CTCCT	2057
Db	748	GAGSACCAGG	ACCTGTGG	GAGATGCTATCC	ATGTCAACGACAG	CCATGGCCCTT	CTCCT	807
Qy	2058	AACGTCCAG	CCCCGGA	AGTACCGTTTCC	GATTCCTCAACG	CTGCGGTCTCTG	TCGTGG	2117
Db	808	AACGTCCAG	CCCCGGA	AGTACCGTTTCC	GATTCCTCAACG	CTGCGGTCTCTG	TCGTGG	867
Qy	2118	CTCCTCTAC	CTCTCAG	GCACAGCTC	CCCAAGTCAGA	ATTCCTTTCCA	AGTCA	2177
Db	868	CTCCTCTAC	CTCTCAG	GCACAGCTC	CCCAAGTCAGA	ATTCCTTTCCA	AGTCA	927
Qy	2178	TCGTATGCT	GGTCTCCT	TCAAGCCCGGTTC	AGACCTCTAAC	CTCTACCTTGC	TGTGGC	2237
Db	928	TCTGATGCT	GGTCTCCT	TCAAGCCCGGTTC	AGACCTCTAAC	CTCTACCTTGC	TGTGGC	987
Qy	2238	GAGGTTTAC	GAGATCAT	TATTTG	TATGCTCCCTC	ACGAATGAGTCA	AGA	2297
Db	988	GAGGTTTAC	GAGATCAT	TATTTG	TATGCTCCCTC	ACGAATGAGTCA	AGA	1008
Qy	2298	AGACTAAC	ACTTTGAG	ACTTCACCA	ACTTTGCTGGCC	AGACTCTTGAC	CTCGCAAG	2357
Db	1009	-----	-----	GACTTCACCA	ACTTTGCTGGCC	AGACTCTTGAC	CTCGCAAG	1053
Qy	2358	GCTGAGAC	CAACGAT	CTCGGCACG	AGGATAGTAC	GTCTCGACTCTC	GAGGTGATG	2417
Db	1054	GCTGAGAC	CAACGAT	CTCGGCACG	AGGATAGTAC	GTCTCGACTCTC	GAGGTGATG	1113
Qy	2418	TTCGTGTG	CAGCTCG	CACTGTGAG	GAACAACGCCAG	GTCCCTCCAC	CTCCGTG	2477
Db	1114	TTCGTGTG	CAGCTCG	CACTGTGAG	GAACAACGCCAG	GTCCCTCCAC	CTCCGTG	1173
Qy	2478	GTTTCCTT	TCCTCCT	CACAGGA	AGCCCGCCGCA	ACAAGCACTTCA	AGTTTGA	2537
Db	1174	GTTTCCTT	TCCTCCT	CACAGGA	AGCCCGCCGCA	ACAAGCACTTCA	AGTTTGA	1233
Qy	2538	AACGACAC	TACCTGAT	CAACGATG	TTGGCTTTG	CGGATGTCAATG	ACGCTGCT	2597
Db	1234	AACGACAC	TACCTGAT	CAACGATG	TTGGCTTTG	CGGATGTCAATG	ACGCTGCT	1293

Qy	2598	AAGCCCGAGCTCGCGCACCGTTGAGTCTCGGAGCTCGAGAACTCCTCTGGAGGCTGGAGC	265
Db	1294	AAGCCCGAGCTCGCGCACCGTTGAGTCTCGGAGCTCGAGAACTCCTCTGGAGGCTGGAGC	1353
Qy	2658	CACCCGCTCCACATTCACCTTGTTGACTTCAAGATCCTCAACGCAACTGGTGGTCTGTGGC	2717
Db	1354	CACCCGCTCCACATTCACCTTGTTGACTTCAAGATCCTCAACGCAACTGGTGGTCTGTGGC	1413
Qy	2718	CAGTCTATGCCTACGAGTCTGCTGCTTTAAGGATGTCTGCTTGGGAGGGGTGAG	2777
Db	1414	CAGTCTATGCCTACGAGTCTGCTGCTTTAAGGATGTCTGCTTGGGAGGGGTGAG	1473
Qy	2778	ACCTGACCATCGAGGGCCCACTACCAACCCCTGGACTTGGAGCTTACATGTGGCACTGTAC	2837
Db	1474	ACCTGACCATCGAGGGCCCACTACCAACCCCTGGACTTGGAGCTTACATGTGGCACTGTAC	1533
Qy	2838	AACCTCATTCACGAGGATAACGACATGATGGCTGTATTCAACGTCACCGCCATGGAGG	2897
Db	1534	AACCTCATTCACGAGGATAACGACATGATGGCTGTATTCAACGTCACCGCCATGGAGG	1593
Qy	2898	AAGGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCCGCTTCCT	2957
Db	1594	AAGGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCCGCTTCCT	1653
Qy	2958	TACAACCGCAACGACTTCCATGCTCGCGTGGAGAACTTCTCGCGCGAGTCCATCACTGCC	3017
Db	1654	TACAACCGCAACGACTTCCATGCTCGCGTGGAGAACTTCTCGCGCGAGTCCATCACTGCC	1713
Qy	3018	CGAGTGCAGGAGCTGGCGGAGCAGGAGCGGTACAAACCGCTCGATCAGATCCTTGAGGAT	3077
Db	1714	CGAGTGCAGGAGCTGGCGGAGCAGGAGCGGTACAAACCGCTCGATCAGATCCTTGAGGAT	1773
Qy	3078	CTTGGAAATCGAGGAGTAA 3095	
Db	1774	CTTGGAAATCGAGGAGTAA 1791	
RESULT 7			
US-10-080-233-1			
; Sequence 1, Application US/10080233			
; Patent No. US20020151450A1			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Huaming			
; TITLE OF INVENTION: No. US20020151450A1e1 Phenol Oxidizing Enzymes			
; FILE REFERENCE: GC567			
; CURRENT APPLICATION NUMBER: US/10/080,233			
; CURRENT FILING DATE: 2002-02-19			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 1791			
; TYPE: DNA			
; ORGANISM: Stachybotrys sp.			
US-10-080-233-1			
Query Match 40.1%; Score 1474; DB 12; Length 1791;			
Best Local Similarity 87.0%; Pred. No. 0;			
Matches 1791; Conservative 0; Mismatches 0; Indels 267; Gaps			
Qy	1038	GTCAATATGCTGTTCAGATCATGGCAACTGGCAGCAGCCCTCCGGGCTCCTGTCTGGAGTC	1097
Db	1	GTCAATATGCTGTTCAGATCATGGCAACTGGCAGCAGCCCTCCGGGCTCCTGTCTGGAGTC	60
Qy	1098	CTCGGCATCCCGATGGACACCGGACGCCACCCCATTTAGAGCTGTGTGATCCCGAAGTGAAG	1157
Db	61	CTCGGCATCCCGATGGACACCGGACGCCACCCCATTTAGAGCTGTGTGATCCCGAAGTGAAG	120
Qy	1158	ACTGAGGTCTTCGCTGACTCCCTCCTTGTGTGACAGCGGATGACGACTGGGAGTCACT	1217
Db	121	ACTGAGGTCTTCGCTGACTCCCTCCTTGTGTGACAGCGGATGACGACTGGGAGTCACT	180
Qy	1218	CCATACAACTTGCCTTTTACAGGTGAGACACCTGTGCCACCTGTTTTTCCCTCGATAACTAAC	1277

Db 181 CCATACAACCTTGCCTTAC----- 198

Qy 1278 TCTTATAGGAATGCCCTGCCAATTCACACTGTCAAGCAGCCCCAAGATGATGTCTTTTGAT 1337

Db 199 -----AGGAATGCCCTGCCAATTCACACTGTCAAGCAGCCCCAAGAT----- 239

Qy 1338 TTTCTACAAGCAACTCGGCCCGACCTAATGTATTTCTAGGATCATTTACCAACCCCTGTAC 1397

Db 240 -----GATCATTTACAACCCCTGTAC 260

Qy 1398 CGGCAAGGACATTTGGTACTATAGATCGAGATCAAGCATTTTCAGCAAAAGGGTGAGTTT 1457

Db 261 CGGCAAGGACATTTGGTACTATAGATCGAGATCAAGCCATTTTCAGCAAG----- 311

Qy 1458 GCTCAGAAACCTTGTGGTAATTAATTCATTTGTTACTGACCCCTTTTCAGATTTTACCCACACTT 1517

Db 312 -----GATTTACCCACACTT 326

Qy 1518 GCGCCCTGCCACTCTCGTCGSGTAGGATGGCATGAGCCCTGGTCTCTACTTTCAATGTTCC 1577

Db 327 GCGCCCTGCCACTCTCGTCGSGTAGGATGGCATGAGCCCTGGTCTCTACTTTCAATGTTCC 386

Qy 1578 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 1637

Db 387 CAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTCGGTCCA 446

Qy 1638 TCTGCACGGCTCCCCATCGCGTGCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCC 1697

Db 447 TCTGCACGGCTCCCCATCGCGTGCCTTTTCGATGGTTGGCTGAAGATGTGACCTTCCC 506

Qy 1698 TGGCAGTACAGGATTTACTACTTTCCCACTACCAATCCGCGCCCTTCTGTGGTACCA 1757

Db 507 TGGCAGTACAGGATTTACTACTTTCCCACTACCAATCCGCGCCCTTCTGTGGTACCA 566

Qy 1758 TGACCACGCTTTCATGAAGGTATGTCTACGAGCCTTTATCTTTCTTGGCTACTCTTTGGCTA 1817

Db 567 TGACCACGCTTTCATGA----- 583

Qy 1818 ACCAATTTCTTTCGTAGACTGCTGAGAAATGCCTACTTTTGGTCAGGCTGGCGCCTACATT 1877

Db 584 -----AGACTGCTGAGAAATGCCTACTTTTGGTCAGGCTGGCGCCTACATT 627

Qy 1878 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTGATATC 1937

Db 628 ATCAACGACGAGGCTGAGGATGCTCTCGGTCTTCTAGTGGCTATGGCGAGTTGATATC 687

Qy 1938 CCTCTGATCTTGACGGCCAAAGTACTATAACCCGATGTACCTGCGTTCGACCGAGGGT 1997

Db 688 CCTCTGATCTTGACGGCCAAAGTACTATAACCCGATGTACCTGCGTTCGACCGAGGGT 747

Qy 1998 GAGGACGAGGACCTGTGGGAGATGTCATCCATGTCAACGACAGCCCATGGCCTTTCCTT 2057

Db 748 GAGGACGAGGACCTGTGGGAGATGTCATCCATGTCAACGACAGCCCATGGCCTTTCCTT 807

Qy 2058 AACGTCCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCGGTCTCGTCTTGG 2117

Db 808 AACGTCCAGCCCGCAAGTACCGTTTCCGATTCCTCAACGCTGCGGTCTCGTCTTGG 867

Qy 2118 CTCCTCTACCTCTGTCAGACGACGCTCTCCCAAGCTCAGAATTCCTTCCCAAGTCAATTGCC 2177

Db 868 CTCCTCTACCTCTGTCAGACGACGCTCTCCCAAGCTCAGAATTCCTTCCCAAGTCAATTGCC 927

Qy 2178 TCTGATGCTGGTCTCTTTCAGACCCCTTTCAGACCTCTAACCTCTACCTTGTCTTGGC 2237

Db 928 TCTGATGCTGGTCTCTTTCAGACCCCTTTCAGACCTCTAACCTCTACCTTGTCTTGGC 987

Qy 2238 GAGCCTTACGAGATCAATTAATTTGGTATGCCCCCTCTCAGAAATGAGTCAAGAACTCTA 2297

Db 988 GAGCCTTACGAGATCAATTAATTTGGTATGCCCCCTCTCAGAAATGAGTCAAGAACTCTA 1008

Qy 2298 AGACTAACACTTTGTAGACTTTCACCAACTTTTGTGGCCAGAGCTTGTACCTGCGCAACGTT 2357

Db 1009 -----GACTTCACCAACTTTTGTGGCCAGAGCTTTGACCTGCGCAACGTT 1053

Qy 2358 GCTGAGACCAACGATGTGGCGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATGCGC 2417

Db 1054 GCTGAGACCAACGATGTGGCGACGAGGATGAGTACGCTCGCACTCTCGAGGTGATGCGC 1113

Qy 2418 TTCGTGCTCAGCTCTGGGACACTGTTGAGGACAACAGCCAGGTCCCTCCACTCTCGGTGAC 2477

Db 1114 TTCGTGCTCAGCTCTGGGACACTGTTGAGGACAACAGCCAGGTCCCTCCACTCTCGGTGAC 1173

Qy 2478 GTTCTTTCCCTCTCAAGAAAGGCCCGCCGACAAGCACTTCAAGTTTGAACGACG 2537

Db 1174 GTTCTTTCCCTCTCAAGAAAGGCCCGCCGACAAGCACTTCAAGTTTGAACGACG 1233

Qy 2538 AACGGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCAATGACGGTGTCTTGCC 2597

Db 1234 AACGGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCAATGACGGTGTCTTGCC 1293

Qy 2598 AAGCCCGAGCTCGGCACCGTTGAGGTCTGGGAGCTCGAGAACTCTCTGGAGGCTGGAGC 2657

Db 1294 AAGCCCGAGCTCGGCACCGTTGAGGTCTGGGAGCTCGAGAACTCTCTGGAGGCTGGAGC 1353

Qy 2658 CACCCCGTCCACATTCACCTTTGACTTCAAGATTCCTCAAGCGAACTGGTGGTCTGGC 2717

Db 1354 CACCCCGTCCACATTCACCTTTGACTTCAAGATTCCTCAAGCGAACTGGTGGTCTGGC 1413

Qy 2718 CAGGTCAATGCCCCACGAGTCTGCTGCTTAAAGGATGCTGCTGGTGGGACGAGGCTGAG 2777

Db 1414 CAGGTCAATGCCCCACGAGTCTGCTGCTTAAAGGATGCTGCTGGTGGGACGAGGCTGAG 1473

Qy 2778 ACCCTGACCATCGAGGCCACTACCAACCCCTGGACTGGACTTACATGTGGCACTGTGAC 2837

Db 1474 ACCCTGACCATCGAGGCCACTACCAACCCCTGGACTGGACTTACATGTGGCACTGTGAC 1533

Qy 2838 AACCTCATTCAGAGGATAACGACATGATGGCTGATTCAACGTCAACGCCATGGAGGAG 2897

Db 1534 AACCTCATTCAGAGGATAACGACATGATGGCTGATTCAACGTCAACGCCATGGAGGAG 1593

Qy 2898 AAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCTTCTT 2957

Db 1594 AAGGATATCTTCAGGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGCGCTTCTT 1653

Qy 2958 TACAACGCCAAGACTTCCATGCTCGCGCTGGAACCTTCTCCGCGGAGTCCATCACTGCC 3017

Db 1654 TACAACGCCAAGACTTCCATGCTCGCGCTGGAACCTTCTCCGCGGAGTCCATCACTGCC 1713

Qy 3018 CGAGTGCAGGAGCTGGCGGACGAGGCGTACAACCCCTCGATGAGATCCTGGAGGAT 3077

Db 1714 CGAGTGCAGGAGCTGGCGGACGAGGCGTACAACCCCTCGATGAGATCCTGGAGGAT 1773

Qy 3078 CTTGGAATCGAGGAGTAA 3095

Db 1774 CTTGGAATCGAGGAGTAA 1791

RESULT 8

US-09-338-723A-3

; Sequence 3, Application US/09338723A

; Patent No. US20020019038A1

; GENERAL INFORMATION:

; APPLICANT: Huaming, Wang

; TITLE OF INVENTION: Phenol Oxidizing Enzymes

; FILE REFERENCE: GC561-2

; CURRENT APPLICATION NUMBER: US/09/338,723A

; CURRENT FILING DATE: 1999-06-23

; PRIOR APPLICATION NUMBER: 09/220,871

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 2905

; TYPE: DNA

; ORGANISM: Bipolaris spicifera

US-09-338-723A-3

Query Match 12.5%; Score 460.8; DB 10; Length 2905;
Best Local Similarity 59.3%; Pred. No. 3.1e-131;
Matches 976; Conservative 0; Mismatches 537; Indels 133; Gaps 6;

Qy 1491 CTGACCCCTTCAGATTTACCCCACTTGGCGCCCTGCCACTCTCTCGGCTACAGTGGCAT 1550
Db 478 CTTACCCAGCAGCTCTATCCAAAGCCTGCGCCCTGCTGGTTAGTAGGCTATGACGGCAT 537

Qy 1551 GAGCCCTGGTCTACTTTCATGTTTCCAGAGACAGAGACTGTAGTTAGTTTCATCAA 1610
Db 538 CTCGCCAGGTCTACGATCATAGTGGCGAGAGAACAGAGCTGTGTACGGTTTATAAA 597

Qy 1611 CAATGCCACCGTGGAGAACTCGGTCCTATCTGCAGGGCTCCCATCTCGCTGCCCTTTTGA 1670
Db 598 CCAGGGTATCGCGAAGCTCCATCCATCTCCACGGCTCCCGCTGCCCTTTTGA 657

Qy 1671 TGGTTGGCTGAAGATGTGACTTCCCTGGCGAGTACAA----- 1709
Db 658 CGGATGGCTGATGATGATGATGATGAAGGGGAATACAAAGGTACGATAGCGTGTGATTC 717

Qy 1710 -----GGATTACTACTTTCCC 1725
Db 718 TACGCATCAGGAAGCCTATATCATATACTAACAGGACTTTCTTCTCAGACTACTACTACCCG 777

Qy 1726 AACTACCAATCCGCCCGCTTCTGTGGTACCATGACCACGCTTTTCATGAAGTA--TGCT 1783
Db 778 AACACCAAGCTGCCAGATTTTGTGGTACCACGATCATGTATGCCATGTGTGAAGTCTT 837

Qy 1784 ACGAGCCCTTATCTTCTTGGCTACCTTTGGCTAACCAACTTCCCTTTCGTAGACTGTGA 1843
Db 838 TACCGACTTTTCATGCTAGTGAACGGAAGGATTAAGCTAATCATCTGTGCAGACGCCAGA 897

Qy 1844 GAATGCCCTACTTTGTGCTAGGCTGGCGCTTACATATCAACAGAGGCTGAGGATGCTCT 1903
Db 898 AAATGCCCTATTTCCGGCAAGCGCGCTTACCTGTATCAGACCGCGCTGAGGATGCTCT 957

Qy 1904 CGGTCTTCTCTAGTGGCTATGGGAGTTCCGATCCCTCTGATCTGACGGCCCAAGTACTA 1963
Db 958 CGGCCTCTCTCAGGTTACGGAATACAGACATCCGCTGGTCTCAGTTCCAACTACTA 1017

Qy 1964 TAAACCGGATGATACCTTGGCTTGCAGCGAGGTGAGACAGAGACCTGTGGGGAGATGT 2023
Db 1018 CAACCCGATGGAACCTTAAAGACCAGTGTGGGGAAGAAAGAGTGTGTGGGGGAGAT 1077

Qy 2024 CATCCATGTCAACGACAGCATGCGCTTCTCTTAACCTCCAGCCCGCAAGTACCGTTT 2083
Db 1078 CATCCATGTCAACGGTCAAGCCCTGGCCATTTCTTAATGTTGAGCCTCGAAAGTATCGTCT 1137

Qy 2084 CCGATTCTCTCAACGCTGCGGTGCTCTGCTGGCTCTACCTCGTCAGGACCCAGCTC 2143
Db 1138 TCGATTCTCTCAACGCGGTGTTCTTAGNACTTTTGCCCTTTACTTTCGTCAAGCAAGCAA 1197

Qy 2144 TCCCAAGCTCAGAAATCTCTTCCAAAGTCAATGCGCTCTGATGCTGTCTCTTCAAGCCCC 2203
Db 1198 CACTGCCACTAGGCTCTCTTTCCAGGCTATTTGCCCTCTGATGCGGGCTACTCACACGCC 1257

Qy 2204 CGTTCAGACCTCTAACCTCTACCTTGTCTTGGTGGCCAGGCTTACGAGATCATTTGGTAT 2263
Db 1258 GGTTCAAACCTCAGATATGTATGTTGCGAGCCGCAAGACGCTACGAGAT----- 1305

Qy 2264 GGCCTCCCTCTCAGGAATGAGTCAAGAACTCTAAGACTATGATAGCTTTCACCAA 2323
Db 1306 -----TGTTGTCGATTTCCGCGC 1323

Qy 2324 CTTTCTGCCAGACTTTGACCTCGCAAGCTTGCTGAGACCAAGATGTGCGGAGCA 2383
Db 1324 CTATCGGCGCAAAAGTTGGATCTCGCAAACTTCGCAAAAGGCCAATGGTATCGGTACGGA 1383

Qy 2384 GATGATGACGCTCGCACTCTCGAGGTGCGCTTCGTCGACGCTCGGACATGTTGA 2443
Db 1384 CGACGACTACGCAAAACACTGACAAGGTCTATCGGTTTCCACGCTCAGCAGCAAAACAGTCT 1443

Qy 2444 GGACAACGACGAGTCCCTCCACTCTCCGTGACGTTCTTCTTCCCTCCTCACAAGGAAG 2503
Db 1444 CGATAACTCCGTGCTACCCGAGCAGCTATCTCAGATCCAGTTCCCGCGGACA---AAAC 1500

Qy 2504 CCCCGCCGACAGCACTTCAAGTTTGAACGCAAGCAACGGACACTACCTGTGATCAACGATGT 2563
Db 1501 CGACATAGACCATCACTTCCGTTTCCATCGTACCAACGGCGAGTGGCGCATCAACGGCAT 1560

Qy 2564 TGGTTTGGCCGATGTCATAGGCTGCTTGGCCAAAGCCGAGCTCGGCACCGTTGAGGT 2623
Db 1561 CGGTTTGCAGACGCTCGAGAACCGTGTCTTTCGCAAGGTACCGCGGTACTGTGCGACT 1620

Qy 2624 CTGGAGCTCGAGAACTCTCTGGAGGCTGGAGCACACCCCTCCACATTCACCTTGTGTA 2683
Db 1621 TTGGAACTTCGAGAACAGCTCCGCGGCTGTGTACACCCCATCCACGTCCTACCTAGTGA 1680

Qy 2684 CTTCAAGATCTCTCAAGCGAACTGG-----TGGTCTGGCCAGGTCATGCCCTACGAGTC 2737
Db 1681 CTTCCGAGTCTCTGCACGCTACGCGGACGAAGGCACCTCGCGGCGTCAATGCCCTATGAGGC 1740

Qy 2738 TGCTGGTCTTAAGGATGTCGTCTGGTGGCAGGGGTGAGACCCTGACCATCGAGGCCCA 2797
Db 1741 CGCGGCTCTAAGGACGCTGTGTGGCTCGCGCGTACAGAGAGGTCCTCTCTCGAAGCACA 1800

Qy 2798 CTACCAACCCCTGGAGCTTACATGTGGCACTGTGCACAACTTCACAACTTCACGAGGATAA 2857
Db 1801 TTACGCCCATGGGAGGAGTCTACATGTTCCACTTGCACAACTTCATCCACGAAGACCA 1860

Qy 2858 CGCATGATGCTGTATTCACGCTACCGCCCATGGAGAGAGGATATCTTCAGGAG-- 2915
Db 1861 AGCATGATGCGCCCTTCGACGTGACTTAACTCCAGAACTTTGGGTACAAACGAGACAC 1920

Qy 2916 -GACTTCCGAGACCCCAAGTGGCGGCGCTTCTTCAACCCCAACGAGCTT 2974
Db 1921 TGATTTCCACGATCTGAGGATCTCGCTGTGTCAGCAAGACCTTTCACCGCGGTGATCT 1980

Qy 2975 CCATGCTCGCTGGAACCTTCTCCGCGAGTCCATCACTACCTGCCGAGTGCAGGAGCTGGC 3034
Db 1981 CACGCGCGATCGGGTATCTTTTCAGAAAGATCCATCAGGCTAGAGTAAATGAGTTGGC 2040

Qy 3035 CGACGAGGCGGTACACCCGCTCG 3060
Db 2041 GCTCGAGCAGCTTACACGGAACCTCG 2066

RESULT 9
US-10-080-210-3
; Sequence 3, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Bipolaris spicifera
US-10-080-210-3

Query Match 12.5%; Score 460.8; DB 12; Length 2905;
Best Local Similarity 59.3%; Pred. No. 3.1e-131;
Matches 976; Conservative 0; Mismatches 537; Indels 133; Gaps 6;

Qy 1491 CTGACCCCTTCAGATTTACCCCACTTGGCGCCCTGCCACTCTCTCGTGGCTACGATGGCAT 1550

Db	478	CTTCA	CCAGCAGG	CTATCCA	AGGCTCGGCC	CTGCTT	AGTAG	AGCTATG	ACGCAT	537		
Qy	1551	GAGCC	TGGTCC	TACTCA	ATGTTCC	CAGAGGA	ACAGAG	ACTGTAG	TAGTTCAT	CAAA	1610	
Db	538	CTCCC	AGGTCCT	TACGAT	CATAGT	CGCGAG	AGGACAG	AGCTGTT	TGACGGT	TATAAA	597	
Qy	1611	CAATG	CCACCG	TGGAGAA	TCGGTCC	ATCTG	CACGGCT	CCCCAT	CGGTCGCC	CCCTTTCGA	1670	
Db	598	CCAGG	TGATCG	GAAGTCC	ATCCAT	CTCCAC	GGCTCCCC	CTCCG	TGCCCC	TTTTTGA	657	
Qy	1671	TGGTT	GGGCTGA	AGATGT	GACCTT	CCCTGG	CCAGTACA	-----	-----	-----	1709	
Db	658	CGATG	GGCTG	ATGATG	ATCATG	AAAGGG	GAATACA	AAAGGT	ACGATAG	CGTGTGATTC	717	
Qy	1710	-----	-----	-----	-----	-----	-----	GGATT	ACTACTT	TTTCCC	1725	
Db	718	TACGC	ATCAG	AAGCCT	CTATCAT	ACTAAC	AGGACTT	TCTTCT	CAGACT	ACTACTACCG	777	
Qy	1726	AATTA	CCAAAT	CGCGCG	CTCTGT	GGTACCA	TACACG	CGCTTTCAT	GAAGGT	A--TGCT	1783	
Db	778	AACA	CCAAAG	CTGCCAG	ATTTTGT	GGTACCA	CGATAT	GCTATG	CATGTT	GTAAGTCTT	837	
Qy	1784	ACNAG	CCCTTAT	CTTCTT	TCCTG	GTACCTT	GGCTAAC	CAACTTCC	TTCGTAG	ACTGCTGA	1843	
Db	838	TACCG	ACTTTT	CTATG	TGAAC	CGGAG	GATTAA	GCTAA	CTCTGT	GACACCGCAGA	897	
Qy	1844	GAATG	CTACTT	TTTGTG	TCAGG	CTGGCG	CTTACAT	TATCAAC	CACGAG	GCTCAGGATGCTCT	1903	
Db	898	AAATG	CCCTAT	TTCCGG	CAAGCG	CGGCCCT	TACCTG	TATCAC	AGCCCG	CTGAGGATGCTCT	957	
Qy	1904	CGGT	CTTCC	TAGTGG	CTATGG	GGAGTT	CGATAT	CCCTCT	GATCGAC	GGCCAA	1963	
Db	958	CGGC	TTTCC	TTCAG	TTTAC	GAAAT	ACGACAT	TCGCT	GGTCTC	AGTTC	CCAA	1017
Qy	1964	TAACG	CGGATG	TACCC	TCGGT	TCGACG	AGGGT	GAGCAC	AGCACTG	TGGGGAGATG	2023	
Db	1018	CAACG	CGGATG	GGAAC	CTTTA	AAGACC	AGTGTGG	GGAAG	ACAAAG	AGTGT	1077	
Qy	2024	CATCC	ATGCA	ACGAG	ACGAT	TGSC	CTTTC	CTTAAC	CTCCAG	CCCGCAG	2083	
Db	1078	CATCC	ATGTC	AAAG	CTGAG	CCCTG	GGCCAT	CTTTAA	TGTTG	AGCTCG	1137	
Qy	2084	CCGAT	TTCC	TCAACG	CTCG	CTGCTG	CTGCTTAC	CTCTAC	CTCTG	CAGGAC	2143	
Db	1138	TCGAT	TCC	TCAACG	CGGCTG	TTTCT	TAGGA	ACTTTG	CCCTT	TAC	1197	
Qy	2144	TCCG	AAGTC	CAGAA	TTTCC	TTTCC	CAAGT	CAATG	CGCTCT	GATGCT	2203	
Db	1198	CAGT	GCCACT	TAGGCT	TTCCCT	TTCCAG	GTCTAT	GGCTCT	GATG	CGGGCT	1257	
Qy	2204	CGTT	CAGAC	CTTA	ACCTCT	ACTT	TCGCTG	TGCG	CAGG	GGTTAC	2263	
Db	1258	GGTT	CAACCT	TCAGAT	GATGAT	GTGTG	CAAG	CGGCA	AGCGT	TACAGAT	1305	
Qy	2264	GCCT	TC	CCCTCT	CACGA	ATGAGT	CAAGAA	CTTAAG	ACTTA	AGACTTT	2323	
Db	1306	-----	-----	-----	-----	-----	-----	-----	-----	-----	1323	
Qy	2324	CTTT	GCTGG	CCAG	ACTTCT	TGACCT	CGGA	CAAGT	TGCTG	AGACCA	2383	
Db	1324	CTAT	GCGG	CCAA	ACCTT	GGATCT	CGCA	AACTT	CGCA	AAAGG	1383	
Qy	2384	GGAT	GATAG	CGCT	CGC	ACTCT	CAGAG	TGAT	GGCTT	CGTCTG	2443	
Db	1384	CGAC	GACT	ACGCA	AAAC	ACTT	GCA	AGGT	CAT	CGGTTT	1443	
Qy	2444	GGAA	CAAC	AGC	AGG	TCCCT	CTCC	ACTCT	CCG	TGACG	2503	
Db	1444	CGAT	AACT	CCG	TGTA	CCG	AGC	AGCT	ATCT	CAGAT	1500	
Qy	2504	CCCC	CGCG	CAAG	CACTT	CAAG	TTTGA	ACG	CAGCA	ACGCA	2563	

Db	1501	CGACATAGACCATCACTTCGGTTTCATTCGTACCAACGGCGAGTGGCGCATCAACGGCAT	1561
Qy	2564	TGGCTTTGCCGATGTCAATGAGCGTGTCTCGCCGAAGCCCGAGCTCGCGACCGTTGAGGT	2623
Db	1561	CGGTTTGCAGACGTTCGAGAACCGTGTTCTTCCCAAGGTACCGCGCGTACTGTCTGAGCT	1620
Qy	2624	CTGGAGACTCGAAGACTCCTCTGGAGGCTGGAGCCACCCCGTCCACATTCACCTTGTGA	2683
Db	1621	TTGSGAACTTTCGAGAACAGCTCCGGCGGTGGTTCACACCCCATCCACGTCACCACTAGTAGA	1680
Qy	2684	CTTCAAGATCCTCAAGCGAACTGG-----TGGTCGTGGCCAGGTTCATGCCCTACGAGTC	2737
Db	1681	CTTCCGAGTCGTTCGACGCTACGGCGACGAAGGCACCTCGCGCGTTCATGCCCTATGAGGC	1740
Qy	2738	TGCTGGTCTTAAAGATGTCTGTGGTGGCGAGGGGTGAGACCCCTGACCATCGAGGCCCA	2797
Db	1741	CGCGGCTCTCAAGGACGCTGTGTGGCTCGCGCGTCCAGAGAGGTCCTCTCGTCTGAAGCACA	1800
Qy	2798	CTACCAACCTGGAGCTGGAGCTTACATGTGGCACTGTTCACAACCTCATTCACGAGGATAA	2857
Db	1801	TTACGCCCATGGGACGGAGTCTACATGTTCACATGTTCACCTGCCCAACCTCATCCACGAAGACCA	1860
Qy	2858	CGACATGATGGCTGTATTCAACGTCACCGCCATCGAGAGAGGAGATATCTTCAGGAG--	2915
Db	1861	AGACATGATGGCCGCTTCGACGTGACTAAACTCCAGAACTTTGGGTACAAACGAGACGAC	1920
Qy	2916	-GACTTCGAGAGCCCCATGAACCCCAAGTGGCGCGCGTTCCTTTACAAACCGCAACGACTT	2974
Db	1921	TGATTTCCAGATCTTGAGATCTCTCGCTGGTTCAGCAAGACCTTTACCGCGGGTGATCT	1980
Qy	2975	CCATGCTTCGGCTTGGAACTTCTCCGCCGAGTCCATCACTGCCCGAGTGCAGAGAGCTGGC	3034
Db	1981	CACGGCGGATCGGGTATCTTTTCAGAAATCCATCAGGGCTAGAGTAAATGAGTTGGC	2040
Qy	3035	CGACGAGGCGGTACAAACGGCGTCG	3060
Db	2041	GCTCGAGCAGCCTTACAGGGAACCTCG	2066
RESULT 10			
US-10-080-210-6			
; Sequence 6, Application US/10080210			
; Patent No. US20020142423A1			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Huaming			
; APPLICANT: Bodie, Elizabeth A.			
; TITLE OF INVENTION: Phenol Oxidizing Enzymes			
; FILE NUMBER: GC561-3			
; CURRENT APPLICATION NUMBER: US/10/080,210			
; PRIOR FILING DATE: 2002-02-19			
; PRIOR APPLICATION NUMBER: US 09/220,871			
; PRIOR FILING DATE: 1998-12-23			
; PRIOR APPLICATION NUMBER: US 09/338,723			
; PRIOR FILING DATE: 1999-06-23			
; NUMBER OF SEQ ID NOS: 17			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 6			
; LENGTH: 2063			
; TYPE: DNA			
; ORGANISM: Curvularia pallescens			
US-10-080-210-6			
Query Match 12.4%; Score 455.6; DB 12; Length 2063;			
Best Local Similarity 59.1%; Pred. No. 9.7e-130;			
Matches 971; Conservative 0; Mismatches 544; Indels 129; Gaps			
Qy	1501	CAGATTTACCCCACTTGGCGCCTGCCACTCTCTGCTCGGCTACGATGGCATGAGCCGTGGT	1560
Db	376	CAGGCTATCCAAGTCTAGCTCCTGCTGGTAGCTATGATGGCATTTCCACAGGC	435
Qy	1561	CCTACTTTCAATGTTCCCAAGAAACAGAGACTAGTTAGTTTCAATCAACAATGCCACC	1620
Db	436	CCTAGCATCTCTGCCGAGAGAACAGAGACCGTTGTACGATTCTGTAACACGAGGTGAT	495

Query Match 12.48; Score 455.6; DB 12; Length 2063;

6.

Qy	1501	CAGATTTACCCACCTTGGCCCTGCCACTCGTCGGCTACGATGGCATGAGCCCTGCT	1560
Db	376	CAGCTCATCCAACTAGCTGCTGCTGCTGGTAGCTATGATGGCATTTTCACAGGC	435
Qy	1561	CCTACTTTCATCTGCCAGAGAACAGAGACTGTATGTAGTTCATCAACAATGCCACC	1620
Db	436	CCTACGATCATCTGCCGAGAGAACAGAGCCGTGTACGATTCGTAAACACGGTGAT	495

Qy 1621 GTGGAGAACTCGGTCCATCTGACGGCTCCCATCGCTGCCCTTTTCGATGGTGGCT 1680
Db 496 CGCGAGAGTTGATTCATCTTCATGGTTCTCCCTCCCTGCCCTTTGACGGATGGCT 555
Qy 1681 GAAGATGTGACCTTCCCTGGCGAGTACAAGAT----- 1713
Db 556 GAAGATTTGATTTATGAAGGGCCAAATTCAAAGGTACAACAGACAATCTTATGCAATCAGG 615
Qy 1714 -----TACTACTTCCCAACTACCAATCCG 1738
Db 616 TGCCTCTTTTATAACAGACTCGTTCTTAGACTACTACTACCCGAAACACAGGCTG 675
Qy 1739 CCGCGCTTCTGTGTPACCATGACACCGCT-TTCATGAAGGTATGCTACGAGCCTTTATCT 1797
Db 676 CCAGATTCCTGTGTGTTACACGATCATGCTATGCTATGTTGAAGTCTTCAGACTAATCAT 735
Qy 1798 TTCCTTGGCTACCTTTGGCTTAACCACTTCTTTCGTAGACTGCTGAGAAATGCTACTTTG 1857
Db 736 GGGAGCGAAACGGAAGATCGGCTGACACTTATCGAGCTGCGGAAATGCTATTTTG 795
Qy 1858 GTCAGGCTGGGCTTACATTTATCAACAGACGAGGCTGAGGATGCTCTCGGTCTTCCCTAGTG 1917
Db 796 GACAGGCTGGGCTTACCTGATCACAGACCCAGCTGAGGACGCCCTCGGCCCTTCTTCGG 855
Qy 1918 GCTATGGCGAGTTGATATCCCTCTGTATCCTGACGGCCAAAGTACTATTAACGCCGATGTA 1977
Db 856 GTTACGGAAATACGACATCCACTGGTGTCTCAGTTTCCAAGTTCTACAACTGATGGA 915
Qy 1978 CCTCGGTTGACCGAGGTTGAGGACGAGGACCTGTGGGAGATGCTATCAGTGTCAAG 2037
Db 916 CTCTCCAGACCACTGTGGGAGAGACACAGTCTGTGGGCGACGTATCCATGTGTCAAG 975
Qy 2038 GACAGCATGGCTTTCTTACCTGTCAGCCGCCCAAGTACCGTTTCCGATTCTCCCAAG 2097
Db 976 GTCAGCCCTGGCCATCTTCAACGTTGAGCCCTCGAAAGTATCGCCTTCGATTCTTCATG 1035
Qy 2098 CTGCGCTGTCTCGTGTGGCTTCTTACCTCGTCAGGACCACTCTCCCAACGTCAGAA 2157
Db 1036 CGGCTGTCTCGGAACCTTGGCCCTTATTTGTCGAAGCAACAAGCCACTGCTACTAGAC 1095
Qy 2158 TTCCTTTCAAGTCAATGGCTCTGATGTGCTCCTTCAAGCCCGCTTCAGACTCTA 2217
Db 1096 TTCCTTTTCAGGTCATGGCTCTGATGAGGGCTACTCACGCAACCCGTTCCAAACCTCAG 1155
Qy 2218 ACCTCTACCTTCTGTGCGGAGCTTACGAGATCATTTATGGTATGCCCTCCCTCTCA 2277
Db 1156 ATATTAGTGCACAGACGAGCCCTACGAGAT----- 1189
Qy 2278 CGAATGAGTCAAGAACTCTAAGACTTAACACTTTGTAGACTTCCAACTTTGCTGCCAGA 2337
Db 1190 -----TGTATTGCACTTTGCGCTTATGCGGCCAGA 1221
Qy 2338 CTCCTTGACCTGGCAACGTTGCTGAGACCAAGATGTGCGGACGAGGATGATGCTC 2397
Db 1222 CGATAGATTTGGCTTAACCTTTGAAAAGGCAATGGGTGCGCACCCGATACGATTATGAA 1281
Qy 2398 GCACCTCGAGGTGATGGCTTCGTCGTCAGCTCTGGCACTCTTGAGGACACACCCAG 2457
Db 1282 ACACCTGACAAGGTATGCGCTTCCATGTACAGCAAGCAAGCACTGCTGCTAATACTCGGTG 1341
Qy 2458 TCCCTCTCCACTCTCGGTGACGTTCTCTTCCCTTCCTTCACAAAGGAAGGCCCGCCGACAAG 2517
Db 1342 TACCGGCACAGTATCTAGATCCAGTTCCTCCCGCCGACA---AACCAGGCTCGACACC 1398
Qy 2518 ACTTCAAGTTTGAACGACGACCAACGACACTACCTGATCAACGATGTTGGCTTTGCCGATG 2577
Db 1399 ACTTCGCTTCCATCGCACCAACAGGAGTGGCGCATCAACGGCATCGGGTTTGCAGAGC 1458
Qy 2578 TCAATGAGGCTGTCTCGGCAACCCGAGCTCGGACACCGTTGAGCTCTGGGAGCTCGAGA 2637
Db 1459 TCCAAACCGTATCTGGCCAAAGGTACCGCGCGGCACTGTGAGCTATGGGAACCTCGAGA 1518

Qy 2638 ACTCCTCTGGAGGCTGGAGCCACCCCTGCCACATTCACCTTGTGACTTCAAGATCCTCA 2697
Db 1519 ACAGCTCCGGCGGTGGTGTGCGACACCCCATCCAGCTCCACTTCCGAGTCTCGTCG 1578
Qy 2698 AGCGAACTGGTG-----GTCGTGGCCAGGTCATGCCCTACGAGTCTGCTCTTAAG 2751
Db 1579 CACGCTACGGTGACGAAGCACTCGGGCGTATGCCCTACGAGTCCCGGCTCTCAAG 1638
Qy 2752 ATGCTGTCTGGCGAGGCTGAGACCCCTGACCATCAGGCGCCACCTACCAACCTCGGA 2811
Db 1639 ACGTGTGTGCTCGGCCGCCACGAGACGGTCTGCTGTCGAGACACACTACGCCCTCGG 1698
Qy 2812 CTGGAGCTTACATGTCGACCTGTCAACACTCATTCACGAGATAACGACATGATGGCT 2871
Db 1699 ACGGAGTCTACATGTTCCACTGCCACAACCTGATCCAGAGACCAAGACATGATGGCG 1758
Qy 2872 TATCAACGTCACCCCATCGAGGAGGAGGATATCTTCA---GGAGGACTTCGAGGACC 2928
Db 1759 CGTTTGAGCTGACTAAGCTCCAGAACTTTGGCTACAAAGACGACGAGATTTCACGACC 1818
Qy 2929 CCATGAACCCCAAGTGGCGCGCTTCTTACAAACCGCAAGCACTTCCATGCTCGCGCTG 2988
Db 1819 CGAAGATTTCTCGCTGGTCTGCAAGACCTTTCACCGCGCTGACTTGACGGCGATCGG 1878
Qy 2989 GAACTTCTCCCGGAGTCCATCACTGCCGAGTCCGAGTGCAGAGCTGGCCGAGAGGACCGT 3048
Db 1879 GTATCTTCTCAGAAGCATCCATCAGGCTTAGAGTGAACGAGTTGGCGCTGGAACAGCGT 1938
Qy 3049 ACAACCGCTCGATGAGATCCTGG 3072
Db 1939 ACAGGAACTGGCACAGGTACGCG 1962

RESULT 11
US-09-942-185-1
; Sequence 1, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Convents, Daniel
; APPLICANT: Doornink, Monique
; APPLICANT: van Gastel, Frans
; APPLICANT: Rodrigues, Ana
; APPLICANT: Topozada, Amr
; APPLICANT: De Vries, Cornelis Hendrikus
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1e1 Phenol
; FILE REFERENCE: C7567
; CURRENT APPLICATION NUMBER: US/09/942,185
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1958
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-942-185-1

Query Match 8.2%; Score 300.4; DB 9; Length 1958;
Best Local Similarity 55.2%; Pred. No. 7.6e-82;
Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;

Qy 1491 CTGACCCCTTTCAGATTTACCCCACTTGGCCCTGCCACTCTCGCTCGCTACGATGGCAT 1550
Db 316 CTCTCTCCACCAAGATCTACCTGATCTGGAGCGGCCCAACATGTTGGATACGATGGCAT 375
Qy 1551 GAGCCCTGTCTACTTTCAATGTTCCCGAGGAAACAGAGACTGTAGTTAGTTTCATCAA 1610
Db 376 GTCCCCGAGCACTACCATCATCATGTTCTCTGTCGGCACTGAGAGTGTGTCGGCTTCGTGAA 435
Qy 1611 CA-----ATGCCACCTGGGAGAACTCGGTCCATCTGACGCTCCCATCGCTGCCGCC 1664
Db 436 CAGCGGAGAGAACACCTCTCTCCCAACAGCGTCCACTTGACGCGCTCTTTCTCTCGAGCTCC 495

Qy 1665 TTTCGATGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAAGATTACTATTCC 1724
Dy 496 CTTTGATGTTGGGCTGAGGACACTACCCAGCCTGGCGAGTACAAGGATTACTACTACC 555
Qy 1725 CAACCTACCAATCCGCCCTCTCTGTGCTACCATGACCAAGCTTTTCATGAAGGATGCTA 1784
Dy 556 CAACAGGAGGCTGCCCGCATGCTTTGTGTACCATGACCATGC----- 597
Qy 1785 CGAGCCTTTATCTTTCTTGGCTACCTTTGGGCTAACCACCTTCTTCGTAGACTGCTGAG 1844
Dy 598 -----CATGTCCATCACGCCCGAG 616
Qy 1845 AATGCTACTTTGGTGCAGGCTGGCGCCTACATATTACAAGAGGAGGTGAGAGTCTCTC 1904
Dy 617 AACGCCTACATGGGTGAGGCTGGTGTCTACATGATCCAGGACCCGGCTGAGGATGCCCTG 676
Qy 1905 GGTCTTCTAGTGGCTAATGGCGAGTTCCATATCCCTCTGATCTCTGACGCCCAAGTACTAT 1964
Dy 677 AACCTCCCGACGGCTACGGCGAGTTGATATCCCTTTGGTTCTGACTGCGCAAGCGATAC 736
Qy 1965 AACGCGATGTTACCTCGTTTCAGCCAGGCGTGAAGACCAAGGACCTGTGGGAGATGTC 2024
Dy 737 AACGAGAGGCACTCTCTCTCCACCAATGGAGAGTTTCCAGCTTCTGGGGTACCGTT 796
Qy 2025 ATCCATGT----- 2032
Dy 797 ATTCAAGTGGTAAGTTGAGCCCATTTGAGATGCTTCAGATCCTAGAAGTATGATATGA 856
Qy 2033 -----CAACGGACAGCCATGGCTTTCTCTTAAG 2061
Dy 857 AATTGTGATGCTTAACCAAGTGCTATCACAGAGGGTCAGCCCTTGGGCTATGCTCAACG 916
Qy 2062 TCCAGCCCCGGAAGTACCGTTTCCGATTTCCTCAACGCTGCCGTGCTCGTGGCTGCC 2121
Dy 917 TGCAGCCGGCAAGTACCGCTTCGCTTCCCTCAAGCTGCCGTCTCAGCGCTTTTCGGCTC 976
Qy 2122 TCTACTCTCGTCAGGACCAAGCTCTCCCAAGCTCAGAAATTTCTTTTCCAAAGTCAATGCTCTG 2181
Dy 977 TGTATCTTGTACCTCTGAGGATTCAGAGACAGACTTTCCTTCCAGGTCATATGGCGCTG 1036
Qy 2182 ATGCTGGTCTCTTCAACGCCCTCTGACACTCTAACTCTACCTTCTGCTGTCGCCGAGC 2241
Dy 1037 ACGGTGGTCTGCTGAGGCCCCCTGTGACACTGACACTCTGTACATCTCTATGGCCGAGC 1096
Qy 2242 GTTACGAGATCATTTGTTGATGCTCCCTCCCTCTCACGAATGAGTCAAGAACTCTAAGAC 2301
Dy 1097 GCTGGAGGTTGTTATC----- 1113
Qy 2302 TAACACTTGTAGCTTACCACCTTTGCTGGCCAGACTCTTTGACCTGGCGAACGTTGCTG 2361
Dy 1114 -----GACTTCTCCACCTTCGCTGGCCAGTCCATCGATTCGCAACCTTCCCTG 1162
Qy 2362 AGACCAAGATGTCGGCGACAGGATGAGTACGCTCGCACTCTCGAGGTGATGGCTTCG 2421
Dy 1163 GTGCTGAGGGCTCGGTTGAGCCTGAGTGTGATTAACACTGACAAAGGTGATGCGATTTCG 1222
Qy 2422 TCGTCAAGTCTGGCACTGTTGAG---GACAACAGCAGGTCCTCCACTCTCCGTGAGC 2478
Dy 1223 TCGTTGATGAGTCTCTGAGTCGCCGACACTTCTGAGGTGCTTCCCAACCTCCGAGATG 1282
Qy 2479 TTCTTTTCCCTCTCTACAAAGGAAGCCCCCGCGAACAGCAC-----TTTCA 2523
Dy 1283 TTCTTTTCCCGAGGGCGCAACTGGGACCCCGCAACCCCACTGATGACGAGACTTTTCA 1342
Qy 2524 AGTTTGAAGCAGCAGCAGCACTACCTGATCAACGATGTTGGCTTTCGCCATGTCAATG 2583
Dy 1343 CTTTGGCGGCTGAATGGAGAGTGGACAATCAACGGAGTTTACCTTCTCGGATTCGAGA 1402
Qy 2584 AGCGTGTCTGGCAAGCCCCGAGCTCGCGACCGTTGAGGTCTGGGAGCTTCGAGAACTCT 2643
Dy 1403 ACCGTCTCGGCAATGTGCCCGGACACTGTTGAGATCTGGGACTTGGAGAACT 1462

Qy 2644 CTGAGAGCTGGAGCCACCCCGTCCACATTCACCTTTGTTGACTTCAAGATTCCTCAAGCGAA 2703
Dy 1463 CCAACGGTGTGACTCACCTGTTCACATTCACCTCGTTGACTTCCGAGTCTCTTCGTT 1522
Qy 2704 CTGGTGGTGTGGCAGGTCATGCCCTACGATCTGCTGTTTAAAGGATGCTGCTCTGTT 2763
Dy 1523 CCAGTGGCCGGTGG---AGTCGAGCCTTATGAGGCTGCTGGTCTCAAGGATGTTGCTGGC 1579
Qy 2764 TGGGAGGGGTGAGACCCCTGACCATCGAGGCCACTACCAACCCCTGGAC----- 2812
Dy 1580 TGGCTCGTGTGAGGTTGCTATGTTGAGGCCCACTACGCTCTTTCCTCCGTAAGTTCTCG 1639
Qy 2813 -----TGGAGCTTACATGTGGCA 2830
Dy 1640 CTTTTTACCTAACTGGTTTTTCACTCATGCTAACATCTACAAGTGGTGTCTACATGTTGA 1699
Qy 2831 CTGTCAACAACCTATTCACGAGGATAACGATGATGCTGTATTCACAGCTCACCGCCAT 2890
Dy 1700 CTGCCAACACTGATCCACGAGGACCAAGCATGATGCTTTCAATGTCACTGTCTT 1759
Qy 2891 GGAGGAGAAGGATATCTTTCAGGAGGACTTGGAGGACCCCATGAACCCCAAGTGGCGGC 2950
Dy 1760 CGGTGACTATGCTTACAACCTACACCGAGTTTCTATGACCCCATGGAGCCTCTCTGAGGCC 1819
Qy 2951 CGTTCTTTACACCCGACAGACTTCCATGCTCGGCTCGAAACTTCTCCGCGAGTCCAT 3010
Dy 1820 CCGCCCTTCTCTCGGAGAGTTTCGAGAATGGCTCGGCTGACTTTCAGCGAGCTTGGCAT 1879
Qy 3011 CACTGCCGAGTGCAGGAGCTGGCCGAGCAGGAGCCGTACAACCCCTCGATGA 3064
Dy 1880 CACTGACCGCATTCAGGAGATGGGTAGCTTCAACCCCTACGCCAGGCTGATGA 1933

RESULT 12
US-09-942-185-3
; Sequence 3, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, wolfgang
; APPLICANT: Convents, Daniel
; APPLICANT: Doornink, Monique
; APPLICANT: van Gastel, Frans
; APPLICANT: Rodrigues, Amr
; APPLICANT: Topozada, Amr
; APPLICANT: De Vries, Cornelis Hendrikus
; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1e1 Phenol
; FILE REFERENCE: C7567
; CURRENT APPLICATION NUMBER: US/09/942,185
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-942-185-3

Query Match 8.2%; Score 300.4; DB 9; Length 2095;
Best Local Similarity 55.2%; Pred. No. 8e-82;
Matches 957; Conservative 0; Mismatches 501; Indels 276; Gaps 8;

Qy 1491 CTGACCCCTTTTCAGATTTACCCCACTTTCGCCCTGCCACTCTCGTCGGCTACGATGGCAT 1550
Dy 380 CTTCTCCACCAAGATCTACCCCTGATCGGAGCGGCCCAACATGGTTGGATAGGATGGCAT 439
Qy 1551 GAGCCCTGGTCTCTACTTTCAATGTTCCAGAGAACAGAGACTGTAGTTAGTTAGTCAAA 1610
Dy 440 GTCCCCAGGACCTACCATCATCTCTTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 499
Qy 1611 CA-----ATCCCCAGCTGGAGAACTCGGTCCATCTGACACGGCTCCCGCATCGCTGCC 1664
Dy 500 CAGCGGAGAGAACACCTCTCCCAACAGCGCTCCACTTGCACGGCTCTTTCTCTCGAGCTCC 559

Qy 1665 TTTCGATGGTTGGGCTGAAGATGTGACCTTCCTGGCGAGTACAAGGATTTACTACTTTCC 1724
Db 560 CTTTGATGGTTGGGCTGAGGACACTACCAGCGCTGGCGAGTACAAGGATTTACTACTACC 619
Qy 1725 CAACCTACCAATCCGCCGCCCTTCTGTGTGATACCATGACACACGCTTTTCATGAAGGTATGTA 1784
Db 620 CAACAGCGACGCTGCCCGCATGCTTTGTGTACCATGACCATGC----- 661
Qy 1785 CGAGCCTTTATCTTCTTGGGCTACCTTTGGGCTAACCAACTTCCTTTCTAGACGCTCTGAG 1844
Db 662 -----CATGTCCATCACCGCCGAG 680
Qy 1845 AATGCTACTTTGGTTCAGGCTGGCGCCTACATTTATCAACGAGGCTGAGGATGCTCTC 1904
Db 681 AACGCTACATGGGTGACGCTGGTGTCTACATGATCCAGGACCCGGCTGAGGATGCCCTG 740
Qy 1905 GGTCTTCTAGTGGCTATGGCGAGTTCGATATCCCTCTGTCTGACGCGCCAAAGTACTAT 1964
Db 741 AACCTCCCACGCGGTACGGCGAGTTTGATATCCCTTTGGTTCTGACTGCCAAAGCGATAC 800
Qy 1965 AACGCGGATGTACCTCGGTTTCGACCGAGGTTGAGGACGAGGCTGTGGGGAGATGTC 2024
Db 801 AACGAGACGCGACTCTTCTTCCACCAATGGAGAGGTTTCCAGCTTCTGGGGTGACGTT 860
Qy 2025 ATCCATGT----- 2032
Db 861 ATTCAAGTGGTAAGTTGAGCCCATTTGAGATGCTTCAGATCTCAGATATCATGATATGA 920
Qy 2033 -----CAACGGACGAGCATGGCTTTTCCTTAACG 2061
Db 921 AATTGTGCATGCTCTAACCAAGTGTCTATCACAGACGGTCAGCCTTGGCCTATGCTCAACG 980
Qy 2062 TCCAGCCCGGCAAGTACGCTTTCCGATTTCCATCAACGCTGCGGTGCTCTCGTGTGGCTCC 2121
Db 981 TGCAGCCCGCAAGTACGCTTCCGCTTCCATCAACGCTGCGGTCTCAGGCTCTTTTCGGTC 1040
Qy 2122 TCTACTCTGTTCAGGACACGCTCTCCCAAGTCCAGAAATTCCTTTCCAACTTCATTTGGCTCTG 2181
Db 1041 TGTATCTGTCTACCTCTGAGGATTCAGAGACGAGTATCCCTTCCAGGTCATGCGCGTG 1100
Qy 2182 ATGCTGGTCTCCTCAAGCCCGGTTCAAGCCTCTAAGCCTCTACCTCTGCTGTGCGCGAGC 2241
Db 1101 ACGGTGGTCTGCTTGGGCGCCTGTGTGACACTGACACTCTGTACATCTCTATGGCGGAGC 1160
Qy 2242 GTTACGAGATCATTTATTGGTATGCCCTCCCTCTCACGAATGAGTCAAGAATCTTAAGAC 2301
Db 1161 GCTGGGAGGTTGTTATC----- 1177
Qy 2302 TAACACTTGTAGACTTCAACCAACTTTTGTGGCCAGACTCTTTGACCTGCGCAACGTTGCTG 2361
Db 1178 -----GACTTCTCCACTTTCGCTGGCCAGTCCATCATGATCCGCAACCTTCCTG 1226
Qy 2362 AGACCAACGATGTCGGCGACGAGGATGAGTAGCTCGCACTCTCGAGGTGATGCGCTTCG 2421
Db 1227 GTGCTGACGGTCTCGGTGTTGAGCCTGAGTTGATTAACACTGACAAGGTTCATGCGATTG 1286
Qy 2422 TCGTCAGCTCTGGCACTGTTGAG---GACAACGACGAGTCCCTCCACTCTCCGTGAGC 2478
Db 1287 TCGTTGATGAAGTCTCTGAGTGGCCGACACTTCTGAGGTGCTGCCCAACCTCCGAGATG 1346
Qy 2479 TTCCCTTTCCTCCTCACAAAGGAAGGCCCGCGCAAGGAC-----TTCA 2523
Db 1347 TTCCCTTTCCTCCGAGGGCGCACTGGGACCCCGCAACCCCACTGATGACGAGACTTTCA 1406
Qy 2524 AGTTTCAACGACGACGACACTACCTGATCAACGATGTTGGCTTTGCCGATGTCGAATG 2583
Db 1407 CCTTGGCGGCTGCTTAATGACAGTGGACAATCAACGGAGTTACCTTCTCGGATTCGAGA 1466
Qy 2584 ACGGTGTCGTGCCAAGCCCGAGCTGGGACCGTTGAGGTCTGGGAGCTCGAGAACTCGT 2643
Db 1467 ACCGTCTGCTCGCAATGTGCCCGCGACACTGTTGAGATCTGGCGACTTTGAGAACT 1526

Qy 2644 CTGGAGGCTGGAGCCACCCCGTCCACATTCACCTTGTGTGACTTCAAGATCCTCAAGCGAA 2703
Db 1527 CCAAGGTTGGACTCACCTCTGTTCACATTCACCTCGTTGACTTCGAGTCTCTTCCTCGTT 1586
Qy 2704 CTGGTGTGCTGGCCAGGTGATGCCCTAGCAGTCTGCTGGTCTTAAGGATGTCGCTCGT 2763
Db 1587 CCACCTGCCCGTGG---AGTCGAGCCTTATGAGGCTGCTGGTCTCAAGGATGTTGCTGGC 1643
Qy 2764 TGGCAGGCGTCAAGCCCTGACCATCGAGGCCCACTACCAACCCCTGGAC----- 2812
Db 1644 TGGCTGCTGAGGTTGCTATGTTGAGGCCCACTACGCTCTTTCCCGTAAGTTCG 1703
Qy 2813 -----TGGAGCTTACATGTGCA 2830
Db 1704 CCTTTTACCTAACTGGTTTTTTCACATCATGCTAACATCTACAAGTGGTGTCTACATTTGA 1763
Qy 2831 CTGTCACAACCTCATTCACGAGGATAACGATGATGCTGTATTCACAGCTACCGCAT 2890
Db 1764 CTGCCACAACCTGATCCACGAGGACGACATGATGCTGCTTTTCAATGTCACTGTTCT 1823
Qy 2891 GGAGGAGAGGATATCTTCAGGAGGACTTCGAGGACCTTCGAGACCCCATGAACCCAAAGTGGCGGC 2950
Db 1824 CGGTGACTATGGCTACAACTACACGAGTTTCATTTGACCCCATGGAGCTCTCTGGAGGCC 1883
Qy 2951 CGTTCCTTACAAACCCCAACGACTTCATCTCGCTCGCTGGAACCTTCTCCGCGAGTCCAT 3010
Db 1884 CGCCCTCTCCTCTCGGAGACTTCGAGATGGCTCGGTGACTTCAGGAGCTTGCAT 1943
Qy 3011 CACTGCCGAGTGCAGGAGCTGGCGGACGAGCCGTACAACCCCTCGATGA 3064
Db 1944 CACTGACCGCATTCAGGATGGCTAGCTTCAACCCCTACGCCACGAGCTGATGA 1997

RESULT 13
US-10-080-210-8
; Sequence 8, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 858
; TYPE: DNA
; ORGANISM: *Amerosporium atrum*
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(858)
; OTHER INFORMATION: n = A,T,C or G
US-10-080-210-8

Query Match 4.1%; Score 150; DB 12; Length 858;
Best Local Similarity 63.4%; Pred. No. 1.le-35;
Matches 269; Conservative 0; Mismatches 140; Indels 15; Gaps 2;
Qy 1836 ACTGCTGAGAATGCCCTACTTTGGTTCAGGCTGGCGCTTACATTTATCAAGACGAGGCTGAG 1895
Db 2 ACCGCCGAGAGCGCTTACTTTGGTCAAGTGGCTTTTACATTTCTGCAGACACCCCGCTGAA 61
Qy 1896 GATGCTCTCGGTCTTCTAGTGGCTATGCGAGTTCGATATCCCTCTGATCCTGACGGCC 1955
Db 62 GATGATTTGGGTCTGCCT-----TCTGGCAAGTATGATGTACTCTTGCATCTGCTCC 115
Qy 1956 AAGTACTATAACGCGGATGGTACCCTTGGCTTCGACCGAGGGTGGAGGACGAGCCTGTGG 2015

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Db 116 AGCAGTACACAGCAGCGGTACCTCTTCGACCCCAAGGAGGAGACCGATTTCACCTGTTTC 175
Qy 2016 GGAGATGTCATCCATGTCTCAACGAGACAGCCATGGCCTTTCTTAAAGGTCCAGCCCGCAAG 2075
Db 176 GCGGATGTCATCCAGCTCAACGAGACAGCCATGGCCTACTTTAAAGTCCAGGCTCGCAAG 235
Qy 2076 TACCGTTTCGGATTCTCAACGCTGCGGTGCTCTGTGCTTGGCTCTCTACCTCTGTCAGG 2135
Db 236 TACCGTCTCGGTTCTCTCAATGCTCTATCAAGCTGCTTCAAGCTCACCTTTCAGAGGT 295
Qy 2136 ACCAGCTCTCCCAAGCTCAGAAATTCCTTTCCAAAGTCATTGCGCTCTGATGCTGCTCTCTT 2195
Db 296 GATGGCAAGTGATCAAC-----TTCTGTGATCGGTGGCGGATGCTGCTCTTG 346
Qy 2196 CAAGCCCCGGTTTCAGACCTCTAACCTCTACCTTGTGTTGCGAGCGGTTCACGAGATCAIT 2255
Db 347 ACCAAGCTGTTTCAGACAGCAACCTTGAGATCTCTATGCGCGAGCGCTGGGAGGTGTT 406
Qy 2256 ATTG 2259
Db 407 TTTG 410

RESULT 14
US-09-738-626-1053
; Sequence 1053, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OKARI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1053
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1053

Query Match 1.6%; Score 60; DB 9; Length 1533;
Best Local Similarity 51.5%; Pred. No. 1e-07;
Matches 138; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

Qy 1835 GACTGCTGAGAATGCTACTTTGGTCAGGCTGGCGCCTACATATATCAACGACGAGGCTGA 1894
Db 483 GACAGGTTTGCTGCTACCGTGGTTGGCGGGGATGATCTGTGGAAGATGAAGCAAC 542
Qy 1895 GGATGCTCTCGTCTCTCTAGTGGGTATGGCGAGTTCGATATCCCTCTGATCCTACGGC 1954
Db 543 AGACAAGCTGGATGCTGCCACCGGAGTAGCGGTGTGACCATATTCCGCTGGTTTTAATGA 602
Qy 1955 CAAGTACTATAACGCGGATGGTACCTGCGTTCGACCGAGGAGGAGGAGGAGGAGGAGGAGG 2014
Db 603 TCACCGCTTCTTAGAGAGGCTTCCCTTGATGAGGAGAACACCTCCCGGATCTTGGGCTGTT 662
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Qy 2015 GGGAGATGTCATCCATGTCAACGGACAGCCATGGCCTTTCTTAAAGTCCAGCCCGGCA 2074
Db 663 GGGCGATACCCCACTGCAATGGCAATTACCAATCGCACTTTGATGCCACACCGCGCG 722
Qy 2075 GPACCGTTTCCGATTCTCTCAACGCTGCC 2102
Db 723 GGTTCGGTTCCGCTGCTCAACGGCTCC 750

RESULT 15
US-09-974-300-2204
; Sequence 2204, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2204
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2204

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Best Local Similarity 65.7%; Pred. No. 0.0058;
Matches 65; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Db 598 CCGGCTTTTTCGGGTGATACCATTTTAGTCAACGGCAAGGTATGGCTTTCGCTGAACGTG 657
Qy 2064 CAGCCCCCGCAAGTACCGTTTCCGATTCTCTCAACGCTGCC 2102
Db 658 GAACCCCGAAAAATACCGTTTTCGGGATCTGAACGCTCC 696

Search completed: February 13, 2003, 05:15:42
Job time : 207.097 secs
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(oiden) uspto

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 18:21:11 ; Search time 4958.71 Seconds
(without alignments)
12009.347 Million cell updates/sec

Title: US-09-218-702-3

Perfect score: 3677

Sequence: 1 ctgctagcctcacttgta.....gataactgaactgggtcaat 3677

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
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 - 22: em_gss_fun:*
 - 23: em_gss_mam:*
 - 24: em_gss_mus:*
 - 25: em_gss_Other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112.4	3.1	600	10	BE188240
2	112.4	3.1	700	10	BE187716
3	60.4	1.6	664	10	BE188099
4	51.8	1.4	580	13	BJ159802
5	50.2	1.4	557	10	AW339201
6	48.6	1.3	599	12	BF258534

c	7	48.4	1.3	465	12	BG053739
	8	47.8	1.3	461	9	AI623533
	9	47	1.3	848	10	BE216983
	10	46.2	1.3	475	12	BF115462
	11	44.8	1.2	463	12	BF059036
	12	44.8	1.2	481	9	AI394530
	13	44.4	1.2	541	9	AI432408
	14	44	1.2	416	9	AI933417
	15	43.4	1.2	467	14	W15474
	16	43.2	1.2	409	9	AA731500
	17	43.2	1.2	426	9	AA807669
	18	43.2	1.2	442	9	AA687287
	19	43.2	1.2	451	9	AI189014
	20	43.2	1.2	463	10	AW576243
	21	43.2	1.2	500	9	AI126707
	22	43.2	1.2	507	9	AA977691
	23	43.2	1.2	538	10	BE379236
	24	43.2	1.2	571	10	AW007209
	25	43.2	1.2	646	14	BM794003
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	28	42.8	1.2	435	10	AW575077
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	31	42.8	1.2	486	9	AA825413
	32	42.8	1.2	496	9	AI860612
	33	42.8	1.2	497	9	AI187025
	34	42.8	1.2	505	9	AA411507
	35	42.8	1.2	508	9	AI200611
	36	42.8	1.2	511	9	AA829600
	37	42.8	1.2	511	9	AI223314
	38	42.8	1.2	511	9	AA262448
	39	42.8	1.2	511	9	AA478433
	40	42.8	1.2	515	9	AA854735
	41	42.8	1.2	526	9	AI077527
	42	42.8	1.2	530	12	BF445939
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ALIGNMENTS

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LOCUS BE188240 600 bp mRNA linear EST 25-SEP-2000
DEFINITION M7ATIG In vitro expressed cDNAs Cladosporium fulvum cDNA similar to
Bilirubin oxidase precursor, mRNA sequence.
ACCESSION BE188240
VERSION BE188240.1 GI:8667479
KEYWORDS EST.
SOURCE Cladosporium fulvum.
ORGANISM Cladosporium fulvum

REFERENCE 1 (bases 1 to 600)
AUTHORS Clark A.J., Rasmussen, S.W. and Oliver, R.P.
TITLE In vitro expressed genes of Cladosporium fulvum
JOURNAL Unpublished (2000)
COMMENT Contact: R.P.Oliver
Necrotrophic Phytopathology Research Centre
Murdoch University
SABC, Perth 6150, Western Australia
Tel: +61-8-9360-7404
Fax: +61-8-9360-6303

High quality sequence stop: 600
POLYA=No.
Location/Qualifiers
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/organism="Cladosporium fulvum"

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BF059036 7k26d11.x
AI394530 cf77b06.x
AI432408 t97c04.x
AI933417 wp67e12.x
W15474 zc19b12.s1
AA731500 nw59f03.s
AA807669 nv66f05.s
AA687287 nv59h08.s
AI189014 qd27h02.x
AW576243 UI-HF-BN0
AI126707 qb94c04.x
AA977691 on32d03.s
BE379236 601237666
AW007209 ws0e06.x
BM794003 K-EST0075
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AA788842 zf25b09.s
AW575077 UI-HF-BK0
BF446871 7n94g10.x
AA481991 zv42c07.s
AA825413 oe64a08.s
AI860612 wk93c05.x
AI187025 qe37h07.s
AA411507 zv27h02.s
AI200611 qf87e08.x
AA829600 ce50a07.s
AI223314 qg71b03.x
AA262448 zs16g09.s
AA478433 zu46f04.s
AA854735 aj65g07.s
AI077527 ox50g11.x
BF445939 7p16ff06.x
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AI279006 qm22f04.x
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/clone_lib="In vitro expressed cDNAs"
/tissue_type="Mycelium"
/note="Vector: Lambda bluescript; A mixture of mycelial cultures grown in liquid B5 for 48 hours and transferred for 24 hours to media lacking carbon, nitrogen or supplemented with hydrogen peroxide"
BASE COUNT 131 a 176 c 162 g 128 t 3 others
ORIGIN
Query Match 3.1%; Score 112.4; DB 10; Length 600;
Best Local Similarity 55.9%; Pred. No. 1.7e-19;
Matches 313; Conservative 0; Mismatches 238; Indels 9; Gaps 5;
Qy 2366 CAACGATGTCGGCCACGAGGATGAGCTCGCAGCTCTCGAGGTGATCGCTTCGTCGT 2425
Db 42 CAACAGGGGGCACAACACACGNGTGNCAATACACCGACGAAGTTCATGAGTTCGTCGT 101
Qy 2426 CAG---CTCTGGCACCTGTTGAGGACACAGCCAGGTCCCTCCACTCTCCGTGACGTTCC 2482
Db 102 TGGAGACAGCGTCCCGACGAGTCCACACACAGTACCATCAACTCTGAACGGTGCAT 161
Qy 2483 TTTCCTCTCACAAGGAGCCCGCGACAGACTTCAAGTTTGAACCCAGCAACGG 2542
Db 162 CGACTGGCCGACGCGAGGACACTATTGACAAGACCTTCAACTTCCAGATGGCGCGC 221
Qy 2543 ACACCTACCTGA---TCAACGATGTTGGCTTTGCGGATGTCATGAGCGTGCTTGGCCAA 2599
Db 222 GGACGTGTGGACCGTCAATGCGTGGATTCAGCGACCCGAACTCGCGTGTGCTGGCTAG 281
Qy 2600 GCCCGAGCTCGGCACCGTTGAGGTCTGGAGCTCGAGAACTCTCTTGAGGCTGGAGCCA 2659
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Qy 2720 GGTCATGCTTACGAGTCTGCTGGCTTTAAGGATGTCGTTGGTGGCAGGGGTGAGAC 2779
Db 402 CCTCATGCCATACGAAGTGTGTTGTTAAAGACGCTGTTATGCTGGCTCTCGCGAGAT 461
Qy 2780 CCTGACCATCGAGGCCCACTACCAACCCCTGGAGCTGAGCTTACATGTGCGACTGTCAAA 2839
Db 462 TGTCAAGCTGCTTGGCTTTAGGGTCTTGGNACG-CTTGACATGTTTCATTGGCCAC-A 519
Qy 2840 CCTCATTCACGAGGATACGACATGATGG-CTGTATTCAACGCTACCGCCATGGAGGAGA 2898
Db 520 CCTTGTACACGAAGATCACACCATGATGCCCGCTTCAACACGACACCCCTTGAACGCTG 579
Qy 2899 AGGGATATCTTCAGGAGGAC 2918
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LOCUS BE187716 700 bp mRNA linear EST 25-SEP-2000
DEFINITION Bilirubin oxidase precursor, mRNA sequence.
ACCESSION BE187716
VERSION BE187716.1 GI:8666955
KEYWORDS EST.
SOURCE Cladosporium fulvum.
ORGANISM Cladosporium fulvum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et Chaetothyriomycetes incertae sedis; Mycosphaerellaceae; mitosporic Mycosphaerellaceae; Cladosporium.
REFERENCE 1 (bases 1 to 700)
* AUTHORS Clark,A.J., Rasmussen,S.W. and Oliver,R.P.
TITLE In vitro expressed genes of Cladosporium fulvum
JOURNAL Unpublished (2000)

Contact: R.P.Oliver
Necrotrophic Phytopathology Research Centre
Murdoch University
SABC, Perth 6150, Western Australia
Tel: +61-8-9360-7404
Fax: +61-8-9360-6303
Email: roliver@central.murdoch.edu.au
High quality sequence stop: 700
POLYA=No.
FEATURES
Location/Qualifiers
1..700
/organism="Cladosporium fulvum"
/strain="Race 4"
/db_xref="taxon:5499"
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/tissue_type="Mycelium"
/note="Vector: Lambda bluescript; A mixture of mycelial cultures grown in liquid B5 for 48 hours and transferred for 24 hours to media lacking carbon, nitrogen or supplemented with hydrogen peroxide"
BASE COUNT 158 a 206 c 183 g 146 t 7 others
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Query Match 3.1%; Score 112.4; DB 10; Length 700;
Best Local Similarity 55.9%; Pred. No. 1.9e-19;
Matches 313; Conservative 0; Mismatches 238; Indels 9; Gaps 5;
Qy 2366 CAACGATGTCGGCCACGAGGATGAGTACGCTCGCAGCTCTCGAGGTGATCGCTTCGTCGT 2425
Db 42 CAACAGGGGGCACAACACACGNGTGNCAATACACCGACGAAGTTCATGAGTTCGTCGT 101
Qy 2426 CAG---CTCTGGCACCTGTTGAGGACACAGCCAGGTCCCTCCACTCTCCGTGAGCTTCC 2482
Db 102 TGGAGACAGCGTCCCGACGAGTCCACACAACTAGCATCAACTCTGAACGGTGCAT 161
Qy 2483 TTTCCTCTCACAAGGAGCCCGCGACAGACTTCAAGTTTGAACCCAGCAACGG 2542
Db 162 CGACTGGCCGACGCGAGGACACTATTGACAAGACCTTCAACTTCCAGATGGCGCGC 221
Qy 2543 ACACCTACCTGA---TCAACGATGTTGGCTTTGCGGATGTCATGAGCGTGCTTGGCCAA 2599
Db 222 GGACGTGTGGACCGTCAATGCGTGGATTCAGCGACCCGAACTCGCGTGTGCTGGCTAG 281
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Db 282 GCCGCCAAGGCACTGTCGAGCGTTGGCGCTCGTGACACTGGCGTCCGGCTGTCCA 341
Qy 2660 CCCCCTCCACATTCACCTTTGAGTTCGAAGATCCTCAAGCGAAGTGTGTTGGGCCA 2719
Db 342 CCCAGTACATATCCATCTTGTCAACATGCAGTCTCTCGGGTACTGTTGGTGGCCGTGG 401
Qy 2720 GGTCATGCTTACGAGTCTGCTGGCTTTAAGGATGTCGTTGGTGGCAGGGGTGAGAC 2779
Db 402 CCTCATGCCATACGAAGTGTGTTGTTAAAGACGCTGTTATGCTGGCTCTCGCGAGAT 461
Qy 2780 CCTGACCATCGAGGCCCACTACCAACCCCTGGAGCTGAGCTTACATGTGCGACTGTCAAA 2839
Db 462 TGTCAAGCTGCTTGGCTTTAGGGTCTTGGNACG-CTTGACATGTTTCATTGGCCAC-A 519
Qy 2840 CCTCATTCACGAGGATACGACATGATGG-CTGTATTCAACGCTACCGCCATGGAGGAGA 2898
Db 520 CCTTGTACACGAAGATCACACCATGATGCCCGCTTCAACACGACACCCCTTGAACGCTG 579
Qy 2899 AGGGATATCTTCAGGAGGAC 2918
Db 580 GGCTACGACTTCAACAGCAC 599
RESULT 3
BE188099
LOCUS BE188099 664 bp mRNA linear EST 25-SEP-2000
DEFINITION CFC377-R In vitro expressed cDNAs Cladosporium fulvum CDNA similar to Bilirubin oxidase precursor, mRNA sequence.

TITLE	Comparison of the moss <i>Physcomitrella patens</i> genome with flowering plants genome
JOURNAL	Unpublished (2002)
COMMENT	Contact: Tadasu Shin-i Center for Genetic Resource Information National Institute of Genetics 1111 Yatai, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6836 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp
FEATURES	A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified lPS phage vector (MO bi Tec, Germany). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCDAG medium for 13-14 days under the continuous light.
	Location/Qualifiers

FEATURES	source	1. 580	Location/Qualifiers
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		/db_xref="taxon:145481"	
		/clone="pphl7c15"	
		/clone_lib="full length cDNA library, chloronemata and young gametophores"	
		/tissue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"	
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	Query Match	1.4%	Score 51.8: DB 13: Length 580:

[illegible]

ACCESSION AW339201.1 GI:5835827
 VERSION
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1. (bases 1 to 557)
 REFERENCE NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Life Technologies catalog #: 11548-013
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL.ac

www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand
Seq primer: -40up from Gibco
High quality sequence stop: 344.

FEATURES

Location/Qualifiers
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/lab_host="DH10B"
/note="organ: pancreas; Vector: pCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

BASE COUNT 162 a 152 c 161 g 78 t 4 others

ORIGIN

Query Match 1.4%; Score 50.2; DB 10; Length 557;
Best Local Similarity 45.7%; Pred. No. 0.026;
Matches 166; Conservative 0; Mismatches 197; Indels 0; Gaps 0;
QY 2765 GGGCAGGGGTGAGACCCCTGACCATCGAGGCCACCTACCAACCCCTGGAGCTTGACAT 2824
Db 80 GGACAGCAGTGAGCTCAGCTCAGCGAGGTCTTCATCCAGCTGCCCTCGCGAAGGAGCT 139
QY 2825 GTGGCACTGTACACACCTCATTCAGGAGGATACACATGATGGCTGATTCACAGCTAC 2884
Db 140 GCCCAGTACTACGAGCTATCCGACGCCCTGGAGCTTCAGAGATTAAGGAGCGCAT 199
QY 2885 CGCCATGGAGGAGGAGGATATCTTCAGGAGGACTTTCAGGAGCCCATGAACCCCAAGTG 2944
Db 200 TCGCAACACAGTACCGCAGCTCAGACCTCAGAGAGGAGCGTCATGCTCCTGTGCCA 259
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Db 260 GAACGCACAGACTTCAACCTGGAGGGTCCCTGATATGAAGACTTCCATGCTTGTGA 319
QY 3005 GTCCATCACTCCCGGAGTGCAGGAGTGGCCGAGGAGCGGTACACCGCTCGATCA 3064
Db 320 GTCGGTCTTCACCGCTGCGCGCAAAATCAGAGGAGGATGACATGAAGGCGAGA 379
QY 3065 GATCTCGAGGAGTCTGGAATCGAGAGGTAAACCCGAGCCCAAGCTCTACAATCGTTT 3124
Db 380 GAGTGAGGANGAGAGAGCGGAGGAGAAAGCCGATCCATCTCGGTCGTCAAN 439
QY 3125 TGA 3127
Db 440 TGA 442

RESULT 6
BF258534
LOCUS
DEFINITION
HVSMEf0015P21f Hordeum vulgare seedling root EST library HVCDNA0007
(Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEf0015P21f, mRNA sequence.

ACCESSION
BF258534
VERSION
BF258534.2 GI:131119477
KEYWORDS
EST.

SOURCE

Hordeum vulgare.
Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 599)

AUTHORS
Wing, R., Close, T.J., Klein, H., A., Wise, R., Begum, D., Frisch, D., Yu
, R.D., Oates, R. and Main, D.,
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling root cDNA library

JOURNAL
COMMENT

Unpublished (2001)
On Nov 16, 2000 this sequence version replaced gi:11187647.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 451
Seq primer: AATTAAACCCTCACTAAAGGG
High quality sequence stop: 552.

FEATURES

Location/Qualifiers
1..599
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEf0015P21f"
/clone_lib="Hordeum vulgare seedling root EST library
HVCDNA0007 (Etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedling roots were
then harvested, total RNA was prepared, poly(A) RNA was
purified, one primary unamplified cDNA library was made,
and 1 million pfu were in vivo excised to give pBluescript
SK(-) cDNA phagemids. These steps were performed in the TJ
Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

source

BASE COUNT 96 a 215 c 206 g 82 t
ORIGIN
Query Match 1.3%; Score 48.6; DB 12; Length 599;
Best Local Similarity 63.0%; Pred. No. 0.074;
Matches 75; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 2016 GGAGATGTCATCCATGTCACAGGACAGCATGGCCCTTCTTAACGTCAGCCCGCCAG 2075
Db 59 GCGCGTGTGCTGCTGCCCAACGCAAGCGCTTCTCGCGTGGCGGCCGCCGC 118
QY 2076 TACCGTTTCCGATTCTCAACGCTGCCGTCTCTCTGCTTGGCTCTTACCTCTCGAG 2134
Db 119 TACCGTCTCCGATCTCTCAACGCTCAACGCCACAGCGCGCTTCTTCGCCCTCTCGCTCTCGG 177

RESULT 7

LOCUS
DEFINITION
BG053739
ACCESSION
BG053739
VERSION
BG053739.1 GI:12509741
KEYWORDS
EST.
SOURCE
Sorghum propinquum.
ORGANISM
Sorghum propinquum

BC053739
RH122_9_B08.b1_A003 Rhizome2 (RH122) Sorghum propinquum cDNA, mRNA
sequence.
BG053739
BG053739.1 GI:12509741
EST.
Sorghum propinquum.
Sorghum propinquum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 465)

AUTHORS Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt, L.H.

TITLE An EST database from Sorghum: Sorghum propinquum rhizomes

JOURNAL Unpublished (2000)

COMMENT Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Seq primer: JEN REV

High quality sequence stop: 421

POLYA-No. Location/Qualifiers

1. .465

/organism="Sorghum propinquum"

/db_xref="taxon:132711"

/clone_lib="Rhizome2 (RHIZ2)"

/note="Organ: Rhizomes; Vector: pBluescript II from Lambda

zap II; Site_1: XhoI; Site_2: EcoRI; The library was made

from poly-A RNA in the cloning vector lambda ZAP II.

Clones to be sequenced were prepared by mass excision."

BASE COUNT 72 a 128 c 193 g 72 t

ORIGIN

Query Match 1.3%; Score 48.4; DB 12; Length 465;

Best Local Similarity 59.4%; Pred. No. 0.073;

Matches 82; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 2016 GGAGATGTCATCCATGTCAACGGACAGCATCGCTTCTTCAAGTCCAGCCCGCAAG 2075

Db 185 GGTGAGGCGGTACCGTCAACGGACAGCGTGGCGTTCCTCGCGGTCCACCGCGCGGC 126

Qy 2076 TACCGTTTCCGATTCCTCAACGCTGCCGTGCTCGTGTGGCTCTTCAAGTCTCGTCAAG 2135

Db 125 TACCGTTTCCGATTCCTCAACGCGACAGCGCGCTACTTCAAGTCTCGCTCTCCAC 66

Qy 2136 ACCAGCTCTCCCAAGTCT 2153

Db 65 GGCATGCCCTTCCAGTCTC 48

RESULT 8

LOCUS A1623533

DEFINITION ts36a05.x1 NCI-CGAP Ut4 Homo sapiens cDNA clone IMAGE:2230640 3',

similar to TR:Q63928 Q63928 BRAHMA RELATED PROTEIN 1 ;, mRNA

sequence.

ACCESSION A1623533

VERSION A1623533.1

KEYWORDS GI:4648464

SOURCE EST.

ORGANISM human.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 461)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 944 Std Error: 0.00

Seq primer: -40Up from Gibco

High quality sequence stop: 438

POLYA-No. Location/Qualifiers

1. .461

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2230640"

/clone_lib="NCI-CGAP_Ut4"

/tissue_type="serous papillary carcinoma, high grade, 2

pooled tumors"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.48 kb. Life Technologies catalog #:

11542-016"

BASE COUNT 131 a 126 c 130 g 74 t

ORIGIN

Query Match 1.3%; Score 47.8; DB 9; Length 461;

Best Local Similarity 46.1%; Pred. No. 0.11; 187; Indels 0; Gaps 0;

Matches 160; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

Qy 2767 GCAGGGGTGAGACCTGTACCATCCAGGCCCCACTACCAACCCCTGGAGCTTGACATGT 2826

Db 85 GCAGCAGTGGACGTCAAGTCCAGGAGGTCTTCATCCAGCTGCCCTCGGAAAGAGCTGC 144

Qy 2827 GGCACGTGTCAACAACCTATTCCAGGAGGATACGACATGATGGCTGTATTCAACGTACCG 2886

Db 145 CCGAGTACTAGAGCTATCCGCAAGCCCGTGGAGCTTCAAGAAGATAAAGGAGCGCATTC 204

Qy 2887 CCATGGAGGAGAAGGATATCTTCAGGAGGACTTCAGAGACCCCATGAACCCCAAGTGGC 2945

Db 205 GCAACACAGATACCGCAGCCTCAACGACCTAGAGAAGGAGCTCATGTCTGTGCCAGA 264

Qy 2947 GCGCGCTTCTTACAAACCGCAACGACTTCCATGTCTCGCGCTGGAAACTTCTCCGCCGAGT 3006

Db 265 ACGCACAGACCTTCAACCTGGAGGGCTCCCTGATCTATGAAGACTCCATCGCTTGGCAGT 324

Qy 3007 CCATCACTGCCCGAGTGCAGGAGCTGGCCGAGCAGGAGCCGCTACAAACGCTTCGATGAGA 3066

Db 325 CGGTCTTCAACGAGCTGGCGCAGAAAATCGAAGAGGAGGTACACAGTGAAGCGGAGGAGA 384

Qy 3067 TCCTGGAGGATCTTGGATCGAGGAGTAAACCCCGAGCCCAAGCTC 3113

Db 385 GTGAGGAGGAGGAAGAGGGCGGAGAGAGGCTCCGAATCCGAATCTC 431

RESULT 9

LOCUS BE216983

DEFINITION BE216983

ACCESSION BE216983

VERSION BE216983.1

KEYWORDS GI:8904523

SOURCE EST.

ORGANISM bread wheat.

Triticum aestivum

848 bp mRNA linear EST 03-JUL-2000

JAL_5A_A06_T3_5', mRNA sequence.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

; Triticeae; Triticum.

1 (bases 1 to 848)

Anderson, J.M., Williams, C.E. and Goodwin, S.B.

Analysis of an EST database reveals a probable CF2 resistance gene

homolog in wheat

Unpublished (2000)

Contact: Anderson, J.M.

Crop Production & Pest Control Research Unit

USDA-ARS

1150 Lilly Hall, West Lafayette, IN 47907, USA

Tel: 765-494-5565
 Fax: 765-496-2926
 Email: janderson@purdue.edu
 Seq primer: T3
 High quality sequence stop: 848.

```

FEATURES
  source
    Location/Qualifiers
      1..848
        /organism="Triticum aestivum"
        /strain="P29"
        /db_xref="taxon:4565"
        ORIGIN
          Query Match      1.3%;      Score 46.2;      DB 12;      Length 475;
          Best Local Similarity 45.8%;      Pred. No. 0.3;
          Matches 159;      Conservative 0;      Mismatches 188;      Indels 0;      Gaps 0;

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QY	2767	GCAGGGTGAGACCCCTGACCATCAGAGCCCATACACCTGACCTTACATCT	2826
QY	2767	GCAGGGTGAGACCCCTGACCATCAGAGCCCATACACCTGACCTTACATCT	2826
Db	93	GCAGCAGTGACGTGACGTGAGGAGGCTTTCATCAGCTGCCTCGCGAAGAGGACTGC	152
QY	2827	GGCACTGTCAACCTCATTACGAGGATTAACGACATGATGGCTGTATTCAACGTCACCG	2886

[illegible]

Accession	Sequence	Position
Ddb	290 GCGCGGTGCTGCTGCCAACGACGAAGGCTTGCCCTTCTCGCGGTGGGGCGCGGGG	349
Qy	2076 TACCGTTTCGGATTCTCAACGGTCGCGGTGCTGTGCTGTGCTCTCTACCTCTCGAC	2134
Db	350 TACCGTTTCGGATCTCAACGCTACGACGCGCGCTTCTCGCTCTCGCTCTCCG	408
Qy	2947 GCGCGTTCCTTACACCGCAACGACTTCGCTCGCTGGAATTCCTCGCGCGAT	3006
Db	273 ACGCAGACAGCTTCAACCTGGAGGGTCCCTGATCATGAAGACTCCATCGTCTTGAT	332
Qy	3007 CCATCCTGCCCTCAGATCAGGAGCTGCGCAGCAGGACGCTACACCGCTCTGATGACA	3066

[illegible]

Accession	BF115462	Result 11
Version	BF115462.1	BF059036
Keywords	EST.	Locus
Source	human	BF059036
		463 bp
		mRNA
		linear
		EST 16-OCT-2000
		close
		WAGE:3476421
		3'
		NCI CCAB C19
		W0005405
		CCNA
		DEUTERON
		7426411
		5'

ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1. (bases 1 to 475)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute Cancer Data Element Project (NCAD)
ACCESSION	BF059036
VERSION	BF059036.1
KEYWORDS	EST. human.
SOURCE	human.
Similar to	TR:063928 Q63928 BRAHMA RELATED PROTEIN 1 ;, MKNA sequence.

JOURNAL COMMENT		Homo sapiens ORGANISM
Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	REFERENCE	1 (bases 1 to 463)
	AUTHORS	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ccgap/ NATIONAL CANCER INSTITUTE, NATIONAL CENTER FOR CHROMOSOME RESEARCH

Soares, Ph.D. CDNA Library Arrayed by: Christina Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: soares@jpllll.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael D. Brennan, Ph.D.
Email: cgabs-r@mail.nih.gov
Contact: Robert Strausberg, Ph.D.
Unpublished (1997)
Tumor Gene Index
JOURNAL COMMENT

Seq primer: -400P from Gibco	
High quality sequence stop: 334.	
Location/Qualifiers	
1. 475	
source	/organism="Homo sapiens"
FEATURES	
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The	
I.M.A.G.E. Consortium DNA Sequencing by: Washington University	
Genome Sequencing Center	
Clone distribution: NCI-CGAP clone distribution information can	
be found through the I.M.A.G.E. Consortium/LLNL, send email to:	

/clone="IMAGE:3571229"	Seq primer: -40UP from Gibco
/clone_lib="NCI_CGAP_Ov18"	High quality sequence stop: 341.
/tissue_type="fibrotheoma"	
/lab_host="PH10B (phage-resistant)"	FEATURES
/note="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a	Location/Qualifiers
	source
	1..463
	/organism="Homo sapiens"

```

strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCGAAGTCGAGCGCGCGACATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors

/clone="IMAGE:3476421"
/clone_lib="NCI_CGAP-Ov18"
/tissue_type="fibrotheoma"

```

```

Seq primer: -40UP from Gibco
High quality sequence stop: 452.
Location/Qualifiers
1. .481
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2105267"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTCAAGTCGGCGCGGCATATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
138 a 128 c 141 g 74 t
BASE COUNT

```

strand cDNA was primed with a NOC I⁻ oligo(dAT) primer [5'-TGTACCACTGTAAGTCGGCGGCATATCTTTTTTTTTTTTTTTTTT-3'] double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 138 a 128 c 141 g 74 t
ORIGIN

		Query Match	1.2%;	Score 44.8;	DB 9;	Length 481;
		Best Local Similarity	45.8%;	Pred. No.	0.73;	
		Matches 154;	Conservative	0;	Mismatches 182;	Indels 0; Gaps 0;

```
QY   2765  GGGCAGGGGTGAGACCCTGACCATCGAGGCCACTACCAACCCCTGGACTGGAGCTTACAT 2824
      ||| ||| |
Db    70   GGACAGCAGTGGAAGTCTCAGCTCAGCAGAGGTCTTCATCCAGCTGCCCTCGGAAAGGAGCT 129
      ||| ||| |

QY   2825  GTGGCTGTGCACAACCTCATTCACGAGGATACGACATGATGCCTGATTCAACGCTCAC 2884
      ||| ||| |
Db    130  GCCGGATCTACGAGCTCATCCGCAAGCCCCTGGAGCTTCAAGAAGATAAAGGAGCCGAT 189
      ||| ||| |

QY   2885  CGCCATGGAGGAGAAGGGATATCTTCAGGAGGACTTCGAGGACCCCCATGAACCCCAAAGTG 2944
      ||| ||| |
Db    190  TCGCAACCAAGATTCCGCGAGCCTCAACGACCTATAGAAGGACGCTCATGCTCTGTGCCA 249
      ||| ||| |

QY   2945  GCgggcggttccittacaacgccgaacgacttcctatgctcgcgctgggaacctctcggccgca 3004
      ||| ||| |
Db    250  GAAGCGCACAGACCTTCAACCTGGAGGGCTCCCTGATCTATGAAGACTCCATCGCTCTTGGCA 309
      ||| ||| |

QY   3005  TTCATCACTGCCCGAGTCAGGAGCTGGCGGACGAGGCGGTACAAACCCCTCGATGA 3064
      ||| ||| |
Db    310  GTCGGTCTTACCACGCTGGCGCAAAAATCGAGAAGGAGATGACAGTGAAGCCGAGGA 369
      ||| ||| |

QY   3065  GATCTGGAGGATCTTTGGAAATCGAGGAGTAAACCCC 3100
      ||| ||| |
Db    370  GAGTGAGGAGGAGGAAGCGCGAGGGCGAGGAGGAGGCTC 405
      ||| ||| |
```

[illegible]


```

Db      333  CGGTCCTCACCCAGCGTGCNCCACAGAAATCGAGAGAAGGAGAGATGACAGTGAAGCGGAGGAGA 392
Qy      3067  TCCTGGAGGATCTTGGAAATCGAGGAGGATAAACCCC 3100
Db      393  GTGAGGAGGAGGAAGAGAGCGCGAGGAGGAAGGGCTC 426

Search completed: February 13, 2003, 03:10:22
Job time : 4977.71 secs

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Search completed: February 13, 2003, 03:10:22
Job time : 4977.71 secs

QY 3067 TCCTGGAGGATCTTGGAAATCGAGGAGTAACCCC 31000

Db 393 GTGAGGAGGAGGAAGAGGGCGGAGGAGGAGGCTC 426

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